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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract:

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## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such  
5 polynucleotides, along with uses for these polynucleotides and proteins, for example in  
therapeutic, diagnostic and research methods.

### 2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as  
10 lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past  
decade. The now routine hybridization cloning and expression cloning techniques clone novel  
polynucleotides "directly" in the sense that they rely on information directly related to the  
discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of  
hybridization cloning; activity of the protein in the case of expression cloning). More recent  
15 "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences  
based on the presence of a now well-recognized secretory leader sequence motif, as well as  
various PCR-based or low stringency hybridization-based cloning techniques, have advanced the  
state of the art by making available large numbers of DNA/amino acid sequences for proteins  
that are known to have biological activity, for example, by virtue of their secreted nature in the  
20 case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based  
techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for  
example, diagnostics, forensics, gene mapping; identification of mutations responsible for  
genetic disorders or other traits, to assess biodiversity, and to produce many other types of data  
25 and products dependent on DNA and amino acid sequences.

### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel  
isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules,  
30 cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic  
variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more  
epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression  
vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such  
35 polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, 5 diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-236 and 473-708. The polypeptides sequences are designated SEQ ID NO: 237-472 and 709-944. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in 10 the Sequence Listing, \* corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-236 and 473-708 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a 15 specific domain or truncation of the peptides encoded by SEQ ID NO: 1-236 and 473-708. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-236 and 473-708 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information 20 from the nucleic acid sequences of SEQ ID NO: 1-236 and 473-708. The sequence information can be a segment of any one of SEQ ID NO: 1-236 and 473-708 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-236 and 473-708.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on 25 a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid 30 sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-236 and 473-708 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-236 and 473-708 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-236 and 473-708; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-236 and 473-708; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-236 and 473-708. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-236 and 473-708; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in SEQ ID NO:237 – 472 or 709-944; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-236 and 473-708; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and “substantial equivalents” thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.



The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

5 The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the  
10 protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA  
15 or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as  
20 expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide  
25 of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition  
30 which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein  
35 expression or biological activity.

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The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides  
5 a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the  
10 invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal  
15 antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate  
20 (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a  
25 compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a  
30 polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that  
35 modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

## 4. DETAILED DESCRIPTION OF THE INVENTION

### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms “a”, “an” and “the” include plural references unless the context clearly dictates otherwise.

The term “active” refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms “biologically active” or “biological activity” refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule.

Likewise “immunologically active” or “immunological activity” refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term “activated cells” as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms “complementary” or “complementarity” refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be “partial” such that only some of the nucleic acids bind or it may be “complete” such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term “embryonic stem cells (ES)” refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term “germ line stem cells (GSCs)” refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-236 and 473-708. The sequence information can be a segment of any one of SEQ ID NO:1-236 and 473-708 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-236 and 473-708. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because  $4^{20}$  possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ( $1/4^{25}$ ) times the increased probability for mismatch at each nucleotide position ( $3 \times 25$ ). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

5 The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

10 The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 500 amino acids, more preferably less than 200 amino acids more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

20 The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

25 The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations



can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about  
10 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a  
15 listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*,  
20 mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about  
25 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using  
30 the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

## 4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-236 and 473-708 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:237-472 and 709-944; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:237-472 and 709-944. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-236 and 473-708 ; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing as SEQ ID NO:237-472 and 709-944; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:237-472 and 709-944. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and

substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides  
5 may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers  
10 from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-236 and 473-708 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions  
15 using any of the polynucleotides of SEQ ID NO:1-236 and 473-708 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-236 and 473-708 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences  
20 (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide  
25 sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid  
30 sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-236 and 473-708, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the  
35 invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can

differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-236 and 473-708, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-236 and 473-708 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-236 and 473-708, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations

will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 5 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal 10 sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent 15 nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 20 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the 25 primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current* 30 *Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

5 The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

10 In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-236 and 473-708, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

15 A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the  
20 invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular  
25 organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-236 and 473-708 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic  
30 acid having any of the nucleotide sequences of SEQ ID NO:1-236 and 473-708 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for  
35 generating the recombinant constructs of the present invention. The following vectors are



provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

5       The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in*  
10 *Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol  
15 transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.  
20 Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid  
25 phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired  
30 characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the  
35 vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-236 and 473-708, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:237-472 and 709-944 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-236 and 473-708 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a

5 "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO:1-236 and 473-708), antisense nucleic acids of the invention can be designed according

10 to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10,

15 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the

20 physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-

25 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil,

30 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a

35 nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the

inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-236 and 473-708). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in

which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*,

5 Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and

10 Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med*

15 *Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using

20 standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication.

25 PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

30 In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition

35 enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

10 The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the



protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:237-472 and 709-944 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-236 and 473-708 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-236 and 473-708 or (b) polynucleotides encoding any one of the amino acid sequences set forth

as SEQ ID NO:237-472 and 709-944 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:237-472 and 709-944 or the corresponding full length or  
5 mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ  
10 ID NO:237-472 and 709-944.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer.*  
15 *Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding  
20 sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also  
25 provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid  
30 fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:237-472 and 709-944.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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#### **4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY**

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

#### **4.7 CHIMERIC AND FUSION PROTEINS**

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

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another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked  
5 in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal  
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,  
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or  
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease  
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be  
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in



the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

#### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10 indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15 or in one of the other physiological pathways described herein.

#### **4.10.1 RESEARCH USES AND UTILITIES**

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

- 5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in  
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,  
15 Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- $\gamma$ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse  
25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin  
30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in  
35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immunol. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

*In vitro* cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell



sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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#### 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

20

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

25

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

30

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the  
10 growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in:  
International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent  
Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.  
15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter,  
Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book  
Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol  
71:382-84 (1978).

#### 20 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A  
25 protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More  
30 specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastbom et al., *Toxicology* 125: 59-66, 1998), skin prick test (Hoffmann et al., *Allergy* 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., *Arch. Toxicol.* 73: 501-9), and murine local lymph node assay (Kimber et al., *J. Toxicol. Environ. Health* 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and  $\beta_2$  microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.



#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily  
5 determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell  
10 population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146,  
15 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

#### **4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY**

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or  
20 thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for  
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res.  
30 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### **4.10.11 CANCER DIAGNOSIS AND THERAPY**

Polypeptides of the invention may be involved in cancer cell generation, proliferation or  
35 metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, 5 Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, 10 Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. 15 exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

*In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of 20 cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction 25 of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### 30 4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and 35 their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant  
5 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

10 Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988;  
15 Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel  
20 overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein  
25 Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

30

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a  
35 solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of  
5 complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and  
10 organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

15 The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a  
20 review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein,  
25 peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

30 Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested  
35 for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be  
5 complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying  
10 previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number  
15 of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the  
20 invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and  
25 inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a  
30 protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

#### **4.10.15 ANTI-INFLAMMATORY ACTIVITY**

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### **4.10.16 LEUKEMIAS**

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

#### **4.10.17 NERVOUS SYSTEM DISORDERS**

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of



therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- 10 (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human  
15 immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral  
20 sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus  
25 callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular  
30 neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- 5 (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

10 Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may  
15 be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the  
20 invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile  
25 muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

30 A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape  
35 (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without  
5 limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of  
10 hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 15           **4.10.19            IDENTIFICATION OF POLYMORPHISMS**

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune  
20 response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

25            Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to  
30 allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction  
35 enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

#### 10           4.10.20       ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129.

15 Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

20 The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound  
25 would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or  
30 other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

##### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

#### 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

#### 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.



For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity.

5 Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the  
10 biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and  
15 polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine,  
20 monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T  
25 lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified  
30 MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in  
35 which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1  $\mu$ g to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

#### 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the  $IC_{50}$  as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

#### 4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

#### 4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}'$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG<sub>1</sub>, IgG<sub>2</sub>, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 237, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will



indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

5 Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

10 A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives,  
15 fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

#### 5.13.1 Polyclonal Antibodies

20 For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a  
25 recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not  
30 limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A,  
35 synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

### 5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin.

Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,  
5 California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

10 The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the  
15 art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting  
20 dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for  
25 example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using  
30 oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of  
35 monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

### 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

### 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

#### 5.13.4 F<sub>ab</sub> Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F<sub>ab</sub> fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F<sub>(ab)<sup>2</sup></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated by reducing the disulfide bridges of an F<sub>(ab)<sup>2</sup></sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

#### 5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

5 Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a  
10 potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen  
15 combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin  
20 light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are  
25 recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino  
30 acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be  
35 prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The  $Fab'$  fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the  $Fab'$ -TNB derivatives is then reconverted to the  $Fab'$ -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other  $Fab'$ -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally,  $Fab'$  fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each  $Fab'$  fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the  $Fab'$  portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the  $V_H$  and  $V_L$  domains of one fragment are forced to pair with the complementary  $V_L$  and  $V_H$  domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on



a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

#### 5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

#### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include

5 diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of

10 radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL),

15 active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987).

20 Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is

25 administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

#### 4.14 COMPUTER READABLE SEQUENCES

30 In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM

35 and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the  
5 presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen  
10 to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase,  
15 Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-236 and 473-708 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the  
20 nucleotide sequences of SEQ ID NO:1-236 and 473-708 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and  
25 BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

30 As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available  
35 computer-based systems are suitable for use in the present invention. As stated above, the

computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

#### 4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which

methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

#### 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One

skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection).

- 5 See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

#### 10 4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-236 and 473-708, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In  
15 detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a  
20 polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a  
25 polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also  
30 comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspaczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560



(1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems.

- 5 Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical  
10 composition.

#### 4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The  
15 hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-236 and 473-708. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO:1-236 and 473-708 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

20 Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a  
25 degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA  
30 polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers,  
35 hybridization screening with libraries or flow-sorted chromosomal preparations specific to

known chromosomes, and the like. The technique of fluorescent *in situ* hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

#### 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the

5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the  
5 light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile  
10 combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

#### 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA,  
15 including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples  
20 may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

25 Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA  
30 fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI\*\*), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

#### 4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm<sup>2</sup>, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid  
5 being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations  
10 may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and  
15 variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

## 20       **5.0    EXAMPLES**

### **5.1.1   EXAMPLE 1**

#### **Novel Nucleic Acid Sequences Obtained From Various Libraries**

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome  
25 using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for  
30 sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

### 5.1.2 EXAMPLE 2

#### Assemblage of Novel Nucleic Acids

5 The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 473-708 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no  
10 additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:473-708 as set forth below. The polypeptides was predicted using a software program called FASTY (available from  
15 <http://fasta.bioch.virginia.edu>) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

### 5.2.2 EXAMPLE 3

#### Novel Nucleic Acids

20 Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e. dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used  
25 in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 217.

Table 1 shows the various tissue sources of SEQ ID NO: 1-217.

The nearest neighbor results for SEQ ID NO: 1-217 were obtained by a BLASTP version  
30 2.0a1 19MP-WashU search against Genpept release 120 and Geneseq October 12, 2000 release 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-217 from Genpept . The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologs with identifiable functions for SEQ ID NO: 1-217 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

#### 5.3.2 EXAMPLE 4

##### Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118, UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 218-236.

Table 1 shows the various tissue sources of SEQ ID NO: 218-236.

The homology results for SEQ ID NO: 218-236 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and Geneseq October 12, 2000 release



21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the homologs for SEQ ID NO: 218-236 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 218-236 are shown in Table 2 below.

5           Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

10           Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

15           The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the  
20           publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal  
25           peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

TABLE 1

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	3 15 19 74 88 174 212-213 229
adult brain	GIBCO	ABD003	1-4 14 33 44 57 73-74 78 88 108 145 148 174 196 209-213 215 218 235
adult brain	Clontech	ABR001	8 118 145 155 174 192 208
adult brain	Clontech	ABR006	2 25 35-36 214 220
adult brain	Clontech	ABR008	1 4 13-14 16 25 33 35-36 41-43 45 50 56 65 80 86 88 95 108 110-112 118 129 141 145 158-159 162 164 169-171 173-174 189 196 208-211 215 218- 220 222-223 228
adult brain	Clontech	ABR011	211
adult brain	Invitrogen	ABR013	48 109 121 158-159 199
adult brain	Invitrogen	ABT004	3-4 14 35-36 88 145 174 196 210-211 222 224 228
cultured preadipocytes	Stratagene	ADP001	2 6-8 13 69 73 193 210 212-213 225 229
adrenal gland	Clontech	ADR002	3-4 7-8 12-14 21 33 38 48 54 74 81 86-87 145 158-159 163 208 211-213 221 229 235
adult heart	GIBCO	AHR001	1-2 9 11 14-15 33 37 39-41 61-62 73-75 102 145-146 148 187 196 210-213 218 222 224-225 235
adult kidney	GIBCO	AKD001	1-4 8 10 12 14-15 33- 34 37 39-40 43-48 54 59 73-74 79-80 88 107-108 118 121 138 145 159 163 169-171 173-174 186 196 209- 215 224 229 235
adult kidney	Invitrogen	AKT002	1 8 12 14 35-36 47-48 86 118 130 148 158- 159 196 210 222-223 225 235
adult lung	GIBCO	ALG001	12 16 37 56 73 88 96- 99 106 114 145 148 155 164 216-217 228- 229

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
lymph node	Clontech	ALN001	12 41 47-48 94 96-99 107-109 121 145 158- 159 172 191
young liver	GIBCO	ALV001	3 8 14 39-40 48 58 64 66 86 104 108 140 145 158-160 169-171 174 189 211-214 216- 217 229 235
adult liver	Invitrogen	ALV002	4 16 37 39-40 66 73 86 105 145 169-171 173 189 192 194-196 209 211 214 222 224 228
adult liver	Clontech	ALV003	214
adult ovary	Invitrogen	AOV001	1 3-4 7 11-16 18 20 34-37 39-40 42-45 48 57-59 70-74 76 78 80 88 96-99 102 108 118 140-141 145-148 155 157-160 162-164 172-175 182 187 196 209-213 220-222 225 228-229 235
adult placenta	Invitrogen	APL001	14 45 222
placenta	Invitrogen	APL002	55 138
adult spleen	GIBCO	ASP001	2-4 8 11-12 33 39-40 44 47-48 74 80 96-99 107-110 121 145 155 158-159 164 172 174 191 211-213 216-217 222 229 235
testis	GIBCO	ATS001	2 35-37 39-40 175 196 212-213 235
adult bladder	Invitrogen	BLD001	5 7-8 14 73 138 141 159 196 235
bone marrow	Clontech	BMD001	2 4 7 12 19 39-40 47- 48 57 63 74 80 94 96- 99 103 107-108 118 121 140 145 149 156 158-160 169-172 186 191 210 212-213 215 229
bone marrow	Clontech	BMD002	1 4 12 14 33 35-36 41 44-45 47-48 74 88 96-99 107-108 110 118 158-160 173 190- 191 209 212-213 223
bone marrow	Clontech	BMD004	7 48 96-99 158-159 212-213
adult colon	Invitrogen	CLN001	2 11-12 80 96-99 140 191

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
adult cervix	BioChain	CVX001	1-2 12 14-15 26 33 35-36 39 42-43 47 54 73 80 88 95 107 129- 137 150 196 212-213 220-221 224 227-229 235
endothelial cells	Stratogene	EDT001	2 4 8 14 33-36 39-40 42-43 56 67-69 73-74 80 88 95 108-109 116 121 132 140 145 163 173 209 211-213 223 225 228-229
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	206-207
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	207
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	207
fetal brain	Clontech	FBR006	2 4 8 25 41 74 111- 112 141 143 162 187 196 210-213 215-217 219-220 222-223 228
fetal brain	Invitrogen	FBT002	4 14 16 18 35-36 65 74 78 80 111-112 139 157 173-174 196 209- 211 220-221
fetal kidney	Clontech	FKD001	7 33 46 65 108 211- 213
fetal kidney	Clontech	FKD002	80 212-213
fetal lung	Clontech	FLG001	108 118 155
fetal lung	Invitrogen	FLG003	3 39-40 145 211 222
fetal liver-spleen	Columbia University	FLS001	1-4 7-8 10 14-17 22 28 33-40 42-44 48 52-53 60 66 68 74 88 96-99 102 108 110- 112 117 136 138 140 143 145 148 154 158- 159 163 169-172 174 181 191 196 201 209- 217 220 222-224 228- 229 231 235
fetal liver-spleen	Columbia University	FLS002	1-2 7-8 11 14-15 27- 28 33-37 39-40 44 53 60 68 73-75 80 86 91 95 108 110 115 122- 128 138 140 143 145 154-155 164 169-172 175 182-186 190 196

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			200-205 209 212-214 216-217 220 222-225 230-231 235
fetal liver-spleen	Columbia University	FLS003	214 223-224
fetal liver	Invitrogen	FLV001	3 8 41 66 73-74 80 88 95 108 110 145 148 154 169-171 173 196 211 214
fetal liver	Clontech	FLV004	7
fetal muscle	Invitrogen	FMS001	7 11 14 37 43 79 139 196 211 224-225 228
fetal muscle	Invitrogen	FMS002	7
fetal skin	Invitrogen	FSK001	7-8 14 33 35-37 39 74 88 108 142 162 172- 175 196 210-213 215 220 222
fetal skin	Invitrogen	FSK002	7 196 235
fetal spleen	BioChain	FSP001	8 96-99
umbilical cord	BioChain	FUC001	7 13-14 20 37 56 102 108 113 145 148 160 176-180 199 209 212- 213 222
fetal brain	GIBCO	HFB001	2 13-15 37 42-43 57 73 88 108 111-112 118 129 163 174 192 196 199 208-213 215 224-225 229 235
macrophage	Invitrogen	HMP001	44
infant brain	Columbia University	IB2002	1 8 14 16 31 37 57 64 77 80 88 108 111-112 151 162 174 192 196 210-213 215 223 225 229
infant brain	Columbia University	IB2003	7 31 57 88 94 148 162 174 196-198 210- 213 215 224-225
infant brain	Columbia University	IBM002	8
infant brain	Columbia University	IBS001	31 42-43 111-112 196 211
Lung, fibroblast	Stratagene	LFB001	4 73 174 196 199 222
lung tumor	Invitrogen	LGT002	2-3 5 7-9 11-12 14 22 24 37 39-40 42-44 47-48 57 73 86 102 106 109-110 121 140 145 148 155 158-160 162 164-166 169-171 186 196 209-213 216- 218 220 222-223 228
lymphocytes	ATCC	LPC001	13 30 39-40 42-44 119 153 158-159 186- 188 209 211 222 226

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			232-234 236
leukocyte	GIBCO	LUC001	4-5 11 13 16 29-30 32 34 39-41 44 47-51 57 74 80 88 96-99 107- 110 116 121 129 145 148 152-155 158-160 163-164 172 186 190- 191 196 210-213 216- 217 219 229 235
leukocyte	Clontech	LUC003	109 121 145 155 160 212-213 235
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	2 4 22 33 140 192 199 211-213 222 228
mammary gland	Invitrogen	MMG001	1-2 4 7-8 12 14 22 35-37 39-40 42-44 47-48 51 59 73-74 80 88 96-99 107 109 116 121 138 145 148 162 167-174 191-192 196 209-213 215 218 221- 222 224-225 228
induced neuron cells	Stratagene	NTD001	163 192 209 224
retinoid acid induced neuronal cells	Stratagene	NTR001	211-213 223
neuronal cells	Stratagene	NTU001	2 8 14 39-40 209 211 215 224
placenta	Clontech	PLA003	145
prostate	Clontech	PRT001	4 8 14 211 218 229 235
rectum	Invitrogen	REC001	12 14 48 73 96-99 143 158-159 169-171 174 196 211 224-225
salivary gland	Clontech	SAL001	4 12 37 47-48 70 74 107 109 114 121 144 158-159 174 196 212- 213 220
small intestine	Clontech	SIN001	12 39-40 47 74 82-83 89-90 96-99 107 117- 118 173 191 222 224 229 235
skeletal muscle	Clontech	SKMs04	88
spinal cord	Clontech	SPC001	1 4 14 27 88 91-92 108 119-120 145 174 212-213 220 235
adult spleen	Clontech	SPLc01	158-159 219 229 235
stomach	Clontech	STO001	4 37 48 93-95 115 138 159 216-217
thalamus	Clontech	THA002	37 94 125 139 174
thymus	Clontech	THM001	8 12 22 25 39-40 84 118 149 160 172 174

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			191 212-213 222
thymus	Clontech	THMc02	4-5 14 33 42-44 48 50 57 59 73-74 78 96-99 109 121 141 145 148 155-162 172 187 191 210 212-213 219 223 228
thyroid gland	Clontech	THR001	4 8-9 14 23 37 39-40 48 54 57 74 86 100- 101 107 118 140 159 169-171 196 209-211 225 229 235
trachea	Clontech	TRC001	11 37 48 85 95-99 114 118 159 172 191 212-213
uterus	Clontech	UTR001	8 102-103 227 235

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
2	Y57899	Homo sapiens	Human transmembrane protein HTMPN-23.	2044	99
3	Y20291	Homo sapiens	Human apolipoprotein E wild type protein fragment 1.	1080	91
4	D42138	Homo sapiens	PIG-B	3001	100
5	AF148145	Mus musculus	putative thymic stromal co-transporter TSCOT	1459	78
6	X68657	Rattus norvegicus	granzyme-like protein II	1138	89
7	Z74615	Homo sapiens	prepro-alpha1(I) collagen	8216	99
8	D13623	Rattus sp.	p34 protein	1482	94
9	Y94263	Homo sapiens	Human phospholipid binding protein 2, PLBP2.	1185	99
11	Y29939	Homo sapiens	Human retinol dehydrogenase type II homologue.	1663	100
12	Y14738	Homo sapiens	immunoglobulin lambda light chain	1144	91
13	AF156549	Mus musculus	putative E1-E2 ATPase	4825	79
14	Y00815	Homo sapiens	put. LAR preprotein (AA -16 to 1881)	9947	99
19	Y11584	Homo sapiens	Human 5' EST secreted protein SEQ ID NO:236.	192	100
25	Y70210	Homo sapiens	Human TANGO 130 protein.	991	95
31	D26093	Gallus gallus	VMO-I	463	52
32	AE000658	Homo sapiens	TCRAV4S1	558	100
33	W64542	Homo sapiens	Human stomach cancer cell clone HP10071 protein.	483	100
34	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	690	100
35	AL049795	Homo sapiens	dJ622L5.8.1 (novel protein (isoform 1))	399	96
36	AL049795	Homo sapiens	dJ622L5.8.1 (novel protein (isoform 1))	458	100



SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
37	Y44273	Homo sapiens	Human Metabotropic Glutamate Receptor-like protein, MGRcm.	2458	99
39	AF111713	Homo sapiens	junctional adhesion molecule	1544	100
40	AF154005	Homo sapiens	junction adhesion molecule	1333	100
41	Y35960	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 209.	500	98
42	AF247174	synthetic construct	RP6-alkaline phosphatase hybrid protein	140	36
43	AF179415	Dendroides canadensis	antifreeze protein 11	132	30
44	W01049	Homo sapiens	Product of 200 gene differentially expressed in T helper cells.	1580	99
45	AL121929	Homo sapiens	bA416N2.2 (similar to murine FISH (an SH3 and PX domain-containing protein, and Src substrate))	5039	100
47	X57816	Homo sapiens	immunoglobulin lambda light chain	1212	100
48	W88464	Homo sapiens	Monoclonal antibody 4B5 heavy chain variable region.	2162	86
50	AE003523	Drosophila melanogaster	CG7510 gene product	280	54
54	AF231128	Danio rerio	Dap1b	165	42
55	AB047612	Macaca fascicularis	hypothetical protein	330	98
56	Y41701	Homo sapiens	Human PRO708 protein sequence.	1070	99
65	Y73351	Homo sapiens	HTRM clone 1484257 protein sequence.	104	39
66	AF188285	Homo sapiens	bone morphogenetic protein 9	2266	100
73	AE002038	Deinococcus radiodurans	ribosomal protein L20	202	41
74	AF157321	Homo sapiens	30 kDa protein	1252	99
79	AC004522	Homo sapiens	gap junction protein; similar to P36383 (PID:g544117)	482	93

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
80	AL355715	Homo sapiens	PCD9	2075	100
86	Y76140	Homo sapiens	Human secreted protein encoded by gene 17.	692	97
88	AL020993	Homo sapiens	dJ5O6.2 (novel protein similar to C. elegans F40E10.6 (isoform 1))	1545	100
91	AC004896	Homo sapiens	similar to contactin associated protein; similar to U87223 (PID:g1857708)	157	58
92	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	124	54
94	Y27593	Homo sapiens	Human secreted protein encoded by gene No. 27.	248	58
95	Y92507	Homo sapiens	Human OXRE-4 with identity to 3-oxo-5-alpha-steroid dehydrogenase.	1715	100
96	AJ006112	Homo sapiens	anti-(ED-B) scFV	1238	100
97	AF174012	Homo sapiens	immunoglobulin heavy chain variable region precursor	692	91
98	AJ006111	Homo sapiens	anti-(ED-B) scFV	1166	93
99	AJ006112	Homo sapiens	anti-(ED-B) scFV	1046	84
102	AF137378	Homo sapiens	integrin alpha 11 subunit precursor	6224	99
106	W62068	Homo sapiens	Human lung tissue gene LU103 protein.	333	97
107	X57802	Homo sapiens	immunoglobulin lambda light chain	1160	95
108	Y41697	Homo sapiens	Human PRO700 protein sequence.	1441	100
109	M12886	Homo sapiens	T-cell receptor beta chain	1590	98
110	U71383	Homo sapiens	OB binding protein-2	2913	99
111	AB035356	Homo sapiens	neurexin I-alpha protein	4390	76
112	L14851	Rattus norvegicus	neurexin III-alpha	5614	97
114	X60660	Rattus rattus	potential ligand-binding protein	382	27
116	L03785	Homo sapiens	myosin regulatory light chain	873	100
118	Y58637	Homo	Protein regulating gene	246	30

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		sapiens	expression PRGE-30.		
121	M12886	Homo sapiens	T-cell receptor beta chain	1536	96
129	AL031985	Homo sapiens	dJ228H13.3 (zinc finger protein)	2364	100
138	Y59664	Homo sapiens	Secreted protein 108-004-5-0-E8-FL.	973	98
139	AF139980	Homo sapiens	LW-1	2275	100
140	Y28279	Homo sapiens	Human G-protein coupled receptor GRIR-1.	742	100
141	AF287892	Homo sapiens	sialic acid binding immunoglobulin-like lectin 8 long splice variant	1320	96
145	X00699	Homo sapiens	precursor	1400	98
146	AB036849	Ciona intestinalis	fibrinogen-like protein	184	40
148	W78169	Homo sapiens	Human secreted protein encoded by gene 44 clone HETFJ05.	2114	98
154	AF109683	Homo sapiens	leukocyte-associated Ig-like receptor 1b	174	25
155	W99070	Homo sapiens	Human PIGR-1.	434	53
158	AF184764	Homo sapiens	IgG1 heavy chain	939	79
159	Y14737	Homo sapiens	immunoglobulin lambda heavy chain	2559	100
160	AF043171	Homo sapiens	T cell receptor alpha chain	1479	100
162	AB000199	Rattus norvegicus	CCA2 protein	822	87
163	AF186273	Homo sapiens	leucine-rich repeats containing F-box protein FBL3	251	32
164	AF227924	Homo sapiens	sialic acid-binding lectin Siglec-9	2459	99
167	AF098807	Homo sapiens	lipoma HMGIC fusion partner	713	63
168	AF098807	Homo sapiens	lipoma HMGIC fusion partner	443	57
169	Y66706	Homo sapiens	Membrane-bound protein PRO1129.	2786	99
170	Y66706	Homo sapiens	Membrane-bound protein PRO1129.	1733	98

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
171	Y66706	Homo sapiens	Membrane-bound protein PRO1129.	1058	93
173	W67898	Homo sapiens	Human secreted protein encoded by gene 16 clone HE9DG49.	838	95
174	Y06115	Homo sapiens	Human organic cation transporter OCT-3.	1876	100
182	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	262	59
186	AE003652	Drosophila melanogaster	CG17996 gene product	115	66
187	AF166350	Homo sapiens	ST7 protein	4716	100
189	AF202889	Homo sapiens	regeneration associated protein 3	1864	100
191	AF090418	Homo sapiens	scFV antibody V-region	1010	85
192	AJ010231	Homo sapiens	RET finger protein-like 2	1522	100
193	U65579	Homo sapiens	mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor	981	89
196	AF161444	Homo sapiens	HSPC326	1467	96
199	D26179	Rattus norvegicus	V-1 protein	479	100
208	L22031	Glycine max	hydroxyproline-rich glycoprotein	99	34
209	AF201931	Homo sapiens	DC1	1662	99
210	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL83.	480	100
211	U53925	Mus musculus	transcription factor C1 (HCF)	297	31
212	AJ251914	Sus scrofa	putative RNA helicase	2199	100
213	AJ251914	Sus scrofa	putative RNA helicase	1571	100
214	X04494	Homo sapiens	precursor polypeptide	1903	100
215	Y66699	Homo sapiens	Membrane-bound protein PRO1108.	2374	100
216	AJ130710	Homo sapiens	QA79 membrane protein, allelic variant airm-1b	2473	100
217	AJ130711	Homo sapiens	QA79 membrane protein, splice product airm-2	1969	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
218	AF233523	Homo sapiens	beta V spectrin	18612	99
219	AF127481	Homo sapiens	non-ocogenic Rho GTPase-specific GTP exchange factor	743	36
220	Y71066	Homo sapiens	Human membrane transport protein, MTRP-11.	2378	99
221	AF132730	Homo sapiens	unknown	1899	100
223	W54097	Homo sapiens	Homo sapiens B223 sequence.	1834	99
224	Y99449	Homo sapiens	Human PRO1760 (UNQ833) amino acid sequence SEQ ID NO:376.	1017	100
225	Y92368	Homo sapiens	G protein-coupled receptor protein 8.	2293	100
227	Y99436	Homo sapiens	Human PRO1474 (UNQ745) amino acid sequence SEQ ID NO:334.	464	100
228	AK024825	Homo sapiens	unnamed protein product	1375	99
229	G03186	Homo sapiens	Human secreted protein, SEQ ID NO: 7267.	307	96
235	AB025606	Arabidopsis thaliana	contains similarity to GTPase activating protein~gene_id:F6N7.7	753	46

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1	PF00152	tRNA synthetases class II.	PF00152D 21.30 8.364e-28 422-461 PF00152C 28.03 9.250e-21 220-257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-11 44-67
2	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 5.263e-09 158-183
3	PD02807	APOLIPOPROTEIN E PRECURSOR APO-E GLYCOPROTEIN PLAS.	PD02807B 8.27 1.000e-40 64-103 PD02807C 8.91 1.000e-40 139-188 PD02807D 7.99 1.000e-40 188-238 PD02807A 12.43 6.143e-25 27-48 PD02807C 8.91 5.645e-09 95-144
5	PD01572	PHOTOSYSTEM II REACTION CENTRE T PROTEIN PHOTOS.	PD01572 8.77 6.917e-09 213-243
6	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 2.125e-15 50-67 BL00134B 15.99 7.618e-13 195-219
7	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL- TERMINAL.	DM01418A 20.83 1.000e-40 1252-1300 DM01418B 22.51 1.000e-40 1351-1393 DM01418C 20.48 5.500e-40 1422-1464
8	BL00224	Clathrin light chain proteins.	BL00224B 16.94 1.082e-09 166-219
9	BL01220	Phosphatidylethanolamine- binding protein family proteins.	BL01220B 16.65 6.774e-23 85-126 BL01220C 14.75 5.857e-17 130-158
11	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081C 15.13 5.846e-11 151-168
12	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 1.529e-14 159-182 BL00290B 13.17 9.000e-12 219-237
13	PR00121	SODIUM/POTASSIUM- TRANSPORTING ATPASE SIGNATURE	PR00121D 16.72 2.694e-12 113-135
14	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 1.500e-24 1420-1441 PR00700D 12.47 4.214e-22 1543-1562 PR00700B 16.80 4.240e-21 1709-1730 PR00700D 12.47 7.158e-20 1834-1853 PR00700C 13.17 5.800e-18 1504-1522 PR00700C 13.17 7.353e-17 1793-1811 PR00700E 17.57 4.000e-14 1865-1881 PR00700F 11.18 7.353e-13 1590-1601 PR00700F 11.18 1.429e-12 1881-1892 PR00700E 17.57 5.304e-12 1574-1590 PR00700A 6.96 8.714e-11 1404-1412
31	PD02382	RECEPTOR CHAIN PRECURSOR	PD02382B 4.60 7.000e-09 105-112

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		TRANSME.	
37	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e-09 150-191
39	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 1.000e-11 102-112
40	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 1.000e-11 62-72
45	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 3.000e-09 953-967
47	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 1.529e-14 150-173 BL00290B 13.17 9.000e-12 210-228
48	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 9.775e-36 20-68 DM00031B 15.41 7.600e-21 84-118 DM00031C 12.79 8.929e-10 131-142
56	BL00523	Sulfatases proteins.	BL00523C 12.64 4.000e-13 314-325 BL00523A 13.36 7.300e-13 222-239 BL00523B 8.64 6.114e-11 268-280
65	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.115e-11 204-221
66	BL00250	TGF-beta family proteins.	BL00250A 21.24 3.000e-24 327-363 BL00250B 27.37 1.000e-15 393-429
73	PR00062	RIBOSOMAL PROTEIN L20 SIGNATURE	PR00062C 16.68 7.245e-15 82-109 PR00062B 16.66 2.658e-11 49-79
79	BL00407	Connexins proteins.	BL00407E 22.17 8.820e-23 169-214 BL00407B 14.23 6.311e-20 39-70 BL00407C 14.61 1.164e-18 70-98 BL00407A 18.57 6.250e-13 2-39 BL00407D 17.61 5.790e-12 131-161
96	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 3.520e-10 281-304
97	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 20-68 DM00031B 15.41 1.000e-36 84-118 DM00031C 12.79 1.600e-15 127-138
98	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 3.520e-10 286-309
99	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 4.000e-12 341-359 BL00290A 20.89 3.520e-10 280-303
102	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 9.719e-13 163-181 PR00453B 14.65 1.818e-12 200-215 PR00453C 12.26 3.769e-10 265-274
107	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 1.563e-15 151-174 BL00290B 13.17 9.000e-12 211-229
108	BL00194	Thioredoxin family proteins.	BL00194 12.16 2.565e-13 46-59 BL00194 12.16 3.348e-13 179-192

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
109	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.200e-12 160-183
111	BL00964	Syndecans proteins.	BL00964B 12.05 2.604e-10 981-1024
112	BL00964	Syndecans proteins.	BL00964B 12.05 2.604e-10 1011-1054
114	BL00400	LBP / BPI / CETP family proteins.	BL00400D 23.26 7.222e-12 251-288
116	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 1.391e-09 43-56
121	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.200e-12 159-182
129	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.875e-15 347-364 BL00028 16.07 6.824e-14 207-224 BL00028 16.07 7.353e-14 403-420 BL00028 16.07 8.650e-13 235-252 BL00028 16.07 8.435e-12 319-336 BL00028 16.07 3.077e-11 291-308 BL00028 16.07 3.769e-11 263-280 BL00028 16.07 5.154e-11 179-196 BL00028 16.07 4.000e-10 375-392
132	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE	PR00836B 16.59 8.347e-09 3-22
139	PR00056	HEAT SHOCK FACTOR (HSF) DOMAIN SIGNATURE	PR00056C 14.47 7.823e-12 153-166
140	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 7.300e-19 82-104
145	PF00969	Class II histocompatibility antigen, beta domain proteins.	PF00969B 9.97 1.000e-40 58-94 PF00969C 27.72 1.000e-40 97-147 PF00969E 11.49 1.000e-39 212-247 PF00969A 22.07 3.520e-38 12-55 PF00969D 14.02 4.789e-36 154-184
146	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 2.579e-24 181-218 BL00514G 15.98 9.111e-12 262-292
155	DM01688	2 POLY-IG RECEPTOR.	DM01688B 15.06 3.628e-09 82-130
158	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 20-68 DM00031B 15.41 5.865e-25 86-120 DM00031C 12.79 4.429e-10 129-140
159	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 20-68 DM00031B 15.41 1.000e-40 84-118 DM00031C 12.79 1.600e-15 134-145
160	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 6.294e-12 85-119
162	PF01073	3-beta hydroxysteriod dehydrogenase/isomerase family.	PF01073A 18.01 9.206e-22 140-193 PF01073B 12.26 6.831e-19 222-267 PF01073C 10.62 2.645e-17 322-370
169	BL00086	Cytochrome P450 cysteine	BL00086 20.87 3.813e-24 480-512



SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		heme-iron ligand proteins.	
170	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.	BL00086 20.87 3.813e-24 502-534
171	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.	BL00086 20.87 3.813e-24 363-395
173	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.	BL00453B 23.86 3.000e-20 87-121 BL00453A 15.57 9.379e-10 63-78
174	BL00216	Sugar transport proteins.	BL00216B 27.64 4.900e-10 240-290
187	BL01209	LDL-receptor class A (LDLRA) domain proteins.	BL01209 9.31 5.500e-11 470-483 BL01209 9.31 2.212e-10 395-408 BL01209 9.31 6.365e-10 433-446 BL01209 9.31 8.962e-10 239-252
189	PD01733	APOLIPOPROTEIN PLASMA LIPID TRANSPORT H.	PD01733B 20.44 6.600e-14 109-164
190	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 8.412e-09 15-39
191	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 61-109 DM00031B 15.41 1.000e-40 125-159 DM00031C 12.79 1.600e-15 174-185 DM00031B 15.41 9.544e-09 245-279
192	PF00622	Domain in SPla and the RYanodine Receptor.	PF00622B 21.00 8.250e-11 161-183
193	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 5.263e-12 152-164 BL00198 10.43 1.346e-10 113-125
199	PF00023	Ank repeat proteins.	PF00023A 16.03 8.000e-12 90-106
208	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 7.288e-09 33-77
210	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e-29 71-107
212	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.000e-26 340-386 BL00039A 18.44 6.114e-17 64-103 BL00039B 19.19 3.681e-11 104-130
213	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.000e-26 314-360 BL00039A 18.44 6.114e-17 64-103 BL00039B 19.19 3.681e-11 104-130
214	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 6.727e-38 238-282 BL00280 24.61 1.514e-30 294-338
216	PF00064	Neuraminidases.	PF00064D 17.65 8.830e-09 11-50
217	PF00064	Neuraminidases.	PF00064D 17.65 8.830e-09 11-50
218	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 7.585e-21 196-226 BL00019C 14.66 9.143e-20 128-164 BL00019A 12.56 5.408e-12 56-67 BL00019B 13.34 9.795e-12 83-106
219	PR00194	TROPOMYOSIN SIGNATURE	PR00194D 9.57 1.240e-10 391-415

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
220	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 4.743e-09 56-100
222	BL00415	Synapsins proteins.	BL00415N 4.29 8.695e-10 335-379
223	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 7.725e-09 302-318
225	PD02918	AMINOGLYCOSIDE N3'-ACETYLTRANSFERASE III.	PD02918A 18.79 3.621e-09 345-385
227	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 4.717e-18 45-68
235	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356G 10.80 8.644e-09 536-550

\* results include in order: accession number subtype, raw score; p-value; position of signature in amino acid sequence.

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
3	Apolipoprotein	Apolipoprotein A1/A4/E family	7.3e-91	315.3
6	trypsin	Trypsin	2.9e-59	189.2
7	Collagen	Collagen triple helix repeat (20 copies)	4.1e-290	977.2
8	LRR	Leucine Rich Repeat	2.9e-13	57.5
9	PBP	Phosphatidylethanolamine-binding protein	1.4e-17	71.9
11	adh_short	short chain dehydrogenase	7e-43	155.9
12	ig	Immunoglobulin domain	2.1e-14	51.4
14	Y_phosphatase	Protein-tyrosine phosphatase	4.8e-299	1006.8
25	SH3	SH3 domain	0.026	5.2
32	ig	Immunoglobulin domain	1.8e-09	35.6
37	7tm_3	7 transmembrane receptor	7.2e-09	29.0
39	ig	Immunoglobulin domain	1.4e-20	71.3
40	ig	Immunoglobulin domain	2.6e-15	54.4
45	SH3	SH3 domain	1.4e-42	154.9
47	ig	Immunoglobulin domain	2.5e-16	57.7
48	ig	Immunoglobulin domain	1.6e-24	84.1
65	zf-C2H2	Zinc finger, C2H2 type	2.7e-06	34.3
66	TGF-beta	Transforming growth factor beta like	6.9e-64	197.9
73	Ribosomal_L20	Ribosomal protein L20	2e-22	74.0
79	connexin	Connexin	1.6e-50	181.3
96	ig	Immunoglobulin domain	2.5e-26	89.9
97	ig	Immunoglobulin domain	1.5e-08	32.6
98	ig	Immunoglobulin domain	3.6e-25	86.1
99	ig	Immunoglobulin domain	7.6e-33	110.9
102	FG-GAP	FG-GAP repeat	6.9e-66	232.3
107	ig	Immunoglobulin domain	1.3e-16	58.6
108	thioredo	Thioredoxin	2.8e-79	267.1
109	ig	Immunoglobulin domain	2.9e-16	57.5
110	ig	Immunoglobulin domain	4.6e-13	47.1
111	laminin_G	Laminin G domain	2.4e-63	223.9
112	laminin_G	Laminin G domain	2.4e-63	223.9
114	LBP_BPI_CETP	LBP / BPI / CETP family	2.6e-06	-2.4
116	efhand	EF hand	1.1e-14	62.2
118	SAP	SAP domain	4.8e-12	53.5
121	ig	Immunoglobulin domain	2.9e-16	57.5
129	zf-C2H2	Zinc finger, C2H2 type	1.7e-64	227.7
139	HSF_DNA-bind	HSF-type DNA-binding domain	1.7e-05	22.3
140	7tm_1	7 transmembrane receptor (rhodopsin family)	1.1e-15	52.0
141	ig	Immunoglobulin domain	9.4e-09	33.3
145	MHC_II_beta	Class II histocompatibility antigen, beta	2.7e-29	110.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
146	fibrinogen_C	Fibrinogen beta and gamma chains, C-term	1.3e-35	125.6
154	ig	Immunoglobulin domain	6.7e-05	20.8
155	ig	Immunoglobulin domain	0.00022	19.2
158	ig	Immunoglobulin domain	7e-19	65.9
159	ig	Immunoglobulin domain	3.5e-28	95.9
160	ig	Immunoglobulin domain	2.4e-06	25.5
162	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	1e-199	676.9
164	ig	Immunoglobulin domain	2.1e-09	35.3
169	p450	Cytochrome P450	8.9e-141	481.1
170	p450	Cytochrome P450	2.1e-131	450.0
171	p450	Cytochrome P450	1.7e-112	387.1
173	FKBP	FKBP-type peptidyl-prolyl cis-trans isomeras	5.1e-27	89.2
174	sugar_tr	Sugar (and other) transporter	0.014	-120.6
187	CUB	CUB domain	2.2e-56	200.7
189	Apolipoprotein	Apolipoprotein A1/A4/E family	1.6e-06	34.6
191	ig	Immunoglobulin domain	1.7e-24	84.0
192	SPRY	SPRY domain	6.2e-13	56.4
193	fer4	4Fe-4S binding domain	1.6e-13	58.4
199	ank	Ank repeat	2.7e-09	44.3
209	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
210	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
211	Kelch	Kelch motif	0.02	20.8
212	DEAD	DEAD/DEAH box helicase	2.8e-52	168.3
213	DEAD	DEAD/DEAH box helicase	2.8e-52	168.3
214	Kunitz_BPTI	Kunitz/Bovine pancreatic trypsin inhibito	3.7e-47	148.6
215	Acyltransferase	Acyltransferase	0.0023	4.4
216	ig	Immunoglobulin domain	1.7e-10	38.9
217	ig	Immunoglobulin domain	1.1e-08	33.1
218	spectrin	Spectrin repeat	0	1209.7
219	PH	PH domain	5.3e-08	33.6
220	Aa_trans	Transmembrane amino acid transporter protein	1.5e-21	85.0
223	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.7e-07	26.4
224	PA	PA domain	0.00022	28.0
227	kazal	Kazal-type serine protease inhibitor domain	5.6e-13	56.6
235	TBC	TBC domain	4.7e-45	163.1

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	1-16	0.907	0.635
2	1-45	0.970	0.723
3	1-31	0.970	0.770
4	1-25	0.929	0.655
5	1-28	0.990	0.860
6	1-18	0.977	0.916
7	1-22	0.990	0.921
8	1-45	0.973	0.605
9	1-22	0.991	0.915
10	1-18	0.910	0.637
11	1-20	0.997	0.915
12	1-21	0.967	0.949
13	1-22	0.985	0.949
14	1-29	0.932	0.690
15	1-15	0.933	0.831
16	1-19	0.985	0.932
17	1-21	0.996	0.951
18	1-18	0.942	0.764
19	1-18	0.954	0.725
20	1-29	0.891	0.625
21	1-31	0.992	0.895
22	1-18	0.974	0.820
23	1-46	0.994	0.917
24	1-32	0.983	0.865
26	1-22	0.975	0.874
27	1-19	0.943	0.723
28	1-21	0.971	0.925
30	1-31	0.970	0.770
31	1-26	0.958	0.844
32	1-19	0.959	0.930
34	1-41	0.958	0.553
35	1-11	0.888	0.610
36	1-29	0.888	0.611
38	1-32	0.917	0.567
39	1-27	0.978	0.895
40	1-25	0.929	0.655
44	1-21	0.972	0.946
46	1-28	0.955	0.806
47	1-19	0.985	0.892
48	1-19	0.981	0.955
49	1-21	0.977	0.675
52	1-23	0.976	0.920
53	1-19	0.988	0.936
55	1-15	0.901	0.782
58	1-24	0.953	0.772
59	1-32	0.992	0.943

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
61	1-19	0.896	0.566
62	1-37	0.915	0.693
66	1-22	0.978	0.889
67	1-24	0.922	0.563
68	1-18	0.962	0.763
69	1-31	0.990	0.773
70	1-21	0.902	0.802
71	1-31	0.922	0.604
72	1-22	0.932	0.645
74	1-32	0.947	0.669
75	1-20	0.973	0.832
76	1-24	0.933	0.597
77	1-42	0.964	0.719
79	1-45	0.973	0.605
82	1-18	0.975	0.870
83	1-25	0.990	0.919
85	1-18	0.946	0.753
87	1-20	0.976	0.854
89	1-27	0.990	0.907
90	1-23	0.890	0.717
92	1-40	0.881	0.660
93	1-36	0.886	0.568
95	1-41	0.994	0.804
96	1-19	0.975	0.901
97	1-19	0.975	0.901
98	1-19	0.975	0.901
99	1-19	0.975	0.901
100	1-18	0.990	0.955
101	1-36	0.998	0.907
102	1-22	0.932	0.756
103	1-15	0.928	0.793
104	1-45	0.992	0.911
105	1-20	0.988	0.926
107	1-19	0.985	0.892
109	1-15	0.983	0.953
110	1-16	0.969	0.894
113	1-19	0.941	0.828
114	1-20	0.989	0.973
115	1-23	0.960	0.786
117	1-22	0.886	0.663
119	1-18	0.960	0.820
120	1-16	0.924	0.582
121	1-16	0.987	0.929
122	1-22	0.992	0.956
123	1-23	0.929	0.588
126	1-41	0.968	0.792
127	1-34	0.930	0.665

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
128	1-42	0.957	0.653
130	1-21	0.897	0.632
131	1-25	0.983	0.845
132	1-13	0.947	0.915
133	1-13	0.930	0.824
134	1-22	0.947	0.857
135	1-25	0.978	0.936
137	1-17	0.960	0.878
141	1-16	0.983	0.952
142	1-23	0.945	0.798
145	1-29	0.979	0.884
146	1-25	0.922	0.765
147	1-37	0.928	0.786
148	1-28	0.981	0.890
150	1-20	0.986	0.965
151	1-20	0.987	0.886
152	1-18	0.922	0.809
153	1-19	0.887	0.607
154	1-16	0.964	0.790
155	1-17	0.984	0.973
156	1-21	0.929	0.692
157	1-21	0.937	0.836
158	1-19	0.897	0.722
159	1-19	0.985	0.932
160	1-21	0.978	0.833
161	1-20	0.940	0.632
165	1-20	0.954	0.696
167	1-20	0.988	0.963
168	1-20	0.986	0.952
169	1-8	0.983	0.634
170	1-8	0.983	0.634
171	1-40	0.994	0.888
173	1-27	0.982	0.925
174	1-17	0.989	0.945
176	1-21	0.987	0.919
177	1-21	0.950	0.596
178	1-22	0.986	0.949
179	1-18	0.942	0.764
181	1-16	0.917	0.618
182	1-23	0.963	0.889
183	1-25	0.992	0.968
184	1-19	0.945	0.638
185	1-31	0.964	0.709
186	1-37	0.978	0.830
187	1-27	0.947	0.799
190	1-41	0.972	0.836
193	1-16	0.900	0.664

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
194	1-35	0.988	0.912
195	1-16	0.944	0.837
196	1-28	0.925	0.626
197	1-20	0.962	0.811
198	1-21	0.947	0.701
199	1-20	0.945	0.854
200	1-34	0.967	0.718
201	1-32	0.994	0.956
203	1-18	0.953	0.786
204	1-24	0.968	0.728
205	1-32	0.920	0.623
206	1-27	0.974	0.843
208	1-31	0.986	0.878
209	1-29	0.997	0.854
214	1-19	0.986	0.967
215	1-37	0.981	0.952
216	1-18	0.974	0.820
217	1-18	0.974	0.820
218	1-21	0.937	0.819
219	1-31	0.914	0.554
224	1-21	0.981	0.945
225	1-25	0.938	0.890
227	1-22	0.965	0.891
230	1-23	0.884	0.746
231	1-14	0.885	0.675
232	1-20	0.930	0.729



TABLE 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/491,404
1	237	473	709	785CIP2B_1	10
2	238	474	710	785CIP2B_2	449
3	239	475	711	785CIP2B_3	1376
4	240	476	712	785CIP2B_4	1425
5	241	477	713	785CIP2B_5	1472
6	242	478	714	785CIP2B_6	1503
7	243	479	715	785CIP2B_7	1513
8	244	480	716	785CIP2B_8	1518
9	245	481	717	785CIP2B_9	1525
10	246	482	718	785CIP2B_10	1533
11	247	483	719	785CIP2B_11	1537
12	248	484	720	785CIP2B_12	1542
13	249	485	721	785CIP2B_13	1549
14	250	486	722	785CIP2B_14	1560
15	251	487	723	785CIP2B_15	1715
16	252	488	724	785CIP2B_16	1731
17	253	489	725	785CIP2B_17	1757
18	254	490	726	785CIP2B_18	1791
19	255	491	727	785CIP2B_19	1809
20	256	492	728	785CIP2B_20	1818
21	257	493	729	785CIP2B_21	1857
22	258	494	730	785CIP2B_22	1869
23	259	495	731	785CIP2B_23	1905
24	260	496	732	785CIP2B_24	1910
25	261	497	733	785CIP2B_25	1917
26	262	498	734	785CIP2B_26	1924
27	263	499	735	785CIP2B_27	1937
28	264	500	736	785CIP2B_28	1965
29	265	501	737	785CIP2B_29	2033
30	266	502	738	785CIP2B_30	2035
31	267	503	739	785CIP2B_31	2194
32	268	504	740	785CIP2B_32	2195
33	269	505	741	785CIP2B_33	2197
34	270	506	742	785CIP2B_34	2199
35	271	507	743	785CIP2B_35	2201
36	272	508	744	785CIP2B_36	2201
37	273	509	745	785CIP2B_37	2253
38	274	510	746	785CIP2B_38	2257
39	275	511	747	785CIP2B_39	2264
40	276	512	748	785CIP2B_40	2264
41	277	513	749	785CIP2B_41	2266
42	278	514	750	785CIP2B_42	2272
43	279	515	751	785CIP2B_43	2272
44	280	516	752	785CIP2B_44	2274

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/491,404
45	281	517	753	785CIP2B_45	2283
46	282	518	754	785CIP2B_46	2285
47	283	519	755	785CIP2B_47	2289
48	284	520	756	785CIP2B_48	2294
49	285	521	757	785CIP2B_49	2295
50	286	522	758	785CIP2B_50	2297
51	287	523	759	785CIP2B_51	2301
52	288	524	760	785CIP2B_52	2312
53	289	525	761	785CIP2B_53	2313
54	290	526	762	785CIP2B_54	2324
55	291	527	763	785CIP2B_55	2337
56	292	528	764	785CIP2B_56	2338
57	293	529	765	785CIP2B_57	2345
58	294	530	766	785CIP2B_58	2359
59	295	531	767	785CIP2B_59	2361
60	296	532	768	785CIP2B_60	2369
61	297	533	769	785CIP2B_61	2379
62	298	534	770	785CIP2B_62	2382
63	299	535	771	785CIP2B_63	2389
64	300	536	772	785CIP2B_65	2400
65	301	537	773	785CIP2B_66	2411
66	302	538	774	785CIP2B_67	2422
67	303	539	775	785CIP2B_68	2425
68	304	540	776	785CIP2B_69	2426
69	305	541	777	785CIP2B_70	2428
70	306	542	778	785CIP2B_71	2431
71	307	543	779	785CIP2B_72	2440
72	308	544	780	785CIP2B_73	2443
73	309	545	781	785CIP2B_74	2451
74	310	546	782	785CIP2B_75	2458
75	311	547	783	785CIP2B_76	2462
76	312	548	784	785CIP2B_77	2470
77	313	549	785	785CIP2B_78	2487
78	314	550	786	785CIP2B_79	2497
79	315	551	787	785CIP2B_80	2504
80	316	552	788	785CIP2B_81	2510
81	317	553	789	785CIP2B_82	2513
82	318	554	790	785CIP2B_83	2519
83	319	555	791	785CIP2B_84	2520
84	320	556	792	785CIP2B_85	2524
85	321	557	793	785CIP2B_86	2528
86	322	558	794	785CIP2B_87	2531
87	323	559	795	785CIP2B_88	2558
88	324	560	796	785CIP2B_89	2567
89	325	561	797	785CIP2B_90	2584
90	326	562	798	785CIP2B_91	2588

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/491,404
91	327	563	799	785CIP2B_92	2594
92	328	564	800	785CIP2B_93	2596
93	329	565	801	785CIP2B_94	2599
94	330	566	802	785CIP2B_95	2601
95	331	567	803	785CIP2B_96	2603
96	332	568	804	785CIP2B_97	2604
97	333	569	805	785CIP2B_98	2604
98	334	570	806	785CIP2B_99	2604
99	335	571	807	785CIP2B_100	2604
100	336	572	808	785CIP2B_101	2610
101	337	573	809	785CIP2B_102	2612
102	338	574	810	785CIP2B_103	2626
103	339	575	811	785CIP2B_104	2629
104	340	576	812	785CIP2B_105	2630
105	341	577	813	785CIP2B_106	2631
106	342	578	814	785CIP2B_107	2639
107	343	579	815	785CIP2B_108	2651
108	344	580	816	785CIP2B_109	2652
109	345	581	817	785CIP2B_110	2661
110	346	582	818	785CIP2B_111	2662
111	347	583	819	785CIP2B_112	2677
112	348	584	820	785CIP2B_113	2677
113	349	585	821	785CIP2B_114	2680
114	350	586	822	785CIP2B_115	2688
115	351	587	823	785CIP2B_116	2693
116	352	588	824	785CIP2B_117	2716
117	353	589	825	785CIP2B_118	2720
118	354	590	826	785CIP2B_119	2721
119	355	591	827	785CIP2B_120	2724
120	356	592	828	785CIP2B_121	2725
121	357	593	829	785CIP2B_122	2727
122	358	594	830	785CIP2B_123	2739
123	359	595	831	785CIP2B_124	2740
124	360	596	832	785CIP2B_125	2747
125	361	597	833	785CIP2B_126	2748
126	362	598	834	785CIP2B_127	2752
127	363	599	835	785CIP2B_128	2755
128	364	600	836	785CIP2B_129	2764
129	365	601	837	785CIP2B_130	2773
130	366	602	838	785CIP2B_131	2778
131	367	603	839	785CIP2B_132	2779
132	368	604	840	785CIP2B_133	2780
133	369	605	841	785CIP2B_134	2781
134	370	606	842	785CIP2B_135	2786
135	371	607	843	785CIP2B_136	2790
136	372	608	844	785CIP2B_137	2791

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/491,404
137	373	609	845	785CIP2B_138	2795
138	374	610	846	785CIP2B_139	2801
139	375	611	847	785CIP2B_140	2802
140	376	612	848	785CIP2B_141	2804
141	377	613	849	785CIP2B_142	2811
142	378	614	850	785CIP2B_143	2820
143	379	615	851	785CIP2B_144	2825
144	380	616	852	785CIP2B_145	2836
145	381	617	853	785CIP2B_146	2841
146	382	618	854	785CIP2B_147	2843
147	383	619	855	785CIP2B_148	2844
148	384	620	856	785CIP2B_149	2845
149	385	621	857	785CIP2B_150	2849
150	386	622	858	785CIP2B_151	2850
151	387	623	859	785CIP2B_152	2866
152	388	624	860	785CIP2B_153	2873
153	389	625	861	785CIP2B_154	2874
154	390	626	862	785CIP2B_155	2878
155	391	627	863	785CIP2B_156	2882
156	392	628	864	785CIP2B_157	2888
157	393	629	865	785CIP2B_158	2894
158	394	630	866	785CIP2B_159	2899
159	395	631	867	785CIP2B_160	2899
160	396	632	868	785CIP2B_161	2903
161	397	633	869	785CIP2B_162	2905
162	398	634	870	785CIP2B_163	2913
163	399	635	871	785CIP2B_164	2920
164	400	636	872	785CIP2B_165	2927
165	401	637	873	785CIP2B_166	2938
166	402	638	874	785CIP2B_167	2952
167	403	639	875	785CIP2B_168	2954
168	404	640	876	785CIP2B_169	2954
169	405	641	877	785CIP2B_170	2958
170	406	642	878	785CIP2B_171	2958
171	407	643	879	785CIP2B_172	2958
172	408	644	880	785CIP2B_173	2959
173	409	645	881	785CIP2B_174	2961
174	410	646	882	785CIP2B_175	2978
175	411	647	883	785CIP2B_176	2981
176	412	648	884	785CIP2B_177	2996
177	413	649	885	785CIP2B_178	2997
178	414	650	886	785CIP2B_179	3001
179	415	651	887	785CIP2B_180	3006
180	416	652	888	785CIP2B_181	3007
181	417	653	889	785CIP2B_182	3010
182	418	654	890	785CIP2B_183	3034

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/491,404
183	419	655	891	785CIP2B_184	3058
184	420	656	892	785CIP2B_185	3060
185	421	657	893	785CIP2B_186	3061
186	422	658	894	785CIP2B_187	3078
187	423	659	895	785CIP2B_188	3081
188	424	660	896	785CIP2B_189	3083
189	425	661	897	785CIP2B_190	3086
190	426	662	898	785CIP2B_191	3090
191	427	663	899	785CIP2B_193	3102
192	428	664	900	785CIP2B_194	3110
193	429	665	901	785CIP2B_195	3117
194	430	666	902	785CIP2B_196	3118
195	431	667	903	785CIP2B_197	3121
196	432	668	904	785CIP2B_198	3124
197	433	669	905	785CIP2B_199	3131
198	434	670	906	785CIP2B_200	3132
199	435	671	907	785CIP2B_201	3135
200	436	672	908	785CIP2B_202	3143
201	437	673	909	785CIP2B_203	3145
202	438	674	910	785CIP2B_204	3156
203	439	675	911	785CIP2B_205	3160
204	440	676	912	785CIP2B_206	3163
205	441	677	913	785CIP2B_207	3167
206	442	678	914	785CIP2B_208	3170
207	443	679	915	785CIP2B_209	3174
208	444	680	916	785CIP2B_210	3176
209	445	681	917	785CIP2B_211	3178
210	446	682	918	785CIP2B_212	3180
211	447	683	919	785CIP2B_213	3791
212	448	684	920	785CIP2B_215	3793
213	449	685	921	785CIP2B_216	3793
214	450	686	922	785CIP2B_217	3794
215	451	687	923	785CIP2B_218	3795
216	452	688	924	785CIP2B_219	3796
217	453	689	925	785CIP2B_220	3796
218	454	690	926	785CIP2C_1	145
219	455	691	927	785CIP2C_3	639
220	456	692	928	785CIP2C_4	652
221	457	693	929	785CIP2C_5	753
222	458	694	930	785CIP2C_6	754
223	459	695	931	785CIP2C_7	1258
224	460	696	932	785CIP2C_8	1316
225	461	697	933	785CIP2C_9	1343
226	462	698	934	785CIP2C_11	1499
227	463	699	935	785CIP2C_12	1659
228	464	700	936	785CIP2C_13	2024

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/491,404
229	465	701	937	785CIP2C_15	2114
230	466	702	938	785CIP2C_16	2119
231	467	703	939	785CIP2C_17	2126
232	468	704	940	785CIP2C_19	2137
233	469	705	941	785CIP2C_20	2143
234	470	706	942	785CIP2C_21	2145
235	471	707	943	785CIP2C_22	2853
236	472	708	944	785CIP2C_24	3076

TABLE 7

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
709	465	301	MGKSLASQFPITLIFSASFSTFCLLDGLFISCPCTSTELPKVNSLLSRPESATT*
710	1181	1345	MLALSSSFLVLSYLLTRWCGSVGFILANCFNM GIRITQSLCFIHRYYRRSPHRPL
711	186	701	MKVLWAALLVTFLAGCQAKVEQAVETEPEPE LRQQTEWQSGQRWELALGRFWDYLRWVQTLS EQVQEELLSSQVTQELRALMDETMKELKAYKS ELEEQLTPVAEETRARLSKELQAAQARLGADM EDVCGRLGAVTAVMVQGHARPEQPRSCGWRV RLPPAQAGVSGSLR*
712	3917	4081	MFRRLTFAQLLFATVLGIAGGVYIFQPVFEQYA KDQKELKEKMQLVQESEEKKS*
713	26	1123	MSLLGFLLSRLGLLLKVLLDWPVEVLYGAAAL NGLFGGFSAFWSGVMALGSLGSSEGRRSVRLIL IDLMLGLAGFCGSMASGHLFKQMAGHSGQGLI LTACSVSCASFALLYSLLVLPESVAKPSQEL PAVDTVSGTVGTYRTLDPDQLDQYAVGHPPS PGKAKPHKTTIALLFVGAIHYDLAVVGTVDVIPL FVLREPLGWNQVQVGYGMAAGYTIFITSFLGV LVFSRCFRDTTMIMIGMVSFGSGALLAFVKET YMFYIARAVMLFALIPVTTIRSAMSKLIKSSY GKVFVILQLSLALTGVVTSTLYNKIYQLTMDM FGGSCFALSSFLSFLAIPISIVAYKQVPLSPYGD IIEK*
714	39	431	MFLFLFFLVAILPVNTEGGEIHWGTESKPHSRPY MAFIKFYDSNSEPHHCGGFLVAKDIVMTAAHC NGRNIKVTLGAHNIKKQENTQVISVVKAKPHE NYDRDSHFNDIMLLKLERKAQLNGCCEDYCPS *
715	970	1755	MLVLLVLRVSLAALVKMELLVRWAPVACLVR EVALEPLALLVLVEMMVLLVLPGLVPPAPLV LLASLVLLVLRVKLVPKGPEALKVPRVCVVS L APLALLVLLALLETLVLRESLVLKVPMVLLVLL VLLASLVPEAPLDPRAPAALLVPRVTAVNLVLL AAKETLVRESLALLVFKDPLALLERKESEEELE VNPDPPLACPDPLASVVDLVAVVSLAQMVLLVP RVPLVNVVLLALLAPKDLLVKLVVPVKLVCLV PRV*
716	3060	2899	MMLLVSLHILFPFMPFSYGLESNNKPKQCLMKL TLQNQLQKQVAFEVFSHTKYN*
717	70	618	MGWTMRLVTAALLGLMMVVTGDEDENSPC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AHEALLDEDTLFCQGLEVFYPELGNGICKVVPD CNNYRQKITSWMEPIVKFPGAVDGYILVMV DPDAPSRAEPRQRFWRHWLVTDIKGADLKEGK IQGQELSALPGSLPHRHTVAFHRYQVLCSSGR EKSSLSFPRKTKLEALGKWTF*
718	79	342	MRRSFWTVMRTAWRCS CSSVDRALSHQAGLQ GQCLSACLLGNLGYPPFISPPAQVLCAARASCH LGSLMAHFETLVHSDKWSCVILK*
719	382	1326	MLFWVLGILLICGFLWTRKGKLIKIEDITDKYIFI TGCDSGFGNLAARTFDKKG FHVIAACLTESGST ALKAETSERLRTVLLDVTDPENVKRTAQWVK NQVGEKGLWGLINNAGVPGVLAPTDWLTLED YREPIEVNLFGLISVTNLMLPLVKKAQGRVINV SSVGGRLAIVGGGYTPSKYAVEGFNDLRRDM KAFGVHVSCEPGLFKTNLADPVKVEKKLAIW EQLSPDIKQQYGEYIEKSLDKLKGKNSYVNM DLSPVVECMDHALTSLFPKTHYAAGKDAKIFW IPLSHMPAALQDFLLKQKARAG*
720	875	516	MSVPTMAWMMLLLGLLAYGSGVESQTVVTQE PSLSVSPGGTVTLTCGLTSGSVSTSFYPSWYQQ TPGQAPRTLIIYSTNTRSSGVPGRFSGSILGSKAA LTITGAQADDES DYCVLICR*
721	431	3643	MNCDVLWCVLLLVCMSLFS AVGHGLWIWRY QEKKS LFYVPKSDGSSLSPVTA AVYSFLTMIIVL QVLIPISLYVSIEIVKACQVYFINQDMQLYDEET DSQLQCRALNITEDLGQIQYIFSDKTGTLTENK MVFRRTVSGVEYSHDANAQRLARYQEADSE EEEVVPRGGSVSQRGSIGSHQSVRVVHRTQSTK SHRRTGSRAEAKRASMLSKHTAFSSPMEKDITP DPKLLEK VSECDKSLAVARHQEHLLAHLSPELS DVFDFLIALTICNTVVVTSPDQPRTKVRVRFEL KSPVKTIEDFLRRFTPSCLTSGCSSIGSLAANKSS HKLGSSFPSTPSSDGMLLRLEERLGQPTSAIASN GYSSQADN WASELAQE QESERELRYEAESPDE AALVYAARAYNCVL VERLHDQVSVELPHLGR LTFELLHTLGFDSVRKRMSV VIRHPLTDEINVY TKGADSVVMDLLQPCSSVDARGRHQKKIRSKT QNYLNVYAAEGLRTL CIAKRVLSKEEYACWLQ SHLEAESSLENSEELLFQSAIRLETNLHLLGATG IEDRLQDGV PETISKLRQAGLQIWVLTGDKQET AVNIA YACKLLDHDEEVITLNATSQEACAALL DQCLCYVQSRGPQRAPEKTKGKVS MRFS SLC P PSTSTASGRPSLVIDGRSMAYALEKNLEDKFL



SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FLAKQCRSVLCCRSTPLQKSMVVKLVRSKLKAMTLAIGDGANDVSMIQVADVGVGISGQEGMQAVMASDFAVPKFRYLERLLILHGHWCYSRLANMVLVFFYKNTMFVGLLFWFQFFCGFSASTMIDQWYLIFFNLLFSSLPPLVTGVLD RDVPANVLLTNPQLYKSGQNMEEYRPRTFWFNMADA AFQSLVCF SIPYLA YYDSNVDLFTWGTPIVTIALLTLLHLGIETKTWTWLNWITCGFSVLLFFTVALIYNASCATCYPPSNPYWTMQALLGDPVFYLTCLMTPVAALLPRLFFRSLQGRVFPTQLQLARQLTRKSPRRCSAPKETFAQGRPXEG LGNRGTHQGGQSRPLCPCPSLLGTHSSRSAPWRPAGSPAQWT*
722	3616	1673	MLWVTGPVLA VILILIVIAILLFKRRTHSPSSKDEQSIGLKDSLLAHSSDPVEMRRLNYQTPGMRDHPPITDLADNIERLKANDGLKFSQEYESIDPGQFTWENS NLEV NKPKNRYANVIA YDHSRVI LTSIDGVPGSDYINANYIDGYRKQNA YIATQGPLPETMGDFWRMVWEQRTATVVMTRLEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFALHKSGSSEKREL RQFQFMAWPDHGVEYPTPILAF LR RVKACNPLDAGPMV VHCSAGVGR TGCFIVIDAMLERMKHEKTVDIYGHVTCMR SQ RNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKL GQVPPGESVTAMELEFKLLASSKAHTSRFISANLPCNKFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASF LDGYRQQA YIATQGPLAESTEDFWRMLWEHNSTIIVMLTKLREMGREKCHQYWP AERSARYQYFVVDPM AEYNMPQYILREFKVTDARDGQSRTIRQFQFTDWPEQGVPKTGEGFIDFIGQVHKTK EQFGQDGPITVHCSAGVGRTGVFITLSIVLERMRYEGVVD MFQT VKTLRTQRPAMVQTEDQYQLCYRAALEYLG SFDHYAT*
723	484	765	MIWIYFAFIFQRLHLIPGKSSARQVSGFSLLSFNPNTIFVKLDWWCFIQLIYSAYLFEKRLLEIDDVFPVILKVVGARIEFHSGIGFGSGL*
724	846	983	MLIAVIACICYLSLLHSYDILFGHFSVLSQGLDKHCLTLFSLGG*
725	154	513	MVIINCSPRFWFLFPFTIQHTCKCPLGVRYHTRHLEQIAANKKHCPYPYEVHYNSSYWRAGIHLHTLHAYLTSYPHYYSFFFFFFGKGVPFCPQGGGAGKGSGLMGSHRGTKPKSFLKKK
726	709	566	MERHGFFLDVCLILGLIPLSIKYS LQKRGKNSA

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			ADNAGWSDLSLGQN*
727	175	342	MYMNTCLYLHVYVLTCSGCNVDMCSRLFLST KLKAHVQIVLYWVFLWSRGNNFLT*
728	109	264	MVILDVLELYHMFVFLGILYDAIFYCFVHAINA DKFFGLKLTKSATVSQNSQ*
729	56	220	MYDFLLLSFIFIVASYWSFLSTIFLDVVCSILHC PVKPQTLLKSLHVDCKST*
730	735	1235	MVGLGGMSQLLLASLLPPVPQGSPTRRKLPASL LVSTALISPVCVRGWMWQNLQNRHGSHTSAR RVPSLPGAGQVGVRWEAGPACRTQPSPQNLAP RPHPSAAQLIENAAALRSAMSGERLFPGEQHLG PLVAPRVPMGGALCPPLPSLSAICKVGAAREA GGR*
731	109	303	MKPYCMYPFLSGLLSSLLFWVESLMLLCVQMV LFLMLCVLDYRIYCIKIYVSIILLMSIWIISI*
732	165	359	MCYFYNTIILTQGSMLFLLFSVVTLYLFSSHPTPISIFSDVFNMYPWIMYSYMFVSVNLYK*
733	7	279	MAAAPGLLVWLLVLRPWRVPGQLDPSTGRR FSEHKLCADDECSMLMYRGEALEDFTGPDCRF VNFKKGDPVYVYYKLARGWPEVWAGSK*
734	81	275	MPGYVPLLLLLLLLLRCSQRGGGVNFGEKDAKV PGTWRDGVVRPGEASWSDRASPERRYGIGE *
735	207	419	MKFLLMSPYRHLFCITQAILSEIAEGIRNDPFK FYLYSVLALFLHYMYVVFVSRSIYYLKLRIKFS*
736	233	457	MRQIAVFQRFMFPLLPWLSCIFSSSQNSIYYVS TFIKCLALKSIKRQRSEINSGFLAIYHALRNQVT RCGGL*
737	39	251	MPRRTRGGLWLCNAHKSCQKYLSSLKLSTLLS PLLVLPFYTPSLKGWGFVLRFYFMVHADCNLF KIII*
738	155	313	MFTHWLGPVYIKQFIVMIVSILTFPVLQGML RNFLYLNIMFVVALLKAIL*
739	60	272	MERGAGAKLLPLLLLRLATGFTCAQADGRNG YTAVIEVTSGGPWGDWAWPEMCPDGFFASGFS LKVGAAQ*
740	49	360	MTQVERVIVFLTLSTLSLAKTTQPIFMDSEYEQ EVNITCSHNNIVTNDYITWYQQFPSQGPRFIIQG YQKKVTNEVAFLCIPADRKSITLNLPRVSLEDT GKK*
741	47	325	MTKLAQWLWGLAILGSTWVALTTGALGLELP LSCQEVLPWPAYLLVSAGCYALGTGVYRVAT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
			FHDCEDAARELQSQIQEARADLARRGLRF*
742	301	438	MSVGLAGAVGRRCHLALAVLHDPLCHHGSLA TICKQPEVCLFTIV*
743	165	413	MPFLLNQCGSLLYYLTLASTDLTLAVPICNSLAI IFTLIVGKALGEDIGGKRAVAGMVLTVIGISLCI TSSVSKTQGGQSTL*
744	165	413	MPFLLNQCGSLLYYLTLASTDLTLAVPICNSLAI IFTLIVGKALGEDIGGKRAVAGMVLTVIGISLCI TSSVSKTQGGQSTL*
745	923	1618	MALIYVMLLLLGAFLGAWPALCGRYKRWRKH GVFVLLTTATSVAIWVWVIMYTYGNKQHNS PTWDDPTLAIALAANAWAFVLFYVIPEVSQVT KSSPEQSYQGDMYPTRGVGYETILKEQKGQSM FVENKAFSMDPEPVAARKRPVSPYSGYNGQLTS VYQPTMALMHKVPSEGAYDIILPRATANSQV MGSANSTLRAEDMYSAQSHQAATPPKDGKNS QVFRNPYVWD*
746	14	370	MVKTDAHLKNPPFAPFRVYTLTSLLLKLSHYS CLWVKKDKFDSSFYNSNNNSNSNHCKSLLSTH YMPGAVISNLCLISCKVSSSPIKQTHGISMLQM KRLKHTLARLAPGTHGGSQN*
747	103	1002	MGTKAQVERKLLCLFILAILLCSLALGSVTVHS SEPEVRIPENNPVKLSLAYSGFSSPRVEWKFDQ GDTTRLVCYNNKITASYEDRVTFLLPTGITFKSV TREDTGTYTCMVSEEGGNSYGEVKVKLIVLVP PSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYT WFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELV FDPLSASDTGEYSCEARNGYGTPMTSNAVRME AVERNVGIVAAVLVTLILLGILVFGIWFAYSR GHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSS FLV*
748	103	1002	MGTKAQVERKLLCLFILAILLCSLALGSVTVHS SEPEVRIPENNPVKLSLAYSGFSSPRVEWKFDQ GDTTRLVCYNNKITASYEDRVTFLLPTGITFKSV TREDTGTYTCMVSEEGGNSYGEVKVKLIVLVP PSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYT WFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELV FDPLSASDTGEYSCEARNGYGTPMTSNAVRME AVERNVGIVAAVLVTLILLGILVFGIWFAYSR GHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSS FLV*
749	970	1263	MPSSFFLLLRFFLRIDGVLIRMNDTRYHEADK TYMLREYTSRESKISSLMHVPPSLFTEPNEISQY

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			LPIKEAVCEKLIFPERIDPNPADSQKSTQVE
750	1207	887	MYTRELLAWIQGLYTWELLAWIQHLNTWELL PWIRRLNSWILLVCPKLLHLWVFGKTMEIFVLV KDMMPFLYKKELCLVPEVISLLIFSHLDTSKELS IYGLTQLI*
751	1207	887	MYTRELLAWIQGLYTWELLAWIQHLNTWELL PWIRRLNSWILLVCPKLLHLWVFGKTMEIFVLV KDMMPFLYKKELCLVPEVISLLIFSHLDTSKELS IYGLTQLI*
752	43	948	MFSHLPFDCVLLLLLLLLLRSSEVEYRAEVGQN AYLPCFYTPAAPGNLVPVCWGKGACPVFECGN VVLRTDERDVNYWTSRYWLNNGDFRKGDVSLT IENVTLADSGIYCCRIQIPGIMNDEKFNKLKLVK PAKVTPAPTLQRDFTAAPRMLTTRGHGPAET QTLGSLPDINLTQISTLANELRDSRLANDLRDSG ATIRIGIYIGAGICAGLALALIFGALIFKWYSHSK EKIQNLSLISLANLPPSGLANAVAEGIRSEENIYT IEENVYVEVEEPNEYCYVSSRQQPSQPLGCRFA MP*
753	2350	2180	MGGVAFLLWLTVFSAWTRLSIFSRLSDLPSFCL PLAGTVSSSLPEGSGCSFSSSTK*
754	369	707	MCHWQNSFLCQSFLTFGSILALLAGKACYPESE SIRELFMWALELYSLPFYLFKLSPLNLPKGLGL IETLSTCWGQKLDPVLETQLQRVRSMA SLIANFF VPFIQKKGQLIT*
755	847	149	MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSP GQTASITCSGDNLGKNKYVAWYQQKAGQSPVL VIYQDDKRPSEIPERFSGSNSGNTATLTISGTQA MDEADYYCQAWDSSTAVMFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGA VTVAWKADSSPVKAGVETTPSKQSNKYAA SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS*
756	1726	1869	MGAGCTPVVLGAALWLWRWFSRWGLGGLCW RPCTCTPCHSASPGAGR*
757	167	310	MLGICLCSICVLRCLCLEKSKIFPPPTSDHSLEGS VTPVENAARSGM*
758	335	778	MSITRLFPALLECFVIVLCGYIAGRANVITSTQA KGLGNFVSRFALPALLFKNMVVLNFSNVDWAF LYSILIAKASVFFIVCVLTLLVASPDSRFSKAGLF PIFATQSNDFALGYPIGKLIFIFQVFKKFNFNLF HLLVTDSYSHI*
759	102	419	MWLGQAFWAWLSFMNRWHSKFLMVRSRGEC

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			GAQRQLLCVFVFRDSLREGMPRRNMVSSEAHG CLLRTAVFYATYPCTSYAKETKPSACLFPLLIIG KWMLWSFKN*
760	27	371	MSSWFLRAGHGLIWVLFRRIGQAAVGVSAAGP GSPKAHLGRVASQHPHGAESRACLLARGLPKA LSSMLAVDCRPRSGPLHRAAHIMAASLISKPVR GCLSEDDIPSPLSDSAY*
761	428	685	MGWDSKLLFLFTCLSCVTTCSVSTCFQAPLGSS SFAPSGIHGTLEFPVVRGAHKNFLPMGPMYLP ITAGQPLTLFVKTSAGRN*
762	293	3	MCHVHCCWKFFIVELLQCVIQGIKCLYFGNICNG TCFLESCFFGMSFQGANFLFFGNHSSSFYCR MSPFPRGEQVLHFICHVCQCQCQCWCSCGG*
763	38	385	MLLVWFLQLNYKIQAIPTYETVMTFFKSFPENC CFLDRDIGQSLRPLFLCLRLHGITKGKDXEVL HLNFFPESWLDQVTNHYHALENGGDMVHLK DLNTQAVRFGLLFNQENTT
764	508	1374	MLAMGALAGFWILCLLYGYLSWGQALEEEE EGALLAQAGEKLEPSTTSTSQPHLIFILADDQGF RDVGYHGSEIKTPTLDKLAAGVKLENYYVQP ICTPSRSQFITGKYQIHTGLQHSIIRPTQPNCLPL DNATLPQKLKEVGYSTHVMVGKWHLGFYRKEC MPTRRGFDTFGSLGSGDYTHYKCDSPGMC GYDLYENDNAAWDYDNGIYSTQMYTQRVQOI LASHNPTKPIFLYIAVQAVHSPLQAPGRYFEHY RSIININRRRYAAMLSCLEAINNVTALK
765	660	875	MRSYKPNPLLPKQLILFLTSYLITLRYLPGVF NILFKTVLLVFFLQDYSLLISANSSSFQVLSVKT YN*
766	316	456	MDLYVVIFWLVIYFSTYIITYIKGNVGLCFQILF QLSFERRPKSVR*
767	231	584	MSFPIHLRFFSLFFLHWLLLSGFSSLLPWASAFV QYSRCPEHTPSLCPGGANNPLLQAPTQMLPPLG CLLCALPASPSYLCWHLLYHAFRNLLIPLISGA PCGSGIPKFSKCLSVS*
768	135	305	MKNLLMVHLWGICTLYLEFSAVSAISFLNHISV KTYFPNSSSFYRATPMVLDLILH*
769	231	401	MLGWQIWRLRPQLLSFHTQDRCHWSITSQCSK PESQESFLSTIHLLEGAQEGTPT*
770	141	314	MRETGILLCFLSALNYITLVTSQKLILSKKMHV NHYLPKKTISKFLYFVKVFHDLVL*
771	55	276	MKQLIYWFSLFFCCSCCHLNRHGNRLHTTEIFP SLFHLVCCADPLPWMPAHSFGSPFWSLSTYPG

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			RNSRGCQ*
772	139	354	MLLFSLNFFFWKIVMFHKNVIFILTCNGFIIVTF KWIDKFILNISILISNTVNVNSHNPHKQKFFGDL SNF*
773	269	457	MQLKFSQLTTSSLSFSSALWLLAFSRVFLADS NLFVKPSSDLGSDTCSADFCDFRKL SFFR*
774	96	1385	MCPGALWVALPLLSLLAGSLQGKPLQSWGRGS AGGNAHSPLGVPGGGLPEHTFNLKMFLENVKV DFLRSLNLSGVPSQDKTRVEPPQYIMIDL YNRYT SDKSTTPASNIVRSFSMEDAISITATEDFPFQKHI LLFNISIPRHEQITRAELRL YVSCQNHVDPSHDL KGSVVIYDVLDTDAWDSATETKTFLVSQDIQ DEGWETLEVSSAVKRWVRSDSTKSKNKLEVT VESHRKGCDTLDISVPPGSRNLPFFVVSNDHSS GTKETRLELREMISHEQESVLKKLSKDGSTEAG ESSHEEDTDGHVAAGSTLARRKRSAGAGSHCQ KTSLRVNFEDIGWDSWIIAPKEYEAYECKGGCF FPLADDVTPTKHAIVQTLVHLKFPTKV GKACC VPTKLSPISVLYKDDMGVPTLKYHYEGMSVAE CGCR*
775	187	354	MFGMIKRRVRRVAVFVGRTVLCGSCNSGIIMHR GKTPPLKMVCRFEESFSCFLNS*
776	22	168	MGFLFLDLSALMQTWVTVIDVSLHHVEIKAPRI RLMWSLPLRRQKYTM*
777	37	357	MLATLACMAIPWTHLGCSCLLACLPFSHHGL SEDIISSEKPSVTMLSKILQHFHPLSHYSAFSET LVLPEYLFCLASFLPHYHVSFLRVRDLVRDN HCILRV*
778	85	225	MHTPHLPNIIVYFILLYICSQYLYLLTIRHNHLT QSLFYNKLLSVL*
779	187	396	MPVTPDPSAVSLFVTPWPLLLCLPWPHRVPGQS HPGLHSRAPVHRLKPGPPARLQLPAAHRNLRH LSIF*
780	9	218	MSWYTCQCLFFLSNLTNRNGATSWYCSRDD MQMVDFFSSTYERIFRPFFVKIKGPDSFRIDMSPI PEDI*
781	398	192	MARSARTFLLSSTWHLTKFPMSAGYFSPCSWL AAVIRLIQRVLMFFFFRYRALVHFTKARITVLT ANL*
782	216	791	MAGPELLDSNIRLWVVLPIVIITFFVGMIRHYV SILLQSDKKLTQEVSQVLSRVLRENGK YI PKQSFLTRKYFNNPEDGFFKTKRKVVPSP MTDPTMLTDMMKGNVTNVLPILIGGWINMT

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			FSGFVTTKVPFPLTLRFKPMQLQQGIELLTLDAS WVSSASLGTSPMVFGLRSIYSSDSGPR*
783	285	440	MLFVVLPLLIIVFNI PMREAVDFLFMIKIKVLK VFYCIACFIKQALVF*
784	277	471	MVTYFIKCFHYEVSFLLWFAVVRNDVDRPVSL SLFSSYSLFSTYPDTCPLFKLPHTLLCCLEEI*
785	256	429	MAVPIMLFYFSLLYKSLAFFESYSFAEYHPPTSG RQGCVKDILKRLIWFLIHLHLDAG
786	412	672	MAVKNALVITWAYYGFVKVTL SLLVFCVYCM YVILHLRMYITHKGACRHM SASWLATNCLWP WGCHSTFHLEIENNNTIILLELCA*
787	778	975	MFGVSGFCLLFTFLELVLLGLGRWWRTWKHK SSSSKYFLTSESTRRHKKATDSLPPVETKEQFQ EA
788	15	1334	MAAARCWRPLL RGPRLSLHTAANAAATATET TCQDVAATPVARYPPIVASMTADSKAARLRRIE RWQATVHAAESVDEKLRLTKMQFMKYMVYP QTFALNADRWYQYFTKTVFLSGLPPPPAEPEPE PEPEPEPALDLAALRAVACDCLLQEHFYLRRRR RVHRYEESEVISLPFLDQLVSTLVGLLSPHPAL AAAALDYRCPVHFYWVRGEEIIPRGHRRGRID DLRYQIDDKPNNQIRISKQLAEFVPLDYSVPPIEP TIKCKPDKLPLFKRQYENHIFVGSKTADPCCYG HTQFHLLPDKLRRLRRQNCADQIEVVFRAN AIASLFAWTGAQAMYQGFWSEADVTRPFVSQ AVITDGKYFSFFCYQLNTLALTTQADQNNPRK NICWGTQSKPLYETIEDNDVKGFNDDEVLLQIVH FLLNRPKEEKSQLEN*
789	680	880	MGLFAIHSSWLLRACFLIENFESVLYISNTHPFI YMGLHRFFSQPSVWILLFLTGPLNTKSYH*
790	85	315	MFKVVFCFGLVWFCFQRAHKPIRFEKHNFINE GNLFMNIPIVTIRSHHRTSCYHKLITCEQQTVF TNIKRHSL*
791	112	273	MNLYLFAVLFFYVFLHIKIIFICFATKWHNLFSK FSYFCILHVKALS LNLGSG*
792	142	297	MYSLSLQLPVL CVLKSFKAYSLLWGVSTGVKE GFAGRTIVNHESYYLRIVW*
793	127	315	MCTLFMHLLFCHLQSIQLKQELRLNYLTLTQF WQRCYSEMIFCLSKVFLHVFQDGLEHHLE*
794	1401	1553	MFATTLGVMGLWSGHICTVFQAVCFGLGFIIQLN WKKACQQGALKTLKEF*
795	181	390	MHLTSLLLFSLHFPTYIIRVNFCLVSNLFQMR STKLLRLIDLDFSFTFSLDLPPVNEYDMYIRNF

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			GK
796	849	1322	MVKSVIFLSFWQGMLLAILEKCGAIPKIHSARV SVGEGTVAAGYQDFIICGEMFFAALALRHAFT YKVYADKRLDAQGRCAPMKSISSSLKETMNP DIVQDAIHNFSPAYQQYTQQSTLEPGPTWRGG AHGLSRSHSLSGARDNEKTLLLSSDDEF*
797	80	271	MGKKVTLLQKCAWLLVCCLFTGIKYLKCF ITDRELLRDVHNALNLRHNFYVNWASLNTF*
798	249	518	MVQLFIPILKFQLGYSVLSLCNHVLEFLFPSSLS GIFSSSLPLLFPPLSLPSPSLPFLRVLLCHPH WSVASNSWAVAILLPQPE*
799	481	651	MYLLILLSTKFSCISSLPGLDYRQDSMLCQGSL APTLIIHLFMCIMIKYKPLIR*
800	148	288	MCVHPYVCTCACMHVCVCLCAWCLSQQPGLG GFSEEVTS�PRPRAL*
801	154	510	MLFLKKIQFLKCNKVFRSLDFCVALLFSSSA VLQITPVDTFSDPHLVLTLVKLLMNILNIAVISL TFPGEYEVSLAFENILMYTHAFIICFCNRQWLK SNSESNLSSNVNLFDC*
802	99	434	MQLHGKGSQDPSTKGHIKALQTVTSFLLCAIY FLSMIISVCNFRLEKQPVFMFCQAIIFSYPSTHP FILILGNKKLKQIFLSVLRHVRYWVKDRSLRLH RFTRGALCVF*
803	1189	233	MAPWAEAEHSALNPLRAVWLTLTAAFLLTLL QLLPPGLLPGCAIFQDLIRYGKTKCGEPSRPAAC RAFDVPKRYFSHFYIISVLWNGFLLWCLTQSLF LGAPFPSWLHGLLRILGAAQFQGGELALSAFLV LVFLWLHSLRRLFECLYVSFVSNVMIHVQYC FGLVYYVLVGLTVLSQVPMDGRNAYITGKNLL MQARWFHILGMMMFIVSSAHQYKCHVILGNL RKNKAGVVIHCNHRIPFGDWFEYVSSPNYLAE LMIYVSMAVTFGFHNLTWWLVVTNVFFNQAL SAFLSHQFYKSKFVSYPKHKRAFLPFLF*
804	92	1246	MEFGLSWLFLVAILKGVQCEVQLVESGGGLVQ PGGSLRLSCAASGFTFSSYAMSWVRQAPGKGL EWVSGLSGSGGSSTYYADSVKGRFTISRDNK GTLYLQMNSLRADDATARYYCAKGGVELASTK PSSIWRNLPIRYWYFDLWGQGTLVTVSSGDGSS GGSGGASTGEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPTTFGQGTQVDIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQ



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			SGNSQESVTEQDSKDYSLSSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC*
805	92	1246	MEFGLSWLFLVAILKGVQCEVQLVESGGGLVQ PGGSLRLSCAASGFTFSSYAMSWVRQAPGKGL EWVSGLSGSGGSSTYYADSVKGRFTISRDN SK GTLYLQMNSLRADDTARYYCAKGGVELASTK PSSIWRLNPIRYWYFDLWGQGTLLTVSSGDGSS GSGGASTGEIVLTQSPGTLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPTTFGQGTKVDIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDYSLSSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC*
806	92	1246	MEFGLSWLFLVAILKGVQCEVQLVESGGGLVQ PGGSLRLSCAASGFTFSSYAMSWVRQAPGKGL EWVSGLSGSGGSSTYYADSVKGRFTISRDN SK GTLYLQMNSLRADDTARYYCAKGGVELASTK PSSIWRLNPIRYWYFDLWGQGTLLTVSSGDGSS GSGGASTGEIVLTQSPGTLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPTTFGQGTKVDIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDYSLSSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC*
807	92	1246	MEFGLSWLFLVAILKGVQCEVQLVESGGGLVQ PGGSLRLSCAASGFTFSSYAMSWVRQAPGKGL EWVSGLSGSGGSSTYYADSVKGRFTISRDN SK GTLYLQMNSLRADDTARYYCAKGGVELASTK PSSIWRLNPIRYWYFDLWGQGTLLTVSSGDGSS GSGGASTGEIVLTQSPGTLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPTTFGQGTKVDIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDYSLSSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC*
808	63	203	MFPPYFSLILLLFTFASKFFLSLNLKKSNIWKARI ESTKTVISKRC*
809	157	387	MQSVIRKQFTALAGFCFWFCLFTLAVLSLTLLI CKLRIMPFKLEGLFQELNKS WHMKLLSQDRELI NMLLLMGRS*

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810	50	3616	MDLPRGLVVAWALS LWP GFTDTFNMDTRKPR VIPGSR TAFFGYTVQQH DISGNKWL VVGAPLET NGYQKTGDVYKCPVIHGNCTKLN LGRVTL SNV SERKDNMRLGLSLATNP KDNSFLACSP LWSHE CGSSYYTTGMCSR VNSNFRFSKTVAPALQRCQ TYMDIVIVLDGS NSIYPWVEVQHFLINILKKFYI GPGQIQVGVVQYGEDVVHEFHLNDYRSVKDV VEAASHIEQRGGTETR TAFGIEFARSEAFQKGG RKGAKKVMIVITDGESH DSPLEKVIQQSERDN VTRYAVAVLGYYNRRGINPETFLNEIKYIASDP DDKHFFNVTDEAALKDIVDALGDRIFSLEGTNK NETSFGLEMSQTGFSSHVVEDGVLLGAVGAYD WNGAVLKETSAGKVIPLRESYLKEFPEELKNH GAYLGYYTVTSVVS SRQGRVYVAGAPRFNHTG KVILFTMHNNRSLTIHQAMRGQQIGSYFGSEITS VDIDGDGVTDVLLVGAPMYFNEGRERGRKVYV YELRQNR FVYNGTLKDSHSYQNARFGSSIASV RDLNQDSYNDVVVGAPLEDNHAGAIYIFHGFR GSILKTPKQRITASELATGLQYFGCSIHGQLDLN EDGLIDLAVGALGNAVILWSRPVVQINASLHFE PSKINIFHRDCKRSGRDATCLAAFLCFTPIFLAP HFQTTTVGIRYNATMDERRYTPRAHLDEGGDR FTNRAVLLSSGQELCERINFHVLD TADYVKPVT FSVEYSLEDPDHGPMLDDGWPTTLRVSVPFWN GCNEDEHCVPDLVLDARSDLP TAMEY CQRVLR KPAQDCSAYTLSFDTTVFIIESTRQRVAVEATLE NRGENAYSTVLNISQSANLQFASLIQKEDSDGSI ECVNEERR LQKQVCNVSYPFFRAKAKVAFRLD FEFSKSIFLHHLEIELAAGSDSNERDSTKEDNVA PLRFHLKYEVDVLFTRSSSLSHYEVKPNSSLER YDGIGPPFSCIFRIQNLGLFPIHGMMMKITIPIAT RSGNRLLKL RDLTDEANTSCNIWGNSTEYRPT PVEEDLRRAPQLNHSNSDVVSINCNIRLV PNQEI NFHLLGNLWLRSLKALKYKSMKIMVNAALQR QFHSPFIFREEDPSRQIVFEISKQEDWQVPIWIIV GSTLGGLLLLALLVLALWKL GFFRSARRRREP GLDPTPKVLE*
811	261	419	MALNIIINPVWFCHCLTCTIHIDFHILFIKIFKHM FFRSLWSSWLSHQLDHI*
812	49	282	MAIFPLWKG VNVLCIFSSFIMLNIYCTLLIWKF IYSAFFCYITSLMIFPFSFFCSFFLDLLK VIVYIFF LYLYSSR*
813	147	293	MGYLLWL VLSILVCTELGLGRLTFPLDSESPRT

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			SYKVRPWVVLEAWVW*
814	418	155	MCLSHLVSLFPAATAFLINKVPLPVDKLAPLPL DNILPFMDPLKLLKTLGISVEHLVEGLRKCVN ELGPEASEAVKKLLEALSHLV*
815	32	742	MAWIPLFLGVLAYCTGAVASYELTQPPSVSVSP GQTASITCSGDLGDKIACWYQLKPGQSPLVVI HQDTPKPSGIPERFSGSNSGNTATLTISGTQAM DEADYYCQAWDSSSYVAFGGGKLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGVV TVAWKADSSPVKAGVETTTPSKQSNKYAVSS YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP TEYLLRVY*
816	160	1701	MPGLGRRAQWLCWWGLLCSGPPPLRPPL PAAAAAAGGQLLDGGSPGRTEQPPSPQSSS GFLYRRLKTQEKREMQEILSVLGLPHRPRPLH GLQQPQPALRQQEEQQQQQQLPRGEPPPGR KSAPLFMLDLYNALSADNDEGASEGERQQS WPHEAASSQRRQPPGAHPLNRKSLAPGS GSGGASPLTSAQDSAFNDADMVMSFVNLVEY DKEFSPQRHHKEFKFNLSQIPEGEVVTAAEFRI YKDCVMGSFKNQTFLLISYQVLQEHQHRDSDLF LLDTRVWVWASKEGWLEFDITATSNLWVVTQ NMGLQLSVVTRDGVHVHPRAAGLVGRDGPYD KQPFMVAFFKVSEVHVRTTRSASSRRRQQRN RSTQSQDVARVSSASDYNSELKTACRKHLY VSFQDLGWQDWIAPKGYAANYCDGECSPFLN AHMNATNHAIVQTLVHLMNPEYVPKPCCAPT KLNALSVLYFDDNSNVILKKYRNMVVRACGCH *
817	7	942	MGCRLCCAVLCLLGAVPMETGVTQTTPRHLV MGMTNKKSLKCEQHLGHNAMEYWKQSAKKP LELMFVYNFKEQTENNSVPSRFSPECNSSLF LHLHTLPEDSALYLCASSQVGGYNEQFFGPG TRLTVLEDLKNVFPPEVAVFEPSEAEISHTQKA TLVCLATGFYPDHVELSWVNGKEVHSGVST DPQPLKEQPALNDSRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPVQIVS AEA WGRADCGFTSESYQQGVLSATILYEILLGK ATLYAVLVLSALVLMAMVVKRKDSRG*
818	1355	1672	MALLCICLCLIFFLIVKARRKQAAGRPEKMDDE DPIMGTITSGSRKKPWPDSPGDQASPPGDAPPL EEQKELHYASLSFSEMKSREPQDQEAPSTTEYS EIKTSK*

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819	3461	3685	MVVGIVAAAALCILILLYAMYKYRNRDEGSYQ VDETRNYISNSAQSNGLTMKEKQSSKSGHKK QKNKDREYYV*
820	3461	3685	MVVGIVAAAALCILILLYAMYKYRNRDEGSYQ VDETRNYISNSAQSNGLTMKEKQSSKSGHKK QKNKDREYYV*
821	129	272	MGSLMPLRPLALHTALGAALNFSLPCEWSTLPS ASEAGRLWGPPSFQ*
822	98	1474	MAWASRLGLLLALLLPVVGASTPGTVVRLNK AALS YVSEIGKAPLQRALQVTVPHFLDWSGEA LQPTRIRILNVHVPRLHLKFIAGFGVRLAAANF TFKVFRAPELELTLPVELLADTRVTQSSIRTPV VSISACSLFSGHANEFDGSNSTSHALLVLVQKHI KAVLSNKLCLISISNLVQGVNVHLGTLIGLNPVG PESQIRYSMVSVPTVTSDYISLEVNAVLFLLGKP IILPTDATPFVLPRHVGTEGSMATVGLSQQLFDS ALLLQKAGALNLDITGQLRSDNLLNTSALG RLIPEVARQFPEPMPVVLKVRLGATPVAMLHT NNATLRLQPFVEVLATASNSAFQSLFSLDVVVN LRLQLSVSKVKLQGTTSVLGDVQLTVASSNVG FIDTDQVRTLMGTVFEEKPLLDHLNALLAMGIA LPGVVNLHYVAPEIFVYEGYVVISSGLFYQS*
823	177	377	MKLVLRLKTSLSVFTTLFSVSSSQYPVLSTICN TPVFSTLFLEACSVNPLPSTVFLVLLYSVACL*
824	1629	1123	MIFVLGQAEGILIMLMTALTVRSEPSLSTCQ QGEDPLDWTVSLLLMAGLCTFFSCILAVFFHTP YRRLQAESGEPSTRNAVGSQTQGRVWTEGEA RKGLGSWGPARRIPELHGEAGASLRGPQEGHG SPHPACHRATPRAQGAATDAPFPPGQTRRQGP SVQVY*
825	381	572	MLLAKRYAKYFIYFIFNPVLIPILQRRILRLGEI HIAGQCRAGSLQSLPLPANLHSILDILA*
826	758	618	MLLCLHLIHCIVFCIISAIPWVLNQCLIFRLYFLC QKKLAMSLN*
827	184	360	MLIGSGYLCFCALQWTELGNVCVCAHICRCH MQVSGITSPVHVHHRVLSCLIHFTS*
828	140	355	MHLLVSHAFLPFPLHGYSGRQGAQWRCHP ARASRERPSEDNLSPAVKEESGFVVSEHLAALH RKLRGCH*
829	21	956	MLLLLLLLGLAGSGLGAVVSQHPSWVICKSGT SVKIECRSLDFQATTMFWRQFPKQSLMLMAT SNEGSKATYEQGVEKDKFLINHASLTSTLTVT SAHPEDSSFYICSAGADSGTQETQYFGPGRILT

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			VLEDLKNVFPPEVAVFEPSEAEISHTQKATLVC LATGFYPDHVELSWVNGKEVHSGVSTDPQP LKEQPALNDSRYCLSSRLRVSAITFWQNPRNHF RCQVQFYGLSENDEWTQDRAKPVTQIVSAEA WGRADCGFTSESYQQGVLSATILYEILLGKATL YAVLVSALVLMAMVKRKDSRG*
830	134	292	MSVGLHLGFLAWFLPFLIPTSPPLLFQLGALPN ESLALYAWLRDCFWENIT*
831	58	258	MSSPCFQCFHLCCTIKVWPLCHHLQKAFPDFS HVFSESDLSSFCEVQLLKICLKQYFLGSLMHCS*
832	68	259	MIKLCHQLYNVYVCFHLLVGLDIAIDYIIVPNIS YLSISIPFVVTNIRGRDIFHPCNVALVM*
833	290	430	MFYENKRREYLQDMLLSYRLLVAILVLLKKLT ELNTITLICKSIIF*
834	112	267	MNIVFVILLFKDMQVLEVFVLLNVLTTLTHIAA GILCTSFCKPFIYNPL*
835	58	240	MIRFALPWFSQIWLSKQTWTRLTHLAFLQEC NSMFYPKVSRITTVFGCLFNPLSSRVCFE*
836	30	296	MTNFFHLLPLPSLFSPSSKTHSFNIHKIIILFF NSIFLYPRDYLKIRNWLQSNLTEREIEWITSIRCL CNSGTTFIFPLTTKST*
837	1089	952	MLYLLFPGVSYLRSFLGRPIGPGITSDFTLILF SNLLDSWPLS*
838	500	670	MPCSVPETLFSLLWLAPSHHSGFSSNEASLRD LLFATAILYSLWHPPYYFLYNTS*
839	84	251	MLFTSFVYGLIFILFDFYFLSFVERDVKIFNCNG EIVLFPFNSVHFCLICLYIHI*
840	99	245	MILNLSSLTLVFAWNYPLHLMISLNVSCSCYSD DISGIYRSVLRQKLG*
841	82	297	MCLILVIWKIHYAELIMLNKRNVNKCRCCLIQK CLSTCHSTVIVLYQCREEEAVMLIKLNFKMKIQ RTICI*
842	36	275	MNLKRLLFLAKMFSAIFSLPHPSHPISIDNI GHWPQSPKVRKEGNEYLLNPNMCQTLDTLL GIGDYLTSTSP*
843	165	437	MAPLPSLTLRPWCVLMLLDLWAAFGTITPSLK HFHHLPSGTQHSLVFVLSLTLHSQSLLMGTSA VCLSACFSSLSTFPGWLLICTLMI*
844	322	462	MFLDLCLGSLSVFIDTHPCMHHGGFKCSQDWC SPAKLLLSAFTKTR*
845	182	358	MLSLVKLLLLCIHDHSINFCIAIQVGLLPSAYR VPGIVLSLENTALIRQTPCSNRAN*
846	98	805	MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELI

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			PDAPLSSAAYSIRSIGERPVLKAPVPKRQKCDH WTPCPSDTYAYRLLSGGGRSKYAKICFEDNLL MGEQLGNVARGINIAIVNYVTGNVTATRCFDM YEGDNSGPMTKFIQSAAPKSLLFMVTYDDGST RLNNDAKNAIEALGSKEIRNMKFRSSWVFIAA KGLELPSEIQREKINHSDAKNNRYSGWPAEIQIE GCI PKERS*
847	1608	1805	MLPFCHLWVPVTLVAAGAAQPAASMVMFPHL PALHHHCPSHRTSQYMPASDGPQAYPDYAD QST*
848	386	592	MNPCFCGFLVLLSCCLSLDSQLHNLIALQITCF KDVEIPNFFCDPSQLPHHACCDTFTNNIVMYFP AA
849	1074	2294	MLLLLLLLPLLWGTKGMEGDRQYGDGYLLQV QELVTVQEGLCVHVPCSFSYPQDGWTDSDPVH GYWFRAGDRPYQDAPVATNNPDREVQAETQG RFQLLGDIWSNDCSLSIRDARKRDKGSYFFRLE RGSMKWSYKSQLNYKTKQLSVFVTDPPWNLT MTVFQGDATASTALGNGSSLSVLEGQSLRLVC AVNSNPPARLSWTRGSLTLCPSRSSNPGLLELP RVHVRDEGEFTCRAQNAQGSQHISLSLSLQNE GTGTSRPVSQVTLAAVGGAGATALAFLSFCIIFI IVRSCRKKSARPAAGVGDGTGMEDAKAIRGSAS QGPLETSWKDGNPLKKPPPAVAPSSGEEGELH YATLSFHKVKPQDPQGQEATDSEYSEIKIHKRE TAETQACLRNHNPPSSKEVRG*
850	100	318	MYYTLCNFVFFTLHMILFPKSLNILLSNQIRSAI VHLKQRTSCIKNQPEPYQRADAMNTNHS�VAV PYVNLI*
851	328	549	MFWMVKILTPKASTFQVTTSVSVPLTSATGAA CSGSCFHSTGCAGRPQTHAGAPCASEQNSRNE VMQTSTNEM*
852	162	440	MHCRQLKEVLQLPLTCSSCCVCTMTVAFPSVQ QVWMETVLTGGLDAAQDEIQAVRLILLPESSP QGPHGNLAPCSAKPFFLPQVMPLGTAP*
853	39	839	MVCLRLPGGSCMAVLTVTLMVLSSPLALAGDT RPRFLEYSTSECHFFNGTERVRFLDRYFYNQEE YVRFSDVGEFRAVTELGRPDEEYWNSQKDFL EDRRAAVDITYCRHNYGVVESFTVQRRVHPKV TVYPSKTQPLQHNLVCSVSGFYPGSIEVRWF RNGQEEKTGVVSTGLIHNGDWTFQTLVMLETV PRSGEVYTCQVEHPSVTSPLTVEWRARSESAQS KMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSG

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			LQPRGFSL*
854	54	1034	MMSPSQASLLFLNVCIFICGEVVQGNVCVHHSTD SSVNVNIVEDGSNAKDESKSNDTVCKEDCEESC DVKTKITREEKHFMCRNLQNSIVSYTRSTKKLL RNMMDEQQASLDYLSNQVNELMNRVLLLTTE VFRKQLDPFPHRPVQSHGLDCTDIKDTIGSVTK TPSGLYIIHPEGSSYPFEVMCDMDYRGGGWTVI QKRIDGIIDFQRLWCDYLDGFGDLLGDAFRGL KKEDNQNAMPFSTSDVDNDGCRPACLVNGQS VKSCSHLHNKTGWWFNECGLANLNGIHHFSG KLLATGIQWGTWTKNNSPVKIKSVSMKIRRM NPYFK*
855	124	336	MRTWSKVIPSLWLKFSRGFILRFHFLMIWPDIP SSMYICMSFITAFKNLFMFGINRIKKISVVS RNTL*
856	159	1028	MGLCVPFAVTTSFSLGLEWDLNVR LHGQHLV QQLVLRVTVRGYLETPQPEKALALSFHGWSGTG KNFVARMLVENLYRDGLMSDCVRMFIA TFHFP HPKYVDLYKEQLMSQIRETQQ LCHQTLFIFDEA EKLHPGLLEV LGPHLERRAPEGHRAESPWTIFL FLSNLRGDIINEVVLKLLKAGWSREEITMEHLE PHLQAEIVETIDNGFGHSRLVKENLIDYFIPFLPL EYRHVRLCARD AFLSQELLYKEETLDEIAQMM VYVPKEEQLFSSQGCKSISQRINYFLS*
857	182	334	MKSSNIFSLFLFLVT FIFLTSIASILFSSWCPFS LIKCNQDLYYSGNGAS*
858	35	172	MLCSLFHILIVTLLLAISFGMSSRNTLNMVNSKI KEHSLHRKLEI*
859	6	215	MFWTLVQGMSLLCLTDVFQALPSICIANSEIYY TVLTLMQFNCLWMVLSGKKVIFSSSELMVRKGR RSWK*
860	204	350	MYLKPLIYFSILIFLSQRSKLSLPYNVHNCMNIG EDRRPQKVQLQLY*
861	263	412	MLPLALIVDLIYPWVQVRGPEDPNHGTTERKR EEVTCLGAARLSLEAAR*
862	169	879	MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHA WPSSVVEAESNVTLKCAHSQNVTFVLRKVND SGYKQEQSSAENEAEPFTDLKPKDAGRYFCA YKTTASHEWSESSEHLQLVVTDKHDELEAPSM KTDTRTIFVAIFSCISILLFLSVFIIYRCSQHSSSS EESTKRTSHSKLPEQEAADLSNMERVSLSTA DPQGVTYAELSTSALSEAASDTTQEPPGSHEYA ALKV*

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863	114	1031	MPLLTLYLLFWLSGYSIATQITGPTTVNGLER GSLTVQCVRSGWETYLKWWCRGAIWRDCKI LVKTSQSEQEVKRDRVSIKDNQKNRTFTVTME DLMKTDADTYWCGIEKTGNDLGVTVQVTIDP ASTPAPTTPTSTTFTAPVTQEETSSSPTLTGHHL DNRHKLLKLSVLLPLIFTILLLLLVAASLLAWR MMKYQQKAAGMSPEQVLQPLEGDLCYADLTL QLAGTSPQKATTKLSSAQVDQVEVEYVTMASL PKEDISYASLTLGAEDQEPTYCNMGLSSHLP RGPEEPTYSTISRP*
864	64	435	MRISCPWCLWNLSLEVGGTVATTAQQHIAEVC RSSQAGRGLHCLHPALGTSGCHPVPCSSSLVG FGWRGYSGEASWGRASSRPAAPTPMPANVQ AGWEQSVRLCHSWRLAALHVTHEES*
865	391	528	MSQQSWFTVYLFYLLRSNIWLEMGIPKYVKEV ELRSLDFTSNYFS*
866	46	612	MDWTWRFLFVVAATGVQSQVQLVQSGAEV KKPGSSVKVSCASGGTFSTYAISWVRQAPGQ GLEWMGGIPIFGTANYAQKFQGRVTITADEST STAYMELSSLRSEDVAVYYCARVWGGSGSYYS IVSTIGATTTVWMSGAREPWSPSPQPPRAHRS SPWHPPPRAPLGAQRPWAAWSRTTSPNR*
867	46	612	MDWTWRFLFVVAATGVQSQVQLVQSGAEV KKPGSSVKVSCASGGTFSTYAISWVRQAPGQ GLEWMGGIPIFGTANYAQKFQGRVTITADEST STAYMELSSLRSEDVAVYYCARVWGGSGSYYS IVSTIGATTTVWMSGAREPWSPSPQPPRAHRS SPWHPPPRAPLGAQRPWAAWSRTTSPNR*
868	133	960	MACPGFLWALVISTCLEFSMAQTVTQSQPEMS VQEAETVTLSTYDTSSESDYYLFWYKOPPSRQ MILVIRQEAYKQQNATENRFSVNFQKAASFSL KISDSQLGDAAMYFCA YRSGRDDKIIFGKGTRL HILPNIQNPDPAVYQLRDSKSSDKSVCLFTDFDS QTNVSQSKSDVYITDKTVLDMRSMDFKNSA VAWSNKSDFACANAFNNSIIPEDTFFPSPESSCD VKLVEKSFETDTNLFQNLVIGFRILLKLVAG FNLLMTLRLWSS*
869	164	310	MVLRLPWGVLAYGNDVGFGFYSLCYQINP PTCPILWLWEVLTVGKS*
870	959	1252	MEFLGPCGLRLVGARPLLPYWLLVFLAALNAL LQWLLRPLVLYAPLLNPYTLAVANTTFTVSTD KAQRHFGYEPFWSWEDSRTRTILWVQAATGSA Q*



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871	52	828	MPPRRVSQLLDLCLWCFMKNISRYLTDIKPLP PNIKDRLIKIMSMQGQITDSNISEILHPEVQTLDL RSCDISDAALLHLSNCRKLKKLNLNASKGNRV SVTSEGIKAVASSCSYLHEASLKRCCLNLTDEGV VALALNCQLLKIIDLGGCLSITDVSLHALGKNC PFLQCVDFSATQVSDSGVIALVSGPCAkkLEEI HMGHCVNLTGAVEAVLTYPQIRILLFHGCP LITDHSREVLEQLVGPnkLKQVTWTVY*
872	313	1704	MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQ EGLCVHVPCSFSYPSHGWIYPGPVVHGYWFRE GANTDQDAPVATNNPARAVWEETRDRFHLLG DPHTENCTLSIRDARRSDAGRYFFRMEKGSIKW NYKHHRLSVNVTALTHRPNILPGTLESGCPQN LTCSVPWACEQGTPPMISWIGTSVSPLDPSTTRS SVLTLIPQPQDHGTS LTCQVTFPGASVTTNKTV HLNVSYPQNL TMTVFQGDGT VSTVLGNGSSL SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGL TLCPSQPSNPGVLELPWVHLRDEDEFTCRAQNP LGSQQVYLVNLSLQSKATSGVTQGA VGGAGAT ALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTI EDANAVRGSA SQPLTEPWAEDSPDQPPAS ARSSVGE GELQYASLSFQMVKPWDSRGQEATD TEYSEIKIHR*
873	590	766	MLFGLALQLLDLKLTTVNQRES DVARVATAE EYSKKGLLGQETLHAGSQTRMQILIS*
874	206	418	MLKLLCAA EVTNVLFNCVFDYGC PKTFCHPWT IFVLFWSSLEGGFIISYKTLTGAL ECRFLITLEIVT SE*
875	241	957	MRSSLTMVGTLWAFSLVTA VTSSTSYFLPYW LFGSQMGKPVSFSTFRR CNYPVRGEGHSLIMVE ECGRYASFNAIPSLAWQMCTVVTGAGCALLL VALAAVLGCCMEELIS RMMGRCMGAAQFVGG LLISSGCALYPLGWNSPEIMQT CGNVSNQFQLG TCRLGWAYYCAGGGAAAAMLICTWLSCFAGR NPKPVILGGKHHEENHFLCYGAWPLPSTLELRK EDRGG RATGKQVTP
876	241	957	MRSSLTMVGTLWAFSLVTA VTSSTSYFLPYW LFGSQMGKPVSFSTFRR CNYPVRGEGHSLIMVE ECGRYASFNAIPSLAWQMCTVVTGAGCALLL VALAAVLGCCMEELIS RMMGRCMGAAQFVGG LLISSGCALYPLGWNSPEIMQT CGNVSNQFQLG TCRLGWAYYCAGGGAAAAMLICTWLSCFAGR NPKPVILGGKHHEENHFLCYGAWPLPSTLELRK

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			EDRGGRATGKQVTP
877	136	1710	MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLA RILAWTYAFYNNCRRLQCFPPPKRNWFWGH LGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIP FIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWL GEGILLSGGDKWSRHRRLTPAFHFNILKSYITI FNKSANIMLDKWQHLLASEGSSCLDMFEHISLM TLDSLQKCFISFDSHCQERPSEYIATILELSALVE KRSQHILQHMDFLYYLSHDGRRFHRACRLVHD FTDAVIRERRRTLPTQGIDDFKDKAKSKTLDI DVLLLSKDEDGKALSDEDIRAEADTFMFGGHD TTASGLSWVLYNLARHPEYQERCRCQEVQELLK DRDPKEIEWDDLAQLPFLTMCVKESLRLHPPAP FISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNP TVWPDPEVYDPFRFDPENSKGRSPLAFIPFSAGP RNCIGQAFAMAEMKVVLALMMLLHFRFLPDHTE PRRKLELIMRAEGGLWLRVEPLNVSLQ*
878	136	1710	MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLA RILAWTYAFYNNCRRLQCFPPPKRNWFWGH LGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIP FIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWL GEGILLSGGDKWSRHRRLTPAFHFNILKSYITI FNKSANIMLDKWQHLLASEGSSCLDMFEHISLM TLDSLQKCFISFDSHCQERPSEYIATILELSALVE KRSQHILQHMDFLYYLSHDGRRFHRACRLVHD FTDAVIRERRRTLPTQGIDDFKDKAKSKTLDI DVLLLSKDEDGKALSDEDIRAEADTFMFGGHD TTASGLSWVLYNLARHPEYQERCRCQEVQELLK DRDPKEIEWDDLAQLPFLTMCVKESLRLHPPAP FISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNP TVWPDPEVYDPFRFDPENSKGRSPLAFIPFSAGP RNCIGQAFAMAEMKVVLALMMLLHFRFLPDHTE PRRKLELIMRAEGGLWLRVEPLNVSLQ*
879	136	1710	MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLA RILAWTYAFYNNCRRLQCFPPPKRNWFWGH LGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIP FIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWL GEGILLSGGDKWSRHRRLTPAFHFNILKSYITI FNKSANIMLDKWQHLLASEGSSCLDMFEHISLM TLDSLQKCFISFDSHCQERPSEYIATILELSALVE KRSQHILQHMDFLYYLSHDGRRFHRACRLVHD FTDAVIRERRRTLPTQGIDDFKDKAKSKTLDI DVLLLSKDEDGKALSDEDIRAEADTFMFGGHD

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			TTASGLSWVLYNLARHPEYQERCRCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESRLRHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNP TVWPDPEVYDPFRFDPENSKGRSPLAFIPFSAGP RNCIGQAFAMAEMKVVLALMLLHFRFLPDHTE PRRKLELIMRAEGGLWLRVEPLNVSQ*
880	856	257	MRLSLPLLLLLLGAWAIPGGLGVMAPLTATAP EVDDDEEMYSAHMPAHLRCDACRAVAYQECGP KTLAKAETKLHTSNSGGRDVSSELVYTDVLD RSCSRNWQDYG VREVDQVKRLTGPG LSEGPEPS ISVMVTGGPWHTRLSRTCLHYLGEFGEDQIYE AHQQGRGALEALLCGGPPGGLLREGVSHKRRALVLDSTLL*
881	782	1222	MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETES PVRTLQVETLVEPPEPCAEPAAFQDTHIHYTG SLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSL LDMCVGEKRRAIIPSHLAYGKRGFPSPVPGTKDN LMRPPGMTSSSQ*
882	940	2040	MALRFLLGFLLAGVDLG VYLMRLELC DPTQRL RVALAGELVG VGGHFLFLGLALVSKDWRFLQ RMITAPCILFLFYGWPGFLFLESARWLIVKRQIEE AQSVLRILAERNRPHGQMLGEEAQEALQDLEN TCPLPATSSFSFASLLNYRNIWKNLLILGFTNFIA HAIRHCYQPVG GGGGSPSDFYLC SLLASGTAALA CVFLGVTVD RFGRRGILL SMTLTG IASLVLLG LWDYLNEAAITTF SVLGLFSSQAAAILSTLLAA EVIPTTVRGRGLGLIMALGALGGLSGPAQRLH MGHGAFLQHVVLAACALLCILSIMLLPETKRK LLPEVLRD GELCRRPSLLRQPPPTRCDHVPLLA TPNPAL*
883	133	306	MVKRKSWTKWCGWLT VVRFLARGFEMHLKS CSRLLFSELA AFAFFEFSLKTVTLRAF*
884	196	357	MCLMKQIIYLLYVGLCSILTAFLFTPHHVLERY RYYCPDFREIKKLGGQYTTN*
885	252	560	MKEALLKCSRLARGLLLCLDCANDHRSPVERN AQTTLILHSSLYSLSLGNQLQGGGEMATTGGST QQAKTYGGLFQIGAMEPALFLLFIFLLASFVWH RAIE*
886	46	189	MLETFLFKLFLFFTLLVNLFITNDQLSVGSIFLSF QLPAFFLDMAEF*
887	68	208	MTFLLHVLVTALSSHSTGRRGTNCFMLLSSGN HPIPCGSLTPYPHL*
888	214	399	MVYLPVSLNGLRLACFSYVLAPIKVKPGGGSET

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			RDGFRIPSTPSLKAGYCDHKHFLPTIHL
889	50	214	MTLLNLYLNSFLLYSKRFEGISFCVQKVSHILCIHYLRSTTIWNKLFFRDVSA*
890	158	700	MHFPVNCFFKSLHIFLLQVFLATFLRKKLSKVAFSCLVEFFYYCYFLDFASSVSFLFCFVLLLRQSLTLSPRLECSDTILAHCNRLRPGSRYSASTSRVAGITGVHHHTYVNFVWTVQKAVHCVGQASWELLTSRDPPTLASHRAGITGMSHRTWAKVFLKRVIFLNREYDLTMFCFL
891	133	333	MLVPTFLSLVCDFSLFVLLLLGCLSFLPPHLPCTSFPLHLWRLLSPFISFLDLLLLSYKMNCHII*
892	71	295	MLPLFKHSPVRIFLFCNLNTQHLSVRNNFVFNCSVSPGILPISLCLAFNHDRSTFFFSIILLKALILSSLQTK*
893	95	331	MKPILLVLSSITRALLLQISSVSWQSCMWRAMPDCLQTDYPISLGFHQRTLLDALCPVTQCHHSAWPCVCQGAQTPI*
894	182	418	MCCELLAVVIATLIKIGLVVLLYFIKLLIHIEFIKRHSILKCESIFNLNVGIRMYPGQVNFCELTQMLDGFGRIQTK
895	104	2683	MACRWSTKESPRWRSALLLFLAGVYGNALAEHSENVHISGVSTACGETPEQIRAPSGIITSPGWSEYPKINCWFIRANPGEIITISFQDFDIQGSRRCNLDWLTITYKNIESYRACGSTIPPPYISSQDHIWIRFHSDDNISRKGFRLAYFSGKSEEPNCA CDQFRCGNGKCIPEAWKCNMDECGDRSDEEICAKEANPPTAAAFQPCAYNQFQCLSRFTKVYTCLPESLKCDGNIDCLDLGDEIDCDVPTCGQWLKYFYGTFSNPYPDFYPPGSNCTWLIDTGDHRKVILRFTDFKLDGTGYGDYVKIYDGLEENPHKLLRVLTAFDSHAPLTVVSSSGQIRVHFCADKVN AARGFNATYQVDGFCLPWEIPCGGNWGCYTEQQRCDGYWHCPNGRDETNCCTMCQKEEFPCSRNGVCYPRSDRCNYQNHCPNGSDEKNCFFCQPGNFHCKNNRCVFESWVCDSQDDCGDGSDEENC PVIVPTRVITA AVIGSLICGLLLVIALGCTCKLYSLRMFERRSFETQLSRVEAELLRREAPPSYGQLIAQGLIPPVEDFPVCSPNQASVLENLRLAVRSQLGFTSVRLPMAGRSSNIWNRIFNFARSRHSGSLALVSADGDEVVPSQSTSREPERNHHTHRSLSVESDDTDTENERRDMAGASGGVAAPLPQKVPPTTAVEATVGACASSSTQSTRGGHADNGRDVTSVEPPSVSPARHQLTSALSRMTQGLRWVRFTLGRSSS

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			LSQNGSPLRQLDNGVSGREDDDDVEMLIPI SDG SSDFDVNDCSRPLLDLASDQGQGLRQPYNATN PGVRPSNRDGPCERCIVHTAQIPDTCLEVTLK NETSDDEALLC*
896	230	391	MSNRTRIRTHVNLCCFCRYTTPKMSFSSACVSL CLMLLFCSPPLLLLLLSSFV*
897	47	1147	MASMAAVLTWALALLSAFSATQARKGFWDYF SQTSGDKGRVEQIHQQKMAREPATLKDSLEQD LNNMNKFLKLRPLSGSEAPRLPQDPVGMRRQ LQEELEEVKARLQPYMAEAHEL VGWNLEGLR QQLKPYTMDLMEQVALRVQELQEQLRVVGED TKAQLLGGVDEAWALLQGLQSRVVHHTGRFK ELFHPYAESLVSGIGRHVQELHRSVAPHAPASP ARLSRCVQVLSRKLTLKAKALHARIQQNLDQL REELSRAFAGTGTEEGAGPDPQMLSEEVQRQL QAFRQDTYLQIAAFTRAIDQETEEVQQQLAPPP PGHSAFAPEFQQTDSGKVL SKLQARLDDLWED ITHSLHDQGHSHLGDP*
898	493	636	MFIGLGISFLNCPSLFAHFILFCPLPLFGIFISYWF VRLLSINRGWK*
899	92	1195	MEFGLSWLFLVAILKGVQCEVQLVESGGGLVQ PGGSLRLSCAASGFTFSSYAMSWVRQAPGKGL EWVSGFTGSGGSGGSTYYADSVKGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKGLLPPRW AYRVYEDSGIFFDYWGQGTLVTVSSSDIQMTQ SPSTLSASVGDRVTITCRASQSISSWLAWYQQK PGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTL TISSLQPDDFATYYCQQLSTYVWTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNMF YPREAKVQWKVDNALQSGNSQESVTEQDSKD STYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC*
900	948	1115	MLCGNTQLLFTVAIILLYVTCLLHWTFLHLEW RVSEGRHHDPLSTTLMHEKMNDN*
901	722	84	MYRLSSSMLLRALAQAMRTGHLIGQSLHSSAV AATYKYVNKKEQESEVDMKSETDNAARILMW TELIRGLGMLRLRYLFREPATINYPFEKGPLSPRF RGEHALRRYPSGEERCIAACKLCEAICPAQAITIE AEPRADGSRRTTRYDIDMTKCIYCGFCQEACPV DAIVEGPNFEFSTETHEELLYNKEKLLNNGDK WEAEIAANIQADYLYR*
902	50	259	MIELAFASFLKCAFSLLILFSFSFPLWFFLSCFA CSYSFSCLLSRISILSPFCHLLPRQSHDLCTNDL*

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903	194	382	MSVLIWCLIFFPLEYSRPKRGLKVDNVCSTVA LSTGSRISNWSNCETCLLAEMFFLDLGS*
904	44	1000	MAAAAVSGALGRAGWRLQLRCLPVARCRQA LVPRAFHASAVGLRSSDEKQKQPPNSFSQQHSE TQGAEKPDPESSHSPRYTDQGGEEEDYESEE QLQHRILTAALFVPAHGWTAEIAEGAQSLG LSSAAASMFCKDGSSELILHFVTQCNTRLTRVLE EEQKLVLGQAEKRKTDQFLRDAVETRLRLMI PYIEHWPRALSILMLPHNIPSSLSLLTSMVDDM WHYAGDQSTDFNWTTRAMLAAIYNTTELVM MQDSSPDFEDTWRFLNRVNDAMNMGHTAK QVKSTGEALVQGLMGAAVTLKNLTGLNQRR*
905	127	297	MGHLLCVWGFTYILPCISLRHSPLOPPGWEGFC RNVSFLLRASLAPHHRKDGFI*
906	233	484	MHVLIRTPCSLILCLANSSHASLPGFSASSFLFK ESCRLLNSSFLLHGLEILSGAAGQCNSFCFSI SQGSLSFNASCLP*
907	572	787	MTLLWPHTAACLSVTLYLPASSAKYFKRGEGR EKFITNPTTRKKKLFWRGKRNDQAFTGIPDQ VSLFPF*
908	259	552	MYLHVLVLSHRILLSPYIPSFKSVPPPVFSILQM APMSILDIDHPRSLGGDSSHFFSSVAQALTFCPF ALRPFNNYSLQRPVFQKAPAFHHFLVKKF*
909	99	371	MFLVFCNIITVITMTSLFLILLSCIFILITCCYKCR YISFSFTFSVTPSGFFVSILQYLAHILLITLQFHF RVCYVNIITLIPLAQIFL*
910	102	278	MQLWGFLNLFPCSSLCFWALGSRGFTLVAV TPINSTGWAHLPHQVHKMRLFSIQLF*
911	142	360	MLMVLKLVICISIFIGKEGHFVISYLPFSLSNIQDT LKSVHQPCSALSGYNMPEKPEECISIKERHPYSQ RLFLE
912	191	481	MGISCKLLLLTRVCYLITPLDLERFPFPNTEQVT FPERRVSVFLLPLSWCLDTRLPREPGCRHRHSSP QDVVGGSHLVTTTLLSLPAREFWTSCIL*
913	256	393	MILFHCEKLYALRSFDFWFMLELLSTWPRALG LLCPGLAIEAHEG*
914	29	265	MKTLKIFTYYFLSLSNIFILTIGLTCASGPLDFTP VFLLGKGSCLKCKYGPVAHLPEALESQPISG CNWKEIPTSS*
915	79	339	MWLFCAWVSTWGQGCPPGRGQMIYASHHLSV HTTSPHHWLSAWALQGGAVFPELAHGASSASS GQADDSTCSFCSPWRVSAEHKSLT
916	57	1163	MWPALLSHLLPLWPLLLLPLPPPAQDSSSSPR

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			TPPAPARPPCARGGPSAPRHVCVWERAPPPSRS PRVPRSRRQVLPGTAPPATPSGFEEGPPSSQYP WAIVWGPTVSREDGGDPNSANPGFLDYGFAAP HGLATPHPNSDSMRGDGDGLILGEAPATLRPFL FGGRGEGVDPQLYVTITISHIVLVATGIIFKFCW DRSQKRRRPSGQQGALRQESQQPLTDLSPAG VTVLGAFGDSPTPTPDHEEPRGGPRPGMPHPKG APAFQLNRSLSGQRFLHTLPLMCVSRPDVVVV CGVLTLSLMNTHPPRFRSPCMLLQRWVGGEGLG APWALIGHGLVPFHTICFSVSPSYSKDAGITLRA PPWEMG*
917	427	1461	MDFLVFLFYLASVLMGLVLICVCSKTHSLKGL ARGGAQIFSCIIPECLQRAMHGLLHYLFHTRNH TFIVLHLVLQGMVYTEYTWVFGYCQELELSL HYLLLPYLLGVNLFFFTLTCTGNPGIITKANEL LFLHVYEFDEVMFPKNVRCSTCDLRKPARSKH CSVCNWCVHRFDHHCVVWVNNCIGAWNIRYFL IYVLTLTASAATVAIVSTTFLVHLVMSDLYQE TYIDDLGHLHVMDTVFLIQYFLTFPRIVFMLG FVVVLSFLLGGYLLFVLYLAATNQTNEWYRG DWAWCQRCPLVAWPPSAEPQVHRNIHSHGLR SNLQEIFLPAFPCHERKKQE*
918	251	538	MELVLVFLCSSLAPMVLASAAEKEKEMDPFHY DYQTLRIGGLVFAVVLFSVGILLILSRCKCSFN QKPRAPGDEEAQVENLITANATEPQKAEN*
919	1355	1507	MGRRKFLPPLLSLLSSSLPLPICHPPAPLTPGLG IPPCGVVGREVFVSVL*
920	588	292	MRVLLQHLFILLDRQTTKNSNLDIGHVFREA LIFLADLKSQPSVTHHQYRHLPSNWLQLLQCG QDKHCCLSHARLGLAQDIHSQNGLRDALMLDF*
921	588	292	MRVLLQHLFILLDRQTTKNSNLDIGHVFREA LIFLADLKSQPSVTHHQYRHLPSNWLQLLQCG QDKHCCLSHARLGLAQDIHSQNGLRDALMLDF*
922	288	1346	MRSLGALLLLSACLAVSAGPVPTPPDNIQVQE NFNISRIYGKWYNLAIGSTCPWLKKIMDRMTV STLVLGEGATEAEISMTSTRWRKGVCETSGA YEKTDTDGKFLYHKSXWNITMESYVVHTNYD EYAIFLTCKFSRHHGPTITAKLYGRAPQLRETL QDFRVVAQGVGIPEDSIFTMADRGECPGEQEP EPILIPVRRAVLPQEEEGSGGGQLVTEVTKE DSCQLGYSAGPCMGMTSRYFYNGTSMACETF

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			QYGGCMGNGNNFVTEKECLQTCRTVAACNLPI VRGPCRAFIQLWAFDAVKGKCVLFPYGGCQG NGNKFYSEKECREYCGVPGDGDEELLRFSN*
923	510	1880	MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIF GVSFGRKLYMKSLLKIFAWATLRMERGAKEK NHQLYKPYTNGIIAKDPTSLEEEIKEIRRSKSSK ALDNTPEFELSDIFYFCRKGMEITMDDEVTKRF SAEELESWNLLSRTNYNFYISLRLTVLWGLG VLIRYCFLPLRIALFTGISLLVVGTTVVGYLP NGRFKEFMSKHVHLMCYRICVRALTAIITYHD RENRPRNGGICVANHTSPIDVILASDGYAMV GQVHGGLMGVIQRAMVKACPHVWFERSEVKD RHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSV MMFKKGSFEIGATVYPVAIKYDPQFGDAFWNS SKYGMVTYLLRMMTSWAIVCSVWYLPMTRE ADEDVQFANRVKSAIARQGGVLDLLWDGGL KREKVKDTFKEEQKLYSKMIVGNHKDRSR*
924	56	1459	MLLLLLLPLLWGRERVEGQKSNRKDYSLTMQS SVTVQEGMCVHVRCFSYPVDSQTDSDPVHGY WFRAGNDISWKAPVATNNPAWAVQEETRDRF HLLGDPQTKNCTLSIRDARMSDAGRYFFRMEK GNIKWNYKYDQLSVNVTALTHRPNILIPGTLES GCFQNLTCSPWACEQGTTPMISWMGTSVSPL HPSTTRSSVLTLPQPQHHGTSLTQVTLPGAG VTNRTIQLNVSYPPQNLTVTVFQGGEGTASTAL GNSSSLSVLEGQSLRLVCAVDSNPPARLSWTW RSLTLYPSQPSNPLVLELQVHLGDEGEFTCRAQ NSLGSQHVS LNLSLQQEYTGKMRPVSGVLLGA VGGAGATALVFLSFCVIFIVVRSCRKKSARPA DVGDIGMKDANTIRGSASQGNLTESWADDNPR HHGLAAHSSGEEREIQYAPLSFHKGEPQDLSGQ EATNNEYSEIKIPK*
925	56	1459	MLLLLLLPLLWGRERVEGQKSNRKDYSLTMQS SVTVQEGMCVHVRCFSYPVDSQTDSDPVHGY WFRAGNDISWKAPVATNNPAWAVQEETRDRF HLLGDPQTKNCTLSIRDARMSDAGRYFFRMEK GNIKWNYKYDQLSVNVTALTHRPNILIPGTLES GCFQNLTCSPWACEQGTTPMISWMGTSVSPL HPSTTRSSVLTLPQPQHHGTSLTQVTLPGAG VTNRTIQLNVSYPPQNLTVTVFQGGEGTASTAL GNSSSLSVLEGQSLRLVCAVDSNPPARLSWTW RSLTLYPSQPSNPLVLELQVHLGDEGEFTCRAQ NSLGSQHVS LNLSLQQEYTGKMRPVSGVLLGA



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			VGGAGATALVFLSFCVIFIVVRSCRKKSARPAADVGDIGMKDANTIRGSASQGNLTESWADDNPRHHGLAAHSSGEEREIQYAPLSFHKGEPQDLSGQEATNNEYSEIKIPK*
926	167	403	MRMLLTGGLPQMCLKFHGTPLTCPQGVPCPHDSQRIQGIPKAPTGREFLAGPQRVPFPWLRSPAHVRGQPSPPGGPTPG
927	161	415	MLCWKTTSGRLKDILAILLTDVLLLLQEKDQKYVFASVDSKPPVISLQKLIVREVANEKAMFMI SASLQGPECIAAAREDPKQ
928	159	365	MQQPEVKTWGGVTAAMVIALAVYMGTCIGCFLTFGAAVDPDVLLSYPSEDMAVAVARALIILSVLTCL
929	1377	1237	MQMWLGAQSAGRCWLRARTATSWWTCSWKRLVRGCCGRKTSSLVW*
930	1524	1673	MRNLSQRVTFRMVFAACSRYSRNMQPCCVLIFLKILLCLFYQSVGQFAN*
931	126	413	MSLCLAFLLHWGHFRTCPLSHVEMHLYPKRCPQRNAESRWSPALVHCSRHIVQVSPSSSSIEAEGSRGSDFWGDGCLGRVLPPIHVTSCSAETPA
932	49	615	MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQIHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSFYVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWA IISIPVNVTSIPTFELLQPPWTFW*
933	1444	1632	MACCLPCRAFPAYPTGVWPTTWLWCWAVLPI PWPASWPWVCCAGPWQGWAAASLCWACSVGAT*
934	442	143	MDWNLQFSLLLWATADISDQLFQPPQKFSWDPLESALCLYSSGSAKDLKGEMQSFWYPARKSPLLHLPALQLFYFGELPCKFLPALVVPGSTLPPSRPL*
935	52	309	MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNECHLCTESLKSNGRVQFLHDGSC*
936	26	1057	MWAAAGGLWRSRAGLRALFRSRDAALFPGCE RGLHCSAVSCKNWLKKFASKTKKKVWYESPS LGSHSTYKPSKLEFLMRSTSKKTRKEDHARLR ALNGLLYKALTDLLCTPEVSQELYDLNVELSK VSLTPDFSACRAYWKTTLSAEQNAHMEAVLQ RSAAHMRHLLMSQQTLRNVPPIVFVQDKGNA ALAELDQLLAVADFGPRDERDNFVQNDFRDPD

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			APQPCGTTEPTTSSSLCGIDHEALNKQIMEYKR RKDKGLGGLVWQQQVAELTTQMKGKRAK PRLEQDSSLKSYLSGEEVEDDLVLGAPEYECY APDTEELEAERGGGRTEDGHSCGASRE*
937	271	98	MTAQHHSIAVLLLNLVTCCEMEYNKVFYSGS FASTSFLIGYCSSSSGFYFVQPSRP*
938	140	370	MLAHLSPFERSLILHLIFSGIAVSIKALTKTWMP EMGSSPVYKAFSLLQCRLSAQKWGSCHSQNTL HWPVWGPQTTL
939	100	411	MALLHICVGHPLLSFPKAGDFSFSQDDPSELT AGAKDKEFSCLLVICLQAPSTRSLFSWQLFLLS FSLVSFTLIYRGEFKKSGEAKDYLTQVQGPIDC GKLL
940	111	386	MFRSNPGFFFFCCCKSCILAI SLGEIPRNEFTEN MSLRESEDLKPDLSAFKSSALYTDVSSPVFFTY QNSRTLPEKPGRYCSTPVSCFSPG*
941	92	328	MCRLYSCARMPLFSTVLFSNVYINDFLQKPEN TTSQPLSNQRVVEVAIPHVGKFMIESKEGGYDD EVPFTALCTIAT*
942	143	481	MGIQWTCEWPSSLSPGWKFIACLWFSMWGSRP PLSQAMSHKQWPMCLCSSISNPEASGTELFTYHF HMMGYIERFWPTEELAQRCSLHKELPCTVFTE KHCSCTFLMVFGVCT*
943	956	1558	MQGMKTQLIQLSTLLRLDLSGFCSYLESQDSGY LYFCFRWLLIRFKREFSFLDILRLWEVMWTELP CTNFHLLLCCAILESEKQQIMEKH YGFNEILKHI NELSMKIDVEDILCKAEAISLQMVCKELPQAV CEILGLQGSEVTTPDSVDGEDENVVMTPCPTSA FQSNALPTLSASGARNDSPQTQIPVSSDVCRLTPA *
944	23	319	MGASLALGFTEVVVLVLGFTVKLGAHLTLLPPL GGHLSPYCAAQAWEGVKQLMCNCSSYPLQCII CCYATPGCYNLSFGILSSCEGIFVYEWLFEMLL *

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-236 and 473-708, a mature protein coding portion of SEQ ID NO:1-236 and 473-708, an active domain coding portion of SEQ ID NO:1-236 and 473-708, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-236 and 473-708.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
  - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10; in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-236 and 473-708, a mature protein coding portion of SEQ ID NO:1-236 and 473-708, an active domain coding portion of SEQ ID NO:1-236 and 473-708, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-236 and 473-708, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:237-472 and 709-944, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-236 and 473-708.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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Cys Thr Arg Thr Leu Thr Asn Thr Met Glu Thr Val Leu Thr Ile Ile	
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gct ctt ttc tac tat cct ttg gaa ggt tca aag tct atg aac agt gtc	1516
Ala Leu Phe Tyr Tyr Pro Leu Glu Gly Ser Lys Ser Met Asn Ser Val	
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Lys Tyr Ser Ser Leu Val Ala Leu Ala Phe Ile Ile Arg Pro Thr Ala	
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Val Ile Leu Trp Thr Pro Leu Leu Phe Arg His Phe Cys Gln Glu Pro	
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Arg Lys Leu Asp Leu Ile Leu His His Phe Leu Pro Val Gly Phe Val	
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Thr Leu Ser Leu Ser Leu Met Ile Asp Arg Ile Phe Phe Gly Gln Trp	
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Thr Leu Val Gln Phe Asn Phe Leu Lys Phe Asn Val Leu Gln Asn Trp	
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Phe Pro Val Ile Leu Gly Thr His Leu Pro Phe Phe Ile His Gly Cys	
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aca ctg ctt gtt tat agc atg ttg agc cac aaa gaa ttc agg ttt att Thr Leu Leu Val Tyr Ser Met Leu Ser His Lys Glu Phe Arg Phe Ile 350 355 360	1948
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aat ttg ttc ctc gcc ctt tat act ggt tta gtt cat caa cga ggt act Asn Leu Phe Leu Ala Leu Tyr Thr Gly Leu Val His Gln Arg Gly Thr 400 405 410	2092
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ccg cca gac ctg act gga aaa agt cat tat ctt gat gaa gca gat gta Pro Pro Asp Leu Thr Gly Lys Ser His Tyr Leu Asp Glu Ala Asp Val 460 465 470 475	2284
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gca tca ttg cct act cac ttg atc acc ttc agc att ttg gaa gag gaa Ala Ser Leu Pro Thr His Leu Ile Thr Phe Ser Ile Leu Glu Glu Glu 495 500 505	2380
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    Met Ser Leu Leu Gly Phe Leu Leu Ser Arg Leu Gly Leu Leu Leu
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aag gtg ctg ctg gac tgg cca gtg gag gtg ctg tac ggg gcg gcg gcg      155
Lys Val Leu Leu Asp Trp Pro Val Glu Val Leu Tyr Gly Ala Ala Ala
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ctg aac ggg cta ttc ggc ggc ttc tcc gcc ttc tgg tcc ggg gtc atg      203
Leu Asn Gly Leu Phe Gly Gly Phe Ser Ala Phe Trp Ser Gly Val Met
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gcg ctg gga tcg ctg ggc tcc tcc gag ggc cgc cgc tct gtg cgc ctc      251
Ala Leu Gly Ser Leu Gly Ser Ser Glu Gly Arg Arg Ser Val Arg Leu
        50             55             60

atc ctc att gac ctg atg ctg ggc ttg gcg ggg ttc tgc ggg agc atg      299
Ile Leu Ile Asp Leu Met Leu Gly Leu Ala Gly Phe Cys Gly Ser Met
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gct tcc ggg cat ctc ttc aag cag atg gct ggg cac tct ggg cag ggc      347
Ala Ser Gly His Leu Phe Lys Gln Met Ala Gly His Ser Gly Gln Gly
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ctg ata ctg acg gcc tgc agc gtg agc tgt gcc tcg ttt gcc ctg ctc      395
Leu Ile Leu Thr Ala Cys Ser Val Ser Cys Ala Ser Phe Ala Leu Leu
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tac agc ctt ttg gtg cta aag gtc cct gag tcg gtg gcc aaa ccc agc      443
Tyr Ser Leu Leu Val Leu Lys Val Pro Glu Ser Val Ala Lys Pro Ser
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cag gag ctc ccc gcc gtg gat acc gtg tct ggc acg gtt ggc aca tac      491
Gln Glu Leu Pro Ala Val Asp Thr Val Ser Gly Thr Val Gly Thr Tyr
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cgc act ctg gat cct gat cag ttg gac caa cag tat gca gtg ggg cac      539
Arg Thr Leu Asp Pro Asp Gln Leu Asp Gln Gln Tyr Ala Val Gly His
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gtg cag gtg ggc tat ggt atg gct gca ggg tac acc atc ttc atc acc 731  
 Val Gln Val Gly Tyr Gly Met Ala Ala Gly Tyr Thr Ile Phe Ile Thr  
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 Ser Phe Leu Gly Val Leu Val Phe Ser Arg Cys Phe Arg Asp Thr Thr  
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 Met Ile Met Ile Gly Met Val Ser Phe Gly Ser Gly Ala Leu Leu Leu  
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gct ttt gtg aaa gag aca tac atg ttc tat att gct cga gcc gtc atg 875  
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 Tyr Gln Leu Thr Met Asp Met Phe Val Gly Ser Cys Phe Ala Leu Ser  
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Phe Phe Leu Val Ala Ile Leu Pro Val Asn Thr Glu Gly Gly Glu Ile	
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Ile Trp Gly Thr Glu Ser Lys Pro His Ser Arg Pro Tyr Met Ala Phe	
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Ile Lys Phe Tyr Asp Ser Asn Ser Glu Pro His His Cys Gly Gly Phe	
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Leu Val Ala Lys Asp Ile Val Met Thr Ala Ala His Cys Asn Gly Arg	
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Asn Ile Lys Val Thr Leu Gly Ala His Asn Ile Lys Lys Gln Glu Asn	
70 75 80 85	
acc cag gtt atc tct gtt gta aaa gcc aaa cct cac gag aac tat gac	341
Thr Gln Val Ile Ser Val Val Lys Ala Lys Pro His Glu Asn Tyr Asp	
90 95 100	
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Arg Asp Ser His Phe Asn Asp Ile Met Leu Leu Lys Leu Glu Arg Lys	
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Leu Ala Asn Cys Thr Ser Ser Asn Thr Leu Gln Glu Val Asn Leu Glu	
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Ser Ile Gln Leu Cys Val Gly Asn Pro Ser Glu Gly Lys Ala Thr Gly	
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Lys Gly Asp Ser Gly Gly Pro Phe Val Cys Asp Gly Met Ala Pro Gly	
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His Trp Gln Leu Ser Ala Trp Val Leu Gly Thr Leu Ser Arg Glu Phe	
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Pro Gln Asn Leu Gln Leu Leu Tyr Arg Gly Phe Arg Lys Pro Met Lys	
230 235 240 245	
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Met Phe Ser Phe Val Asp Leu Arg Leu Leu Leu  
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gtc gag ggc caa gac gaa gac atc cca cca atc acc tgc gta cag aac 268  
Val Glu Gly Gln Asp Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn  
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Gly Leu Arg Tyr His Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg  
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Ile Cys Val Cys Asp Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys  
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Thr Gly Val Glu Gly Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg  
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15

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cct ggc cct gct gga gag gaa gga aag cga gga gct cga ggt gaa ccc Pro Gly Pro Ala Gly Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro 460 465 470 475			1564
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670	675	680	
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Phe Asp Phe Ser Phe Leu Pro Gln Pro Pro Gln Glu Lys Ala His Asp				
1200	1205	1210		
ggt ggc cgc tac tac cgg gct gat gat gcc aat gtg gtt cgt gac cgt				3820
Gly Gly Arg Tyr Tyr Arg Ala Asp Asp Ala Asn Val Val Arg Asp Arg				
1215	1220	1225		
gac ctc gag gtg gac acc acc ctc aag agc ctg agc cag cag atc gag				3868
Asp Leu Glu Val Asp Thr Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu				
1230	1235	1240		
aac atc cgg agc cca gag ggc agc cgc aag aac ccc gcc cgc acc tgc				3916
Asn Ile Arg Ser Pro Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys				
1245	1250	1255		
cgt gac ctc aag atg tgc cac tct gac tgg aag agt gga gag tac tgg				3964
Arg Asp Leu Lys Met Cys His Ser Asp Trp Lys Ser Gly Glu Tyr Trp				
1260	1265	1270	1275	
att gac ccc aac caa ggc tgc aac ctg gat gcc atc aaa gtc ttc tgc				4012
Ile Asp Pro Asn Gln Gly Cys Asn Leu Asp Ala Ile Lys Val Phe Cys				
1280	1285	1290		
aac atg gag act ggt gag acc tgc gtg tac ccc act cag ccc agt gtg				4060
Asn Met Glu Thr Gly Glu Thr Cys Val Tyr Pro Thr Gln Pro Ser Val				
1295	1300	1305		
gcc cag aag aac tgg tac atc agc aag aac ccc aag gac aag agg cat				4108
Ala Gln Lys Asn Trp Tyr Ile Ser Lys Asn Pro Lys Asp Lys Arg His				
1310	1315	1320		
gtc tgg ttc ggc gag agc atg acc gat gga ttc cag ttc gag tat ggc				4156
Val Trp Phe Gly Glu Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly				
1325	1330	1335		
ggc cag ggc tcc gac cct gcc gat gtg gcc atc cag ctg acc ttc ctg				4204
Gly Gln Gly Ser Asp Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu				
1340	1345	1350	1355	
cgc ctg atg tcc acc gag gcc tcc cag aac atc acc tac cac tgc aag				4252
Arg Leu Met Ser Thr Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys				
1360	1365	1370		
aac agc gtg gcc tac atg gac cag cag act ggc aac ctc aag aag gcc				4300
Asn Ser Val Ala Tyr Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala				
1375	1380	1385		
ctg ctc ctc cag ggc tcc aac gag atc gag atc cgc gcc gag ggc aac				4348
Leu Leu Leu Gln Gly Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn				
1390	1395	1400		
agc cgc ttc acc tac agc gtc act gtc gat ggc tgc acg agt cac acc				4396
Ser Arg Phe Thr Tyr Ser Val Thr Val Asp Gly Cys Thr Ser His Thr				
1405	1410	1415		
gga gcc tgg ggc aag aca gtg att gaa tac aaa acc acc aag acc tcc				4444
Gly Ala Trp Gly Lys Thr Val Ile Glu Tyr Lys Thr Thr Lys Thr Ser				
1420	1425	1430	1435	
cgc ctg ccc atc atc gat gtg gcc ccc ttg gac gtt ggt gcc cca gac				4492
Arg Leu Pro Ile Ile Asp Val Ala Pro Leu Asp Val Gly Ala Pro Asp				

1440	1445	1450	
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Gln Glu Phe Gly Phe Asp Val Gly Pro Val Cys Phe Leu			
1455	1460		
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gcaacccaaa ctgaaccccc ccaaaagcca aaaaatggga gacaatttca catggacttt			4661
ggaaaaatatt tttttccttt gcattcatct ctcaaaactta gtttttatct ttgaccaaac			4721
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gagccggggc ccgctcagcc ggcgttacc	atg acc aag gcc ggt agc aag ggc		653
	Met Thr Lys Ala Gly Ser Lys Gly		
	1 5		
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Gly Asn Leu Arg Asp Lys Leu Asp Gly Asn Glu Leu Asp Leu Ser Leu			
10 15 20			
agc gac ctg aat gag gtc ccg gtg aag gag ctg gct gcc ctt cca aag			749
Ser Asp Leu Asn Glu Val Pro Val Lys Glu Leu Ala Ala Leu Pro Lys			
25 30 35 40			
gcc acc atc ctg gat ctg tct tgt aat aaa ctg act act cta ccg tcg			797
Ala Thr Ile Leu Asp Leu Ser Cys Asn Lys Leu Thr Thr Leu Pro Ser			
45 50 55			
gat ttc tgt ggc ctc aca cac ctg gtg aag cta gac ctg agt aag aac			845

Asp Phe Cys Gly Leu Thr His Leu Val Lys Leu Asp Leu Ser Lys Asn	
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aag ctg cag cag ctg cca gca gac ttt ggc cgt ctg gtc aac ctc cag	893
Lys Leu Gln Gln Leu Pro Ala Asp Phe Gly Arg Leu Val Asn Leu Gln	
75 80 85	
cac ctg gat ctc ctc aac aac aag ctg gtc acc ttg cct gtc agc ttt	941
His Leu Asp Leu Leu Asn Asn Lys Leu Val Thr Leu Pro Val Ser Phe	
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gct cag ctc aag aac ctg aag tgg ttg gac ctg aag gat aac ccc ctg	989
Ala Gln Leu Lys Asn Leu Lys Trp Leu Asp Leu Lys Asp Asn Pro Leu	
105 110 115 120	
gat cct gtc ctg gcc aag gtg gca ggt gac tgc ttg gat gag aag cag	1037
Asp Pro Val Leu Ala Lys Val Ala Gly Asp Cys Leu Asp Glu Lys Gln	
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Cys Lys Gln Cys Ala Asn Lys Val Leu Gln His Met Lys Ala Val Gln	
140 145 150	
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Ala Asp Gln Glu Arg Glu Arg Gln Arg Arg Leu Glu Val Glu Arg Glu	
155 160 165	
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Ala Glu Lys Lys Arg Glu Ala Lys Gln Arg Ala Lys Glu Ala Gln Glu	
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Arg Glu Leu Arg Lys Arg Glu Lys Ala Glu Glu Lys Glu Arg Arg Arg	
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aag gag tat gat gcc ctc aaa gca gtc aag cgg gag cag gag aag aaa	1277
Lys Glu Tyr Asp Ala Leu Lys Ala Val Lys Arg Glu Gln Glu Lys Lys	
205 210 215	
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Pro Lys Lys Glu Ala Asn Gln Ala Pro Lys Ser Lys Ser Gly Ser Arg	
220 225 230	
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Pro Arg Lys Pro Pro Pro Arg Lys His Thr Arg Ser Trp Ala Val Leu	
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Lys Leu Leu Leu Leu Leu Leu Leu Phe Gly Val Ala Gly Gly Leu Val	
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Ala Cys Arg Val Thr Glu Leu Gln Gln Gln Pro Leu Cys Thr Ser Val	
265 270 275 280	
aac acc atc tat gac aat gcg gtc cag ggt cta cgc cgc cat gag atc	1517
Asn Thr Ile Tyr Asp Asn Ala Val Gln Gly Leu Arg Arg His Glu Ile	
285 290 295	
ctc cag tgg gtc ctc cag acc gac tct cag cag tga gctt gtccccagca	1567
Leu Gln Trp Val Leu Gln Thr Asp Ser Gln Gln *	
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&lt;210&gt; 9

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&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (168)..(839)

&lt;400&gt; 9

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ccctggaagc tgctgtcct tctccctgtg cttaaccaga ggtgccc  atg ggt tgg      176
                                         Met Gly Trp
                                         1

aca atg agg ctg gtc aca gca gca ctg tta ctg ggt ctc atg atg gtg      224
Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met Val
      5              10              15

gtc act gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc ctc      272
Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala Leu
      20              25              30              35

ttg gac gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac cca      320
Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro
      40              45              50

gag ttg ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac tac      368
Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys Asn Asn Tyr
      55              60              65

aga cag aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg ggg      416
Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro Gly
      70              75              80

gcc gtg gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat gcc      464
Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp Ala
      85              90              95

cct agc aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg gta      512
Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu Val
     100              105              110              115

aca gat atc aag ggc gcc gac ctg aag gaa ggg aag att cag ggc cag      560
Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile Gln Gly Gln
      120              125              130

gag tta tca gcc tac cag gct ccc tcc cca ccg gca cac agt ggc ttc      608
Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe
      135              140              145

cat cgc tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc tct      656
His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser
      150              155              160

ctc ctt ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac aga      704
Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg
      165              170              175

ttt ctg aac cgc ttc cac ctg ggc gaa cct gaa gca agc acc cag ttc      752
Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe
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atg acc cag aac tac cag gac tca cca acc ctc cag gct ccc aga gga	800
Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg Gly	
200 205 210	
agg gcc agc gag ccc aag cac aaa acc agg cag aga tag ctgcctgcta	849
Arg Ala Ser Glu Pro Lys His Lys Thr Arg Gln Arg *	
215 220	
gatatccggc ttgtccatcc gggcatgtgg ccacactgct caccaccgac gatgtgggta	909
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gaa	972

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<212> DNA
<213> Homo sapiens
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<222> (114) .. (365)
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	Met
	1
cga cgc tcc ttc tgg act gta atg cgc act gcg tgg aga tgt tcg tgt	164
Arg Arg Ser Phe Trp Thr Val Met Arg Thr Ala Trp Arg Cys Ser Cys	
	5 10 15
tcc agt gta gac agg gcg ttg tca cat cag gca gga cta cag gga caa	212
Ser Ser Val Asp Arg Ala Leu Ser His Gln Ala Gly Leu Gln Gly Gln	
	20 25 30
tgt ttg tca gcc tgt ctt ctg ggc aac ttg ggg tat cct ccc ttt ata	260
Cys Leu Ser Ala Cys Leu Leu Gly Asn Leu Gly Tyr Pro Pro Phe Ile	
	35 40 45
tca cct cct gcc cag gtg ctc tgc gcc gcc aga gca tca tgt cat ttg	308
Ser Pro Pro Ala Gln Val Leu Cys Ala Ala Arg Ala Ser Cys His Leu	
	50 55 60 65
gga tcc ctg atg gca att ttg aga ctt tgg ttc aca gta aag att ggt	356
Gly Ser Leu Met Ala Ile Leu Arg Leu Trp Phe Thr Val Lys Ile Gly	
	70 75 80
cct gtg tga tcttaaa gtaatgtggc ttaaaaacaa atggctgtca gggaattgta	412
Pro Val *	
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gtgtacctat cacacacagg gggaaaa atg ctc ttt tgg gtg cta ggc ctc Met Leu Phe Trp Val Leu Gly Leu 1 5	1431
cta atc ctc tgt ggt ttt ctg tgg act cgt aaa gga aaa cta aag att Leu Ile Leu Cys Gly Phe Leu Trp Thr Arg Lys Gly Lys Leu Lys Ile 10 15 20	1479
gaa gac atc act gat aag tac att ttt atc act gga tgt gac tcg ggc Glu Asp Ile Thr Asp Lys Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly 25 30 35 40	1527
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atc gct gcc tgt ctg act gaa tca gga tca aca gct tta aag gca gaa Ile Ala Ala Cys Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu 60 65 70	1623
acc tca gag aga ctt cgt act gtg ctt ctg gat gtg acc gac cca gag Thr Ser Glu Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu 75 80 85	1671
aat gtc aag agg act gcc cag tgg gtg aag aac caa gtt ggg gag aaa Asn Val Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys 90 95 100	1719
ggt ctc tgg ggt ctg atc aat aat gct ggt gtt ccc ggc gtg ctg gct Gly Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala 105 110 115 120	1767
ccc act gac tgg ctg aca cta gag gac tac aga gaa cct att gaa gtg Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu Val 125 130 135	1815
aac ctg ttt gga ctc atc agt gtg aca cta aat atg ctt cct ttg gtc Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro Leu Val 140 145 150	1863
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gtc tca tgc att gaa cca gga ttg ttc aaa aca aac ttg gca gat cca Val Ser Cys Ile Glu Pro Gly Leu Phe Lys Thr Asn Leu Ala Asp Pro 205 210 215	2055
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 Lys Leu Lys Gly Asn Lys Ser Tyr Val Asn Met Asp Leu Ser Pro Val  
 250 255 260  
 gta gag tgc atg gac cac gct cta aca agt ctc ttc cct aag act cat 2247  
 Val Glu Cys Met Asp His Ala Leu Thr Ser Leu Phe Pro Lys Thr His  
 265 270 275 280  
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 Leu Ala Asn Pro Lys Ala Val \*  
 315 320  
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 aacctggact catttagatc gtgcttattt ggattgcaaa agggagtccc accatcgctg 2517  
 gtggtatccc agggtcctg ctcaagtttt ctttgaaaag gagggctgga atggtacatc 2577  
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&lt;210&gt; 12

&lt;211&gt; 912

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54) .. (776)

&lt;400&gt; 12

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 Ser Val Pro Thr Met Ala Trp Met Met Leu Leu Leu Gly Leu Leu Ala  
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 Tyr Gly Ser Gly Val Asp Ser Glu Thr Val Val Thr Gln Glu Pro Ser  
 20 25 30  
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Phe	Ser	Val	Ser	Pro	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys	Gly	Leu	Asn	
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Ser	Gly	Ser	Val	Ser	Asp	Ser	Phe	Tyr	Pro	Ser	Trp	His	Gln	Gln	Thr	
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Pro	Gly	Gln	Pro	Pro	Arg	Thr	Leu	Ile	Tyr	Asn	Thr	His	Ile	Arg	Ala	
			70					75						80		
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Ser	Gly	Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser	Ile	Val	Gly	Asn	Lys	Ala	
			85				90						95			
gcc	ctc	acc	atc	acg	ggg	gcc	cag	gct	gac	gat	gag	tgt	gtt	tat	tac	392
Ala	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Asp	Asp	Glu	Cys	Val	Tyr	Tyr	
	100						105					110				
tgt	gta	ctc	tac	atg	ggc	aat	gac	att	tcg	ctg	ttc	ggc	gga	ggg	aca	440
Cys	Val	Leu	Tyr	Met	Gly	Asn	Asp	Ile	Ser	Leu	Phe	Gly	Gly	Gly	Thr	
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aga	ctg	acc	gtc	cta	ggt	cag	ccc	aag	gct	gcc	ccc	tcg	gtc	act	ctg	488
Arg	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	
	130				135				140						145	
ttc	ccg	ccc	tcc	tct	gag	gag	ctt	caa	gcc	aac	aag	gcc	aca	ctg	gtg	536
Phe	Pro	Pro	Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	
			150					155						160		
tgt	ctc	ata	agt	gac	ttc	tac	ccg	gga	gcc	gtg	aca	gtg	gcc	tgg	aag	584
Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	
			165				170						175			
gca	gat	agc	agc	ccc	gtc	aag	gcg	gga	gtg	gag	acc	acc	aca	ccc	tcc	632
Ala	Asp	Ser	Ser	Pro	Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	
	180						185					190				
aaa	caa	agc	aac	aac	aag	tac	gcg	gcc	agc	agc	tac	ctg	agc	ctg	acg	680
Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	
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cct	gag	cag	tgg	aag	tcc	cac	aaa	agc	tac	agc	tgc	cag	gtc	acg	cat	728
Pro	Glu	Gln	Trp	Lys	Ser	His	Lys	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	
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Glu	Gly	Ser	Thr	Val	Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*	
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&lt;210&gt; 13

&lt;211&gt; 6116

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (464) .. (4048)

&lt;400&gt; 13

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Val Leu Trp Cys Val Leu Leu Leu Val Cys Met Ser Leu Phe Ser Ala
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Val Gly His Gly Leu Trp Ile Trp Arg Tyr Gln Glu Lys Lys Ser Leu
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ttt tat gtc ccc aag tct gat gga agc tcc tta tcc cca gtc aca gct      619
Phe Tyr Val Pro Lys Ser Asp Gly Ser Ser Leu Ser Pro Val Thr Ala
                40                      45                      50

gca gtt tac tca ttt tta aca atg ata ata gtt ctg cag gtt ttg atc      667
Ala Val Tyr Ser Phe Leu Thr Met Ile Ile Val Leu Gln Val Leu Ile
                55                      60                      65

cca att tcc tta tac gtt tcc att gaa att gtt aaa gca tgc caa gtg      715
Pro Ile Ser Leu Tyr Val Ser Ile Glu Ile Val Lys Ala Cys Gln Val
                70                      75                      80

tac ttc att aac cag gac atg cag ttg tat gac gaa gaa aca gac tgc      763
Tyr Phe Ile Asn Gln Asp Met Gln Leu Tyr Asp Glu Glu Thr Asp Ser
   85                      90                      95                      100

cag ctg cag tgc cga gct ctg aac atc acg gaa gac tta gga cag ata      811
Gln Leu Gln Cys Arg Ala Leu Asn Ile Thr Glu Asp Leu Gly Gln Ile
                105                      110                      115

cag tac att ttc tca gat aaa act ggc act ttg aca gag aat aag atg      859
Gln Tyr Ile Phe Ser Asp Lys Thr Gly Thr Leu Thr Glu Asn Lys Met
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gtt ttc cga aga tgc act gtg tct ggt gta gaa tat tct cat gat gca      907
Val Phe Arg Arg Cys Thr Val Ser Gly Val Glu Tyr Ser His Asp Ala
                135                      140                      145

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Asn Ala Gln Arg Leu Ala Arg Tyr Gln Glu Ala Asp Ser Glu Glu Glu
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cac cgg cgc acg ggc agc cgg gcc gag gcc aag agg gcc agc atg ctg His Arg Arg Thr Gly Ser Arg Ala Glu Ala Lys Arg Ala Ser Met Leu 200 205 210	1099
tcc aag cac acg gcc ttc agc agc ccc atg gag aag gat atc acg ccc Ser Lys His Thr Ala Phe Ser Ser Pro Met Glu Lys Asp Ile Thr Pro 215 220 225	1147
gac cca aag ctg ctg gag aag gtg agt gag tgt gac aag agc cta gcc Asp Pro Lys Leu Leu Glu Lys Val Ser Glu Cys Asp Lys Ser Leu Ala 230 235 240	1195
gtg gcg agg cat cag gag cac ctg ctg gcc cac ctc tcg ccc gag ctg Val Ala Arg His Gln Glu His Leu Leu Ala His Leu Ser Pro Glu Leu 245 250 255 260	1243
tct gac gtc ttt gat ttc ttc atc gca ctc acc atc tgc aac aca gtc Ser Asp Val Phe Asp Phe Phe Ile Ala Leu Thr Ile Cys Asn Thr Val 265 270 275	1291
gtc gtc acg tcc ccg gat cag cca cga aca aag gtg agg gtg agg ttt Val Val Thr Ser Pro Asp Gln Pro Arg Thr Lys Val Arg Val Arg Phe 280 285 290	1339
gag ctg aag tcc ccg gtg aag acg ata gaa gac ttc ctg cgg agg ttc Glu Leu Lys Ser Pro Val Lys Thr Ile Glu Asp Phe Leu Arg Arg Phe 295 300 305	1387
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gcc aac aag tcc agc cac aag ttg ggc tcc agc ttc ccg tcc acc ccg Ala Asn Lys Ser Ser His Lys Leu Gly Ser Ser Phe Pro Ser Thr Pro 325 330 335 340	1483
tcc agc gac ggc atg ctt ctc agg ctg gag gag agg ctg ggc cag ccc Ser Ser Asp Gly Met Leu Leu Arg Leu Glu Glu Arg Leu Gly Gln Pro 345 350 355	1531
acc tcg gcc atc gcc agc aac ggc tac agc agc cag gcg gac aac tgg Thr Ser Ala Ile Ala Ser Asn Gly Tyr Ser Ser Gln Ala Asp Asn Trp 360 365 370	1579
gcc tcg gag ctt gct cag gag cag gag tca gag cgc gag ctg cgg tac Ala Ser Glu Leu Ala Gln Glu Gln Glu Ser Glu Arg Glu Leu Arg Tyr 375 380 385	1627
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Leu Pro His Leu Gly Arg Leu Thr Phe Glu Leu Leu His Thr Leu Gly	
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Phe Asp Ser Val Arg Lys Arg Met Ser Val Val Ile Arg His Pro Leu	
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Thr Asp Glu Ile Asn Val Tyr Thr Lys Gly Ala Asp Ser Val Val Met	
455 460 465	
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Asp Leu Leu Gln Pro Cys Ser Ser Val Asp Ala Arg Gly Arg His Gln	
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Lys Lys Ile Arg Ser Lys Thr Gln Asn Tyr Leu Asn Val Tyr Ala Ala	
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Glu Gly Leu Arg Thr Leu Cys Ile Ala Lys Arg Val Leu Ser Lys Glu	
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Glu Tyr Ala Cys Trp Leu Gln Ser His Leu Glu Ala Glu Ser Ser Leu	
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Glu Asn Ser Glu Glu Leu Leu Phe Gln Ser Ala Ile Arg Leu Glu Thr	
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Asn Leu His Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Asp	
550 555 560	
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Gly Val Pro Glu Thr Ile Ser Lys Leu Arg Gln Ala Gly Leu Gln Ile	
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585 590 595	
gcc tgc aaa ctg ctg gac cac gac gag gag gtc atc acc ctg aat gcc	2299
Ala Cys Lys Leu Leu Asp His Asp Glu Glu Val Ile Thr Leu Asn Ala	
600 605 610	
acc tcc cag gag gcg tgt gca gcc ctg cta gac cag tgc cta tgc tac	2347
Thr Ser Gln Glu Ala Cys Ala Ala Leu Leu Asp Gln Cys Leu Cys Tyr	
615 620 625	
gtg cag tcc aga ggc ccc cag aga gcc cct gag aag acc aag ggc aaa	2395
Val Gln Ser Arg Gly Pro Gln Arg Ala Pro Glu Lys Thr Lys Gly Lys	
630 635 640	
gtg agc atg agg ttc tcc tct ctc tgc cca ccc tcc acg tcc act gcc	2443
Val Ser Met Arg Phe Ser Ser Leu Cys Pro Pro Ser Thr Ser Thr Ala	
645 650 655 660	
tct ggc cgc aga ccc agc ctc gtg atc gat ggg aga agc ctg gcc tac	2491
Ser Gly Arg Arg Pro Ser Leu Val Ile Asp Gly Arg Ser Leu Ala Tyr	
665 670 675	

gct ctc gag aaa aac ctg gag gac aaa ttc ctc ttc ctt gcc aag cag Ala Leu Glu Lys Asn Leu Glu Asp Lys Phe Leu Phe Leu Ala Lys Gln 680 685 690	2539
tgc cgc tcc gtc ctc tgc tgt cgg tgc acg cct ctg cag aag agc atg Cys Arg Ser Val Leu Cys Cys Arg Ser Thr Pro Leu Gln Lys Ser Met 695 700 705	2587
gtg gtg aag ctg gtg cgg agc aag ctc aag gcc atg acc ctg gcc ata Val Val Lys Leu Val Arg Ser Lys Leu Lys Ala Met Thr Leu Ala Ile 710 715 720	2635
ggg gat gga gcc aat gat gtc agc atg atc cag gtg gca gat gtg ggt Gly Asp Gly Ala Asn Asp Val Ser Met Ile Gln Val Ala Asp Val Gly 725 730 735 740	2683
gtg gga atc tcc ggc cag gag ggt atg cag gca gtg atg gcc agc gac Val Gly Ile Ser Gly Gln Glu Gly Met Gln Ala Val Met Ala Ser Asp 745 750 755	2731
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ggg cat tgg tgc tac tcc cga ctt gcc aac atg gtg ctg tac ttc ttc Gly His Trp Cys Tyr Ser Arg Leu Ala Asn Met Val Leu Tyr Phe Phe 775 780 785	2827
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935 940 945	
acg tgc tat cct ccg tcc aac cct tac tgg act atg caa gcc tta ctg	3355
Thr Cys Tyr Pro Pro Ser Asn Pro Tyr Trp Thr Met Gln Ala Leu Leu	
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ttc	cct	tcc	atc	gac	atg	ggg	cct	cag	ctg	aag	gtg	gtg	gag	aag	gca	785
Phe	Pro	Ser	Ile	Asp	Met	Gly	Pro	Gln	Leu	Lys	Val	Val	Glu	Lys	Ala	
		135				140					145					
cgc	aca	gcc	acc	atg	cta	tgt	gcc	gca	ggc	gga	aat	cca	gac	cct	gag	833
Arg	Thr	Ala	Thr	Met	Leu	Cys	Ala	Ala	Gly	Gly	Asn	Pro	Asp	Pro	Glu	
		150				155				160					165	
att	tct	tgg	ttc	aag	gac	ttc	ctt	cct	gta	gac	cct	gcc	acg	agc	aac	881
Ile	Ser	Trp	Phe	Lys	Asp	Phe	Leu	Pro	Val	Asp	Pro	Ala	Thr	Ser	Asn	
				170					175						180	
ggc	cgc	atc	aag	cag	ctg	cgt	tca	ggt	gcc	ttg	cag	ata	gag	agc	agt	929
Gly	Arg	Ile	Lys	Gln	Leu	Arg	Ser	Gly	Ala	Leu	Gln	Ile	Glu	Ser	Ser	
			185					190					195			
gag	gaa	tcc	gac	caa	ggc	aag	tac	gag	tgt	gtg	gcg	acc	aac	tcg	gca	977
Glu	Glu	Ser	Asp	Gln	Gly	Lys	Tyr	Glu	Cys	Val	Ala	Thr	Asn	Ser	Ala	
		200					205					210				
ggc	aca	cgt	tac	tca	gcc	cct	gcg	aac	ctg	tat	gtg	cga	gtg	cgc	cgc	1025
Gly	Thr	Arg	Tyr	Ser	Ala	Pro	Ala	Asn	Leu	Tyr	Val	Arg	Val	Arg	Arg	
		215				220					225					
gtg	gct	cct	cgt	ttc	tcc	atc	cct	ccc	agc	agc	cag	gag	gtg	atg	cca	1073
Val	Ala	Pro	Arg	Phe	Ser	Ile	Pro	Pro	Ser	Ser	Gln	Glu	Val	Met	Pro	
		230				235					240				245	
ggc	ggc	agc	gtg	aac	ctg	aca	tgc	gtg	gca	gtg	ggg	gca	ccc	atg	ccc	1121
Gly	Gly	Ser	Val	Asn	Leu	Thr	Cys	Val	Ala	Val	Gly	Ala	Pro	Met	Pro	
				250					255					260		
tac	gtg	aag	tgg	atg	atg	ggg	gcc	gag	gag	ctc	acc	aag	gag	gat	gag	1169
Tyr	Val	Lys	Trp	Met	Met	Gly	Ala	Glu	Glu	Leu	Thr	Lys	Glu	Asp	Glu	
			265					270					275			
atg	cca	gtt	ggc	cgc	aac	gtc	ctg	gag	ctc	agc	aat	gtc	gta	cgc	tct	1217
Met	Pro	Val	Gly	Arg	Asn	Val	Leu	Glu	Leu	Ser	Asn	Val	Val	Arg	Ser	
		280					285					290				
gcc	aac	tac	acc	tgt	gtg	gcc	atc	tcc	tcg	ctg	ggc	atg	atc	gag	gcc	1265
Ala	Asn	Tyr	Thr	Cys	Val	Ala	Ile	Ser	Ser	Leu	Gly	Met	Ile	Glu	Ala	
		295				300					305					
aca	gcc	cag	gtc	aca	gtg	aaa	gct	ctt	cca	aag	cct	ccg	att	gat	ctt	1313
Thr	Ala	Gln	Val	Thr	Val	Lys	Ala	Leu	Pro	Lys	Pro	Pro	Ile	Asp	Leu	
					315					320					325	
gtg	gtg	aca	gag	aca	act	gcc	acc	agt	gtc	acc	ctc	acc	tgg	gac	tct	1361
Val	Val	Thr	Glu	Thr	Thr	Ala	Thr	Ser	Val	Thr	Leu	Thr	Trp	Asp	Ser	
				330					335					340		
ggg	aac	tcg	gag	cct	gta	acc	tac	tat	ggc	atc	cag	tac	cgc	gca	gcg	1409
Gly	Asn	Ser	Glu	Pro	Val	Thr	Tyr	Tyr	Gly	Ile	Gln	Tyr	Arg	Ala	Ala	
			345					350					355			
ggc	acg	gag	ggc	ccc	ttt	cag	gag	gtg	gat	ggg	gtg	gcc	acc	acc	cgc	1457
Gly	Thr	Glu	Gly	Pro	Phe	Gln	Glu	Val	Asp	Gly	Val	Ala	Thr	Thr	Arg	
		360					365					370				
tac	agc	att	ggc	ggc	ctc	agc	cct	ttc	tcg	gaa	tat	gcc	ttc	cgc	gtg	1505

Tyr	Ser	Ile	Gly	Gly	Leu	Ser	Pro	Phe	Ser	Glu	Tyr	Ala	Phe	Arg	Val		
375						380					385						
ctg	gcg	gtg	aac	agc	atc	ggg	cga	ggg	ccg	ccc	agc	gag	gca	gtg	cg	1553	
Leu	Ala	Val	Asn	Ser	Ile	Gly	Arg	Gly	Pro	Pro	Ser	Glu	Ala	Val	Arg		
390					395				400						405		
gca	cgc	acg	gga	gaa	cag	gcg	ccc	tcc	agc	cca	ccg	cgc	cgc	gtg	cag	1601	
Ala	Arg	Thr	Gly	Glu	Gln	Ala	Pro	Ser	Ser	Pro	Pro	Arg	Arg	Val	Gln		
			410					415						420			
gca	cgc	atg	ctg	agc	gcc	agc	acc	atg	ctg	gtg	cag	tgg	gag	cct	ccc	1649	
Ala	Arg	Met	Leu	Ser	Ala	Ser	Thr	Met	Leu	Val	Gln	Trp	Glu	Pro	Pro		
			425					430					435				
gag	gag	ccc	aac	ggc	ctg	gtg	cgg	gga	tac	cgc	gtc	tac	tat	act	ccg	1697	
Glu	Glu	Pro	Asn	Gly	Leu	Val	Arg	Gly	Tyr	Arg	Val	Tyr	Tyr	Thr	Pro		
		440					445					450					
gac	tcc	cgc	cgc	ccc	ccg	aac	gcc	tgg	cac	aag	cac	aac	acc	gac	gcg	1745	
Asp	Ser	Arg	Arg	Pro	Pro	Asn	Ala	Trp	His	Lys	His	Asn	Thr	Asp	Ala		
	455					460					465						
ggg	ctc	ctc	acg	acc	gtg	ggc	agc	ctg	ctg	cct	ggc	atc	acc	tac	agc	1793	
Gly	Leu	Leu	Thr	Thr	Val	Gly	Ser	Leu	Leu	Pro	Gly	Ile	Thr	Tyr	Ser		
470					475					480					485		
ctg	cgc	gtg	ctt	gcc	ttc	acc	gcc	gtg	ggc	gat	ggc	cct	ccc	agc	ccc	1841	
Leu	Arg	Val	Leu	Ala	Phe	Thr	Ala	Val	Gly	Asp	Gly	Pro	Pro	Ser	Pro		
			490						495					500			
acc	atc	cag	gtc	aag	acg	cag	cag	gga	gtg	cct	gcc	cag	ccc	gcg	gac	1889	
Thr	Ile	Gln	Val	Lys	Thr	Gln	Gln	Gly	Val	Pro	Ala	Gln	Pro	Ala	Asp		
			505					510					515				
ttc	cag	gcc	gag	gtg	gag	tcg	gac	acc	agg	atc	cag	ctc	tcg	tgg	ctg	1937	
Phe	Gln	Ala	Glu	Val	Glu	Ser	Asp	Thr	Arg	Ile	Gln	Leu	Ser	Trp	Leu		
		520					525					530					
ctg	ccc	cct	cag	gag	cgg	atc	atc	atg	tat	gaa	ctg	gtg	tac	tgg	gcg	1985	
Leu	Pro	Pro	Gln	Glu	Arg	Ile	Ile	Met	Tyr	Glu	Leu	Val	Tyr	Trp	Ala		
		535				540					545						
gca	gag	gac	gaa	gac	caa	cag	cac	aag	gtc	acc	ttc	gac	cca	acc	tcc	2033	
Ala	Glu	Asp	Glu	Asp	Gln	Gln	His	Lys	Val	Thr	Phe	Asp	Pro	Thr	Ser		
550					555				560						565		
tcc	tac	aca	cta	gag	gac	ctg	aag	cct	gac	aca	ctc	tac	cgc	ttc	cag	2081	
Ser	Tyr	Thr	Leu	Glu	Asp	Leu	Lys	Pro	Asp	Thr	Leu	Tyr	Arg	Phe	Gln		
			570						575					580			
ctg	gct	gca	cgc	tcg	gat	atg	ggg	gtg	ggc	gtc	ttc	acc	ccc	acc	att	2129	
Leu	Ala	Ala	Arg	Ser	Asp	Met	Gly	Val	Gly	Val	Phe	Thr	Pro	Thr	Ile		
			585				590						595				
gag	gcc	cgc	aca	gcc	cag	tcc	acc	ccc	tcc	gcc	cct	ccc	cag	aag	gtg	2177	
Glu	Ala	Arg	Thr	Ala	Gln	Ser	Thr	Pro	Ser	Ala	Pro	Pro	Gln	Lys	Val		
		600					605					610					
atg	tgt	gtg	agc	atg	ggc	tcc	acc	acg	gtc	cgg	gta	agt	tgg	gtc	ccg	2225	
Met	Cys	Val	Ser	Met	Gly	Ser	Thr	Thr	Val	Arg	Val	Ser	Trp	Val	Pro		
		615				620					625						
ccg	cct	gcc	gac	agc	cgc	aac	ggc	gtt	atc	acc	cag	tac	tcc	gtg	gcc	2273	

Pro Pro Ala Asp Ser Arg Asn Gly Val Ile Thr Gln Tyr Ser Val Ala	
630 635 640 645	
tac gag gcg gtg gac ggc gag gac cgc ggg cgg cat gtg gtg gat ggc	2321
Tyr Glu Ala Val Asp Gly Glu Asp Arg Gly Arg His Val Val Asp Gly	
650 655 660	
atc agc cgt gag cac tcc agc tgg gac ctg gtg ggc ctg gag aag tgg	2369
Ile Ser Arg Glu His Ser Ser Trp Asp Leu Val Gly Leu Glu Lys Trp	
665 670 675	
acg gag tac cgg gtg tgg gtg cgg gca cac aca gac gtg ggc ccc ggc	2417
Thr Glu Tyr Arg Val Trp Val Arg Ala His Thr Asp Val Gly Pro Gly	
680 685 690	
ccc gag agc agc ccg gtg ctg gtg cgc acc gat gag gac gtg ccc agc	2465
Pro Glu Ser Ser Pro Val Leu Val Arg Thr Asp Glu Asp Val Pro Ser	
695 700 705	
ggg cct ccg cgg aag gtg gag gtg gag cca ctg aac tcc act gct gtg	2513
Gly Pro Pro Arg Lys Val Glu Val Glu Pro Leu Asn Ser Thr Ala Val	
710 715 720 725	
cat gtc tac tgg aag ctg cct gtc ccc agc aag cag cat ggc cag atc	2561
His Val Tyr Trp Lys Leu Pro Val Pro Ser Lys Gln His Gly Gln Ile	
730 735 740	
cgc ggc tac cag gtc acc tac gtg cgg ctg gag aat ggc gag ccc cgt	2609
Arg Gly Tyr Gln Val Thr Tyr Val Arg Leu Glu Asn Gly Glu Pro Arg	
745 750 755	
gga ctc ccc atc atc caa gac gtc atg cta gcc gag gcc cag tgg cgg	2657
Gly Leu Pro Ile Ile Gln Asp Val Met Leu Ala Glu Ala Gln Trp Arg	
760 765 770	
cca gag gag tcc gag gac tat gaa acc act atc agc ggc ctg acc ccg	2705
Pro Glu Glu Ser Glu Asp Tyr Glu Thr Thr Ile Ser Gly Leu Thr Pro	
775 780 785	
gag acc acc tac tcc gtt act gtt gct gcc tat acc acc aag ggg gat	2753
Glu Thr Thr Tyr Ser Val Thr Val Ala Ala Tyr Thr Thr Lys Gly Asp	
790 795 800 805	
ggg gcc cgc agc aag ccc aaa att gtc act aca aca ggt gca gtc cca	2801
Gly Ala Arg Ser Lys Pro Lys Ile Val Thr Thr Thr Gly Ala Val Pro	
810 815 820	
ggc cgg ccc acc atg atg atc agc acc acg gcc atg aac act gcg ctg	2849
Gly Arg Pro Thr Met Met Ile Ser Thr Ala Met Asn Thr Ala Leu	
825 830 835	
ctc cag tgg cac cca ccc aag gaa ctg cct ggc gag ctg ctg ggc tac	2897
Leu Gln Trp His Pro Pro Lys Glu Leu Pro Gly Glu Leu Leu Gly Tyr	
840 845 850	
cgg ctg cag tac tgc cgg gcc gac gag gcg cgg ccc aac acc ata gat	2945
Arg Leu Gln Tyr Cys Arg Ala Asp Glu Ala Arg Pro Asn Thr Ile Asp	
855 860 865	
ttc ggc aag gat gac cag cac ttc aca gtc acc ggc ctg cac aag ggg	2993
Phe Gly Lys Asp Asp Gln His Phe Thr Val Thr Gly Leu His Lys Gly	
870 875 880 885	
acc acc tac atc ttc cgg ctt gct gcc aag aac cgg gct ggc ttg ggt	3041

Thr Thr Tyr Ile Phe Arg Leu Ala Ala Lys Asn Arg Ala Gly Leu Gly	
890 895 900	
gag gag ttc gag aag gag atc agg acc ccc gag gac ctg ccc agc ggc	3089
Glu Glu Phe Glu Lys Glu Ile Arg Thr Pro Glu Asp Leu Pro Ser Gly	
905 910 915	
ttc ccc caa aac ctg cat gtg aca gga ctg acc acg tct acc aca gaa	3137
Phe Pro Gln Asn Leu His Val Thr Gly Leu Thr Thr Ser Thr Thr Glu	
920 925 930	
ctg gcc tgg gac ccg cca gtg ctg gcg gag agg aac ggg cgc atc atc	3185
Leu Ala Trp Asp Pro Pro Val Leu Ala Glu Arg Asn Gly Arg Ile Ile	
935 940 945	
agc tac acc gtg gtg ttc cga gac atc aac agc caa cag gag ctg cag	3233
Ser Tyr Thr Val Val Phe Arg Asp Ile Asn Ser Gln Gln Glu Leu Gln	
950 955 960 965	
aac atc acg aca gac acc cgc ttt acc ctt act ggc ctc aag cca gac	3281
Asn Ile Thr Thr Asp Thr Arg Phe Thr Leu Thr Gly Leu Lys Pro Asp	
970 975 980	
acc act tac gac atc aag gtc cgc gca tgg acc agc aaa ggc tct ggc	3329
Thr Thr Tyr Asp Ile Lys Val Arg Ala Trp Thr Ser Lys Gly Ser Gly	
985 990 995	
cca ctc agc ccc agc atc cag tcc cgg acc atg ccg gtg gag caa gtg	3377
Pro Leu Ser Pro Ser Ile Gln Ser Arg Thr Met Pro Val Glu Gln Val	
1000 1005 1010	
ttt gcc aag aac ttc cgg gtg gcg gct gca atg aag acg tct gtg ctg	3425
Phe Ala Lys Asn Phe Arg Val Ala Ala Ala Met Lys Thr Ser Val Leu	
1015 1020 1025	
ctc agc tgg gag gtt ccc gac tcc tat aag tca gct gtg ccc ttt aag	3473
Leu Ser Trp Glu Val Pro Asp Ser Tyr Lys Ser Ala Val Pro Phe Lys	
1030 1035 1040 1045	
att ctg tac aat ggg cag agt gtg gag gtg gac ggg cac tcg atg cgg	3521
Ile Leu Tyr Asn Gly Gln Ser Val Glu Val Asp Gly His Ser Met Arg	
1050 1055 1060	
aag ctg atc gca gac ctg cag ccc aac aca gag tac tcg ttt gtg ctg	3569
Lys Leu Ile Ala Asp Leu Gln Pro Asn Thr Glu Tyr Ser Phe Val Leu	
1065 1070 1075	
atg aac cgt ggc agc agc gca ggg ggc ctg cag cac ctg gtg tcc atc	3617
Met Asn Arg Gly Ser Ser Ala Gly Gly Leu Gln His Leu Val Ser Ile	
1080 1085 1090	
cgc aca gcc ccc gac ctc ctg cct cac aag ccg ctg cct gcc tct gcc	3665
Arg Thr Ala Pro Asp Leu Leu Pro His Lys Pro Leu Pro Ala Ser Ala	
1095 1100 1105	
tac ata gag gac ggc cgc ttc gat ctc tcc atg ccc cat gtg caa gac	3713
Tyr Ile Glu Asp Gly Arg Phe Asp Leu Ser Met Pro His Val Gln Asp	
1110 1115 1120 1125	
ccc tcg ctt gtc agg tgg ttc tac att gtt gtg gta ccc att gac cgt	3761
Pro Ser Leu Val Arg Trp Phe Tyr Ile Val Val Val Pro Ile Asp Arg	
1130 1135 1140	
gtg ggc ggg agc atg ctg acg cca agg tgg agc aca ccc gag gaa ctg	3809

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Val Gly Gly Ser Met Leu Thr Pro Arg Trp Ser Thr Pro Glu Glu Leu	
1145 1150 1155	
gag ctg gac gag ctt cta gaa gcc atc gag caa ggc gga gag gag cag	3857
Glu Leu Asp Glu Leu Leu Glu Ala Ile Glu Gln Gly Gly Glu Glu Gln	
1160 1165 1170	
cgg cgg cgg cgg cgg cag gca gaa cgt ctg aag cca tat gtg gct gct	3905
Arg Arg Arg Arg Arg Gln Ala Glu Arg Leu Lys Pro Tyr Val Ala Ala	
1175 1180 1185	
caa ctg gat gtg ctc ccg gag acc ttt acc ttg ggg gac aag aag aac	3953
Gln Leu Asp Val Leu Pro Glu Thr Phe Thr Leu Gly Asp Lys Lys Asn	
1190 1195 1200 1205	
tac cgg ggc ttc tac aac cgg ccc ctg tct ccg gac ttg agc tac cag	4001
Tyr Arg Gly Phe Tyr Asn Arg Pro Leu Ser Pro Asp Leu Ser Tyr Gln	
1210 1215 1220	
tgc ttt gtg ctt gcc tcc ttg aag gaa ccc atg gac cag aag cgc tat	4049
Cys Phe Val Leu Ala Ser Leu Lys Glu Pro Met Asp Gln Lys Arg Tyr	
1225 1230 1235	
gcc tcc agc ccc tac tcg gat gag atc gtg gtc cag gtg aca cca gcc	4097
Ala Ser Ser Pro Tyr Ser Asp Glu Ile Val Val Gln Val Thr Pro Ala	
1240 1245 1250	
cag cag cag gag gag ccg gag atg ctg tgg gtg acg ggt ccc gtg ctg	4145
Gln Gln Gln Glu Glu Pro Glu Met Leu Trp Val Thr Gly Pro Val Leu	
1255 1260 1265	
gca gtc atc ctc atc atc ctc att gtc atc gcc atc ctc ttg ttc aaa	4193
Ala Val Ile Leu Ile Ile Leu Ile Val Ile Ala Ile Leu Leu Phe Lys	
1270 1275 1280 1285	
agg aaa agg acc cac tct ccg tcc tct aag gat gag cag tcg atc gga	4241
Arg Lys Arg Thr His Ser Pro Ser Ser Lys Asp Glu Gln Ser Ile Gly	
1290 1295 1300	
ctg aag gac tcc ttg ctg gcc cac tcc tct gac cct gtg gag atg cgg	4289
Leu Lys Asp Ser Leu Leu Ala His Ser Ser Asp Pro Val Glu Met Arg	
1305 1310 1315	
agg ctc aac tac cag acc cca ggt atg cga gac cac cca ccc atc ccc	4337
Arg Leu Asn Tyr Gln Thr Pro Gly Met Arg Asp His Pro Pro Ile Pro	
1320 1325 1330	
atc acc gac ctg gcg gac aac atc gag cgc ctc aaa gcc aac gat ggc	4385
Ile Thr Asp Leu Ala Asp Asn Ile Glu Arg Leu Lys Ala Asn Asp Gly	
1335 1340 1345	
ctc aag ttc tcc cag gag tat gag tcc atc gac cct gga cag cag ttc	4433
Leu Lys Phe Ser Gln Glu Tyr Glu Ser Ile Asp Pro Gly Gln Gln Phe	
1350 1355 1360 1365	
acg tgg gag aat tca aac ctg gag gtg aac aag ccc aag aac cgc tat	4481
Thr Trp Glu Asn Ser Asn Leu Glu Val Asn Lys Pro Lys Asn Arg Tyr	
1370 1375 1380	
gcg aat gtc atc gcc tac gac cac tct cga gtc atc ctt acc tct atc	4529
Ala Asn Val Ile Ala Tyr Asp His Ser Arg Val Ile Leu Thr Ser Ile	
1385 1390 1395	
gat ggc gtc ccc ggg agt gac tac atc aat gcc aac tac atc gat ggc	4577

Asp Gly Val Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Asp Gly  
 1400 1405 1410

tac cgc aag cag aat gcc tac atc gcc acg cag ggc ccc ctg ccc gag 4625  
 Tyr Arg Lys Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu  
 1415 1420 1425

acc atg ggc gat ttc tgg aga atg gtg tgg gaa cag cgc acg gcc act 4673  
 Thr Met Gly Asp Phe Trp Arg Met Val Trp Glu Gln Arg Thr Ala Thr  
 1430 1435 1440 1445

gtg gtc atg atg aca cgg ctg gag gag aag tcc cgg gta aaa tgt gat 4721  
 Val Val Met Met Thr Arg Leu Glu Glu Lys Ser Arg Val Lys Cys Asp  
 1450 1455 1460

cag tac tgg cca gcc cgt ggc acc gag acc tgt ggc ctt att cag gtg 4769  
 Gln Tyr Trp Pro Ala Arg Gly Thr Glu Thr Cys Gly Leu Ile Gln Val  
 1465 1470 1475

acc ctg ttg gac aca gtg gag ctg gcc aca tac act gtg cgc acc ttc 4817  
 Thr Leu Leu Asp Thr Val Glu Leu Ala Thr Tyr Thr Val Arg Thr Phe  
 1480 1485 1490

gca ctc cac aag agt ggc tcc agt gag aag cgt gag ctg cgt cag ttt 4865  
 Ala Leu His Lys Ser Gly Ser Ser Glu Lys Arg Glu Leu Arg Gln Phe  
 1495 1500 1505

cag ttc atg gcc tgg cca gac cat gga gtt cct gag tac cca act ccc 4913  
 Gln Phe Met Ala Trp Pro Asp His Gly Val Pro Glu Tyr Pro Thr Pro  
 1510 1515 1520 1525

atc ctg gcc ttc cta cga cgg gtc aag gcc tgc aac ccc cta gac gca 4961  
 Ile Leu Ala Phe Leu Arg Arg Val Lys Ala Cys Asn Pro Leu Asp Ala  
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ggg ccc atg gtg gtg cac tgc agc gcg ggc gtg ggc cgc acc ggc tgc 5009  
 Gly Pro Met Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Cys  
 1545 1550 1555

ttc atc gtg att gat gcc atg ttg gag cgg atg aag cac gag aag acg 5057  
 Phe Ile Val Ile Asp Ala Met Leu Glu Arg Met Lys His Glu Lys Thr  
 1560 1565 1570

gtg gac atc tat ggc cac gtg acc tgc atg cga tca cag agg aac tac 5105  
 Val Asp Ile Tyr Gly His Val Thr Cys Met Arg Ser Gln Arg Asn Tyr  
 1575 1580 1585

atg gtg cag acg gag gac cag tac gtg ttc atc cat gag gcg ctg ctg 5153  
 Met Val Gln Thr Glu Asp Gln Tyr Val Phe Ile His Glu Ala Leu Leu  
 1590 1595 1600 1605

gag gct gcc acg tgc ggc cac aca gag gtg cct gcc cgc aac ctg tat 5201  
 Glu Ala Ala Thr Cys Gly His Thr Glu Val Pro Ala Arg Asn Leu Tyr  
 1610 1615 1620

gcc cac atc cag aag ctg ggc caa gtg cct cca ggg gag agt gtg acc 5249  
 Ala His Ile Gln Lys Leu Gly Gln Val Pro Pro Gly Glu Ser Val Thr  
 1625 1630 1635

gcc atg gag ctc gag ttc aag ttg ctg gcc agc tcc aag gcc cac acg 5297  
 Ala Met Glu Leu Glu Phe Lys Leu Leu Ala Ser Ser Lys Ala His Thr  
 1640 1645 1650

tcc cgc ttc atc agc gcc aac ctg ccc tgc aac aag ttc aag aac cgg 5345

Ser Arg Phe Ile Ser Ala Asn Leu Pro Cys Asn Lys Phe Lys Asn Arg	
1655 1660 1665	
ctg gtg aac atc atg ccc tac gaa ttg acc cgt gtg tgt ctg cag ccc	5393
Leu Val Asn Ile Met Pro Tyr Glu Leu Thr Arg Val Cys Leu Gln Pro	
1670 1675 1680 1685	
atc cgt ggt gtg gag ggc tct gac tac atc aat gcc agc ttc ctg gat	5441
Ile Arg Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe Leu Asp	
1690 1695 1700	
ggt tat aga cag cag aag gcc tac ata gct aca cag ggg cct ctg gca	5489
Gly Tyr Arg Gln Gln Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ala	
1705 1710 1715	
gag agc acc gag gac ttc tgg cgc atg cta tgg gag cac aat tcc acc	5537
Glu Ser Thr Glu Asp Phe Trp Arg Met Leu Trp Glu His Asn Ser Thr	
1720 1725 1730	
atc atc gtc atg ctg acc aag ctt cgg gag atg ggc agg gag aaa tgc	5585
Ile Ile Val Met Leu Thr Lys Leu Arg Glu Met Gly Arg Glu Lys Cys	
1735 1740 1745	
cac cag tac tgg cca gca gag cgc tct gct cgc tac cag tac ttt gtt	5633
His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr Phe Val	
1750 1755 1760 1765	
gtt gac ccg atg gct gag tac aac atg ccc cag tat atc ctg cgt gag	5681
Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln Tyr Ile Leu Arg Glu	
1770 1775 1780	
ttc aag gtc acg gat gcc cgg gat ggg cag tca agg aca atc cgg cag	5729
Phe Lys Val Thr Asp Ala Arg Asp Gly Gln Ser Arg Thr Ile Arg Gln	
1785 1790 1795	
ttc cag ttc aca gac tgg cca gag cag ggc gtg ccc aag aca ggc gag	5777
Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Val Pro Lys Thr Gly Glu	
1800 1805 1810	
gga ttc att gac ttc atc ggg cag gtg cat aag acc aag gag cag ttt	5825
Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys Glu Gln Phe	
1815 1820 1825	
gga cag gat ggg cct atc acg gtg cac tgc agt gct ggc gtg ggc cgc	5873
Gly Gln Asp Gly Pro Ile Thr Val His Cys Ser Ala Gly Val Gly Arg	
1830 1835 1840 1845	
acc ggg gtg ttc atc act ctg agc atc gtc ctg gag cgc atg cgc tat	5921
Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg Met Arg Tyr	
1850 1855 1860	
gag ggc gtg gtc gac atg ttt cag acc gtg aag acc ctg cgt aca cag	5969
Glu Gly Val Val Asp Met Phe Gln Thr Val Lys Thr Leu Arg Thr Gln	
1865 1870 1875	
cgt cct gcc atg gtg cag aca gag gac cag tat cag ctg tgc tac cgt	6017
Arg Pro Ala Met Val Gln Thr Glu Asp Gln Tyr Gln Leu Cys Tyr Arg	
1880 1885 1890	
gcg gcc ctg gag tac ctc ggc agc ttt gac cac tat gca acg taa cta	6065
Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr *	
1895 1900 1905	
ccgctccct ctcctccgcc acccccgccg tggggctccg gaggggaccc agctcctctg	6125



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agccataccg accatcgctcc agccctccta cgcagatgct gtcactggca gagcacagcc 6185
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<210> 15
<211> 1309
<212> DNA
<213> Homo sapiens

<220>

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&lt;221&gt; CDS

&lt;222&gt; (484) .. (765)

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catttataat aagaatgagt tattcatttg taagccgttc agtaatttat ctactattcc      120
taaattggca taatgttaga taatctatct tgaatcacct ttaattacat gtcagaatgc      180
cttaactacc ctaacttgac aaaacagaat tctttggtag acgcggtggg ggcgggggtgg      240
ggggctctgga cggagctctct atttaaggag aaatcatcat gctatgataa aacacagaag      300
catgagtggc aagtggcggg gtatttattt tgcacaaact atttgagtc tctgtgtatt      360
taaaaagtaa agaaagttgc atccagaagg gttttgttag aatgaatata tttatattag      420
gactgacaac ttcagctctt ttgttttagt tttcaattat ttttggttaag agtatgtagc      480
ctt  atg atc tgg ata tat ttt gca ttc att ttc caa cgc cta cat tta      528
      Met Ile Trp Ile Tyr Phe Ala Phe Ile Phe Gln Arg Leu His Leu
        1             5             10             15

att cct ggt aag agc agt gct cgt caa gtt tct ggt ttt tct ctg ctc      576
Ile Pro Gly Lys Ser Ser Ala Arg Gln Val Ser Gly Phe Ser Leu Leu
          20             25             30

tca ttt aac ccg tca aac aca atc ttt gta aag cta gat tgg tgg tgt      624
Ser Phe Asn Pro Ser Asn Thr Ile Phe Val Lys Leu Asp Trp Trp Cys
          35             40             45

ttt ata caa ctt att tac tca gct tac ctt ttt gag aaa cga ttg tta      672
Phe Ile Gln Leu Ile Tyr Ser Ala Tyr Leu Phe Glu Lys Arg Leu Leu
          50             55             60

gaa att gac gat gtg ttt gtt cca gtg ata ctg aaa gta gtg ggg gca      720
Glu Ile Asp Asp Val Phe Val Pro Val Ile Leu Lys Val Val Gly Ala
          65             70             75

aga att gag ttt cac agt gga att ggc ttt gga tct ggc cta tag att      768
Arg Ile Glu Phe His Ser Gly Ile Gly Phe Gly Ser Gly Leu *
          80             85             90

agtgacataa aatattttct ctattttccc ctgtttcttt tgtgttatgc acttaatttt      828
atgactgccg ggggggtcag ctggagtgct gcttaacaag tatctctcct actctcagtg      888
gtcagaggct gtgttggaac catagtagaa ttttccaggt cacagacca agcttccatg      948
ggttgttact gtgctgtacc acttggtggg tctgattctg aacctgatgt gtgtgttaat      1008
tatattttta gcaacacaca cacacacaca cgcctcatgt aatggacttt tataacaaaa      1068
gaaaaaattt ggattttctaa tttacaaatg gcaaattatt tatccctctc tggatgcacc      1128
aaagaccagt aaagtttata gcttttccat ctatatttat aaagcaatac tgtattataa      1188
aatcaatat ttttatcaca tgcttgaaat ttttattttg ttgttttaaa atgtgcactc      1248
taaacatata agaaccttat ttcttctat gaacttaagc tgcttgcgca caaaaaaaaaa      1308
a                                                                 1309

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<210> 16  
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 <213> Homo sapiens  
  
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 tcgtgaggct gaggtgcagc atgtctagac tgggagccct gggtggtgcc cgtgccgggc 180  
 tgggactgtt gctgggtacc gccgccggcc ttggattcct gtgcctcctt tacagccagc 240  
 g atg gaa acg gac cca gcg tca tgg ccg cag cca gag cct gcc caa 286  
 Met Glu Thr Asp Pro Ala Ser Trp Pro Gln Pro Glu Pro Ala Gln  
 1 5 10 15  
 ctc cct gga cta tac gca gac ttc aga tcc cgg acg cca cgt gat gct 334  
 Leu Pro Gly Leu Tyr Ala Asp Phe Arg Ser Arg Thr Pro Arg Asp Ala  
 20 25 30  
 cct gcg ggc tgt ccc agg tgg ggc tgg aga tgc ctc agt gct gcc cag 382  
 Pro Ala Gly Cys Pro Arg Trp Gly Trp Arg Cys Leu Ser Ala Ala Gln  
 35 40 45  
 cct tcc acg gga agg aca gga gaa ggt gct gga ccg cct gga ctt tgt 430  
 Pro Ser Thr Gly Arg Thr Gly Glu Gly Ala Gly Pro Pro Gly Leu Cys  
 50 55 60  
 gct gac cag cct tgt ggc gct gcg gcg gga ggt gga gga gct gag aag 478  
 Ala Asp Gln Pro Cys Gly Ala Ala Ala Gly Gly Gly Gly Ala Glu Lys  
 65 70 75  
 cag cct gcg agg gct tgc ggg gga gat tgt tgg gga ggt ccg atg cca 526  
 Gln Pro Ala Arg Ala Cys Gly Gly Asp Cys Trp Gly Gly Pro Met Pro  
 80 85 90 95  
 cat gga aga gaa cca gag agt ggc tcg gcg gcg aag gtt tcc gtt tgt 574  
 His Gly Arg Glu Pro Glu Ser Gly Ser Ala Ala Lys Val Ser Val Cys  
 100 105 110  
 ccg gga gag gag tga ctccactggc tccagctctg tctacttcac ggctcctcg 629  
 Pro Gly Glu Glu \*  
 115  
 ggagccacgt tcacagatgc tgagagtga ggggggtgag ttgtctctct tggaggcagt 689  
 tatggctaca gccaggttgt gttttgtaaa agtattatca atggaaaatt caaaccaagc 749  
 tgctgcaaat gatttttggga acaggtaaga gtataataaa tacagaagag ttgaaacaaa 809  
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 atctgttata ttagtttatt acatagttat gatataattat ttgggcattt ttctgtctta 929  
 tcacaaggac ttgataagca ttgtttgact ttgttccttt ccttgggtgg ctgagctggt 989

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atacggagat gtctaagcac gaagcatgct cctccctggg agtcaccctc ttcccacagg 1049
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agtggcccag gagggtctgac gataggcctt tctgtgaggc ggggcagctg gcacgagtct 1169
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gccactgtc cccctctct cccacaccat ctatccgtca accttcaatc cgcctctgac 1529
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ccgataaatc c 1600

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<210> 17
<211> 735
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (402)..(482)

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aaaaagggtt ccccccggt tttttggtg ccccccccc tccccgtaa acccggggtt 120
attctaaaaa ggttttaggc ccgtagggc ccttccaat ttgttttaa aaattcaatt 180
ccggcccccc tttttttttt ttttttcaga aaggattttg gttttgtccc ccggtgggag 240
cccattaacc cagatcctt ccccgcccc cccccctggg ggcaaaagg gaccctttt 300
ccaaaaaaa aaaaaaaaa agaataataa tgtgggtatg atgtgagata cgcagcaaa 360
gtatgtaata taatgctgc cctccagtag ctgtattgt a atg tac ttc ata 413
Met Tyr Phe Ile
1

tgg ata ggg aca gtg ttt ctt att tgc tgc tat ctg ttc caa gtg tct 461
Trp Ile Gly Thr Val Phe Leu Ile Cys Cys Tyr Leu Phe Gln Val Ser
5 10 15 20

agt gtg gta cct aac acc taa tg ggcacttaca tgtgtgttga atagtgaag 514
Ser Val Val Pro Asn Thr *
25

ggaaaaggaa ccagaatcta ggagaacagt taattattac cattctccct cattctctt 574
catctcagtt ttaggtgaaa taggcaaaag aatttcacta cttaaacaat ttgaagtga 634

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ggtgagaaat aagagagaaa atgcaaggaa gaaaaaactg tgtgacgtct tctatgtaca 694  
agccagttct cgtgccgaat tcttgccctc gagggccaaa t 735

<210> 18  
<211> 1031  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (133)..(264)

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aagcacgggc tt atg gga ccc ggg ttc ctt cag tgc tca ccc acg aag 168  
Met Gly Pro Gly Phe Leu Gln Cys Ser Pro Thr Lys  
1 5 10  
aag ggc tcc caa acg gcc cca ctc gac ggc tca ccg gag gat ggt cct 216  
Lys Gly Ser Gln Thr Ala Pro Leu Asp Gly Ser Pro Glu Asp Gly Pro  
15 20 25  
gcg cag tgg gtg ttt gtt gaa cag ata aga gac aac aaa aca gac taa 264  
Ala Gln Trp Val Phe Val Glu Gln Ile Arg Asp Asn Lys Thr Asp \*  
30 35 40  
gaagaggcct gttctatgaa ccggggaaaag tgaaggaatc acaaagagcg gctcgcctta 324  
gggcaatcct ggggaaaaga tggagaggca tggatttttc ttggatgtgt gcctcctcct 384  
ggggctcatc cctctgagca tcaaatttc attgcaaaag agggggaaaa actctgctgc 444  
ggacaatgct ggatggtctg atctctccct tggccagaat taacggggca attcctaacc 504  
cctgttggtc ctcagaatca cctggcctat gcacactccc gctaaaccac tgaagtccaa 564  
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ggctaattta gtcattcatg cctttttaga gcaaattaca tgtggagagg gtggggcaca 864  
ctgaatttta ttttagccaa atgcccctta tctccttatg caattgatat ttttatattg 924  
aacattagag gattgggtcat ttgtcatcaa gtcgtctgta atacagaaaa cgataaatac 984  
aacctaacag ttcaaacatg acgagttaaa taaatgatgg ttaaaaa 1031

<210> 19  
<211> 780

<212> DNA  
<213> Homo sapiens

<220>  
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<222> (271) .. (435)

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aaaaatgagac cacaaggag tatgctataa atcaaatttg ccaaccaatt atgtagatat 180  
tactcattct aggactaatg atgatggtaa agaagttgcc agtggtatgg caatgaaaat 240  
ttcagaaagg aggagttgat gatcttctag atg tat atg aac acc tgt cta 291  
Met Tyr Met Asn Thr Cys Leu  
1 5  
tat ctg cat gta tat gtt ttg acc tgc agt ggt tgc aat gtt gat atg 339  
Tyr Leu His Val Tyr Val Leu Thr Cys Ser Gly Cys Asn Val Asp Met  
10 15 20  
tgt tca aga tta ttc ctg tct aca aaa ctg aag gcc cat gtt caa att 387  
Cys Ser Arg Leu Phe Leu Ser Thr Lys Leu Lys Ala His Val Gln Ile  
25 30 35  
gtt ctt tat tgg gtg ttt tta tgg tca cgt ggt aac aat ttt ctt acc 435  
Val Leu Tyr Trp Val Phe Leu Trp Ser Arg Gly Asn Asn Phe Leu Thr  
40 45 50 55  
taacctacaa aaggttctct tgatgaacat ttttatttat atttactaat ctttttaaaa 495  
aaaagctttc atagcattat ataatcagat gaagaaagcc cagtagaata aaaaaaaaaat 555  
tcattagcct agcctatatt atgttttctg tcaaaggaaa acaaattctc aaataggaat 615  
tctaaaaata ttactaaag taaaataact acttaaaatg ttttattcca gttggaagga 675  
aggtacaggg agaaatcgca attatttagg ggagaagtat atttattata agatggtgtc 735  
ctcaaattag cctaccatgg cacgtagggg cagcagctat attag 780

<210> 20  
<211> 644  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (66) .. (221)

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ggatt atg gta att ctg gat gtc ctt gaa ctg tat cac atg tgg ttt 107  
Met Val Ile Leu Asp Val Leu Glu Leu Tyr His Met Trp Phe  
1 5 10  
ctt ggc ata tta tat gat gca att ttt tat tgc ttt gtc cat gca ata 155

Leu Gly Ile Leu Tyr Asp Ala Ile Phe Tyr Cys Phe Val His Ala Ile  
 15 20 25 30  
 aac gct gat aaa ttt ttc ggt tta aaa ttt acc aag tct gct act gta 203  
 Asn Ala Asp Lys Phe Phe Gly Leu Lys Phe Thr Lys Ser Ala Thr Val  
 35 40 45  
 tcc cag aat tct caa tga aagaaa atatttacag tttttaacat tacaggtaga 257  
 Ser Gln Asn Ser Gln \*  
 50  
 aaaaggatca aagtgatttt cttatttttc tatctaattc atggaaaaaa gaacacaggc 317  
 agggaggggc tttgctcctg ttccccaatt ttctttgtcc aaatgggtca gccttgaatt 377  
 caagaggagt ggtgcaggat ttaattgttc ccacttgtct tccttgtgca aaactgcagc 437  
 tagaagagca aatgataagt tgagaatatt taacactcag caacaatacc aggaacttgt 497  
 tcaaactttg tttttgaagc ttcttgacct tccaatgatt tattttcttc acacatgggt 557  
 tcattagaac ttcacttgga gaagaagaga aatagcatat aacaacattc ttcacttata 617  
 accagaatat tccaagcctt tccaaag 644

<210> 21  
 <211> 825  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (113)..(277)

<400> 21  
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 atgttaaaga actatctttc caaacgtaa acactgcctt ccctttactt aa atg 115  
 Met  
 1  
 tac gat ttt ctt ttg ctc ttg agt ttt att ttc ata gtg gca tct tac 163  
 Tyr Asp Phe Leu Leu Leu Leu Ser Phe Ile Phe Ile Val Ala Ser Tyr  
 5 10 15  
 tgg tct ttc ctt tcc acc ata ttt ttg gat gtt gtg tgt tcc att tta 211  
 Trp Ser Phe Leu Ser Thr Ile Phe Leu Asp Val Val Cys Ser Ile Leu  
 20 25 30  
 cat tgc cca gtt aaa cca cag aca ctc ctg aag tca tgt tta cat gtg 259  
 His Cys Pro Val Lys Pro Gln Thr Leu Leu Lys Ser Cys Leu His Val  
 35 40 45  
 gac tgc aag tca acc tag ttggca tgttgatcta agctacaaat tgcactgctg 313  
 Asp Cys Lys Ser Thr \*  
 50 55  
 ttttgccgaa cccaacagtc ggtttcttgc cattatttgc ggtattttta cttaaaactc 373  
 acggtaatcc ttctcaccac atctagtttg ttttaattga tctaacaaac actgcttggt 433

tgaattcaaa tggaggatcc atggaagctc tcccacccca ccctttgata cttgataagg 493  
 ggtcaaacag tacttctttt aaattcagat aattctttga atgaactatg aaatacttca 553  
 gagggaaagg aaatatcgat tctgagatgg agagtaaaag aacaaggaga tattcattac 613  
 tgttgagat aatttcttgc aatgaaagga aaaaattaga cggtggatat ttttggttgt 673  
 ggtggttgta tagtgaggat aggtggacaa tagaaaaatc ttccttgggg attgaagttc 733  
 taaatctaga acttaattct gaagctggca cctttacttg gacagcccac tatgggaggg 793  
 aatctaaaaa cctacctttg attagaaacc tg 825

<210> 22  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (709) .. (966)

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 caccctatct ggggtgccct aaacaggggt gtgggagctc aggcattggg gccgggcttt 180  
 aagcaccttc ccagacccca agaccctctg tcagcagcag ctgtgcccc aagcccaggc 240  
 tcactgtgta aatcccaacc ccatgagccc caggccacac cagacccct ctgcaggccg 300  
 ctgtgagcat tctccattga gaaacatctg cccactaga caccggcccc tccccctgca 360  
 gcctcctgcc ccattagca cctgaattgc agcaaattgtg acccagaaac accgcctggg 420  
 ggatgcagcc agcgggtgga gcgtggagag ggatggggtg gccatgtgaa cccctcactc 480  
 agccccattc caaggcctga agtcccgta ccttcctcca gcctcctgg cggccccac 540  
 tttacagatg gcacaactga gacttgggag tggagggcac agggctcctc ccatggggac 600  
 cctgggagcc accagaggcc ccagatgctc ctgcccctct gggaacagtc tttcccaga 660  
 cattgcactc ctcaaagctg cattttcaat taactgtgcc gctgaggg atg tgg cct 717  
 Met Trp Pro  
 1

ggg tgc cag gtt ttg agg gct ggg ctg agt cct gca ggc agg gcc cgc 765  
 Gly Cys Gln Val Leu Arg Ala Gly Leu Ser Pro Ala Gly Arg Ala Arg  
 5 10 15

ttc cca ccg gac acc tac ctg ccc agc ccc agg cag gga ggg aac cct 813  
 Phe Pro Pro Asp Thr Tyr Leu Pro Ser Pro Arg Gln Gly Gly Asn Pro  
 20 25 30 35

gcg tgc aga tgt gtg act gcc atg aat gcg gtt ttg caa gtt ttg cca 861  
 Ala Cys Arg Cys Val Thr Ala Met Asn Ala Val Leu Gln Val Leu Pro  
 40 45 50



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cat cca gcc cct gac aca aac agg gct gat gag ggc tgt gga gac cag      909
His Pro Ala Pro Asp Thr Asn Arg Ala Asp Glu Gly Cys Gly Asp Gln
          55                      60                      65

gag gga agc agg gag ctt cct ccg ggt ggg gct gcc ttg ggg cac agg      957
Glu Gly Ser Arg Glu Leu Pro Pro Gly Gly Ala Ala Leu Gly His Arg
          70                      75                      80

ggg cag taa gctggcc aacagaagct gactcatgcc ccccaacccc accatacaga      1013
Gly Gln *
          85

tgtggaaact aaggccagag ggacagagca gcctcccacg tcctggggtg aacaccacac      1073

aggatcagtg gcctccgcga cggctggtag gagggaaagta ggcaaggaga gagggatgta      1133

ctcatctgga tgggatggcc actgccttcc cagactgtcc caagcttggg acattctgat      1193

ccccctgcag tccccaggaa gcggagcctc agagtctctt ggcttctagt cctcctgcga      1253

ggccctggga tggctcctca tggagaaacc aggttcccag tccccggctg ggcacagatg      1313

gtaccgggat ggctgaggcc atgaccctac ccctgtgagg ggcacagctc aaagggtctt      1373

ggcctcatcc cctgatacca accaccatgg ggtaatacct ggggtcgggtg aattagggaa      1433

agccaggtag cctctgggca gcacaagcca ggagcactac tgcctatagg gttaggagag      1493

gcccggggga gtgggtgccca gaccggggca gcatctcttc ctaccagct agcccgaaaag      1553

ctggtgaacc gtgtgcaccc tccccattgc tccggtaaag ggacagatgc cctgccagc      1613

cccaggagag cacctagtcg cgcacacgga gtccccaggc acacctctga agggggaatt      1673

ccaccgcact ggactaatgt tcatcaagg      1702

```

```

<210> 23
<211> 629
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (109)..(303)

```

```

<220>
<221> misc_feature
<222> (1)...(629)
<223> n = a,t,c or g

```

```

<400> 23
aacattttcca gaaccagaca gcatcctcac ttgtaccac taaaggtaac tactagtgtg      60

acttctatct ttgttggttg gttgtatcca ttcttgta tcataaag atg aaa cca      117
                               Met Lys Pro
                               1

tat tgt atg tat cct ttt ctg tct ggc ctg ctt agc tcc tta tta ttt      165
Tyr Cys Met Tyr Pro Phe Leu Ser Gly Leu Leu Ser Ser Leu Leu Phe
          5                      10                      15

```

```

tgg tta gag tca ttg atg ttg tta tgt gtg cag atg gtt ctt ttt tta      213
Trp Leu Glu Ser Leu Met Leu Leu Cys Val Gln Met Val Leu Phe Leu
  20                      25                      30                      35

atg cta tgt gta ttg gat tac agg ata tat tgc atc aaa att tat gta      261
Met Leu Cys Val Leu Asp Tyr Arg Ile Tyr Cys Ile Lys Ile Tyr Val
                      40                      45                      50

tcc att ata tta tta atg agc att tgg att att tca att taa gactatt      310
Ser Ile Ile Leu Leu Met Ser Ile Trp Ile Ile Ser Ile *
                      55                      60                      65

ttgaatacaa ttactgtaat tgtcttgttc atatcatgtg ttcaacatat gcacttactc      370

ctaagagagg aattttagg tcataggata tgtgtatgat cagcttgggt atacactacc      430

agttttctcc tgtcaaccag gcatgagaaa tctaattgcc ctatgtgctg actaaaacat      490

gaaattggga ggctctaat tctaaccctt ctggagaggg cccccccccc cccctggggg      550

gggggccttc cccccccacc ccgngggggn naatttttaa ataaagtcgt ggtaagtta      610

tagatttttt taaaaaatt                                              629

```

<210> 24  
 <211> 757  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (165)..(359)

<220>  
 <221> misc\_feature  
 <222> (1)..(757)  
 <223> n = a,t,c or g

```

<400> 24
tatagagacc actagtccaa gtggaggaat tcctcccttc tagccccctt ccttacctgg      60

taagtcaaat gaaccaaag tcaaacagtt tggaaaggag agttgaagca gaaggaaact      120

tccttctgcc cctttgaatt tgttactttt tcttccaatt aaaa atg tgt tat ttt      176
                               Met Cys Tyr Phe
                               1

tac aat acc att ata ttg aca ttg caa ggg tcc ctg atg ttt tta ttg      224
Tyr Asn Thr Ile Ile Leu Thr Leu Gln Gly Ser Leu Met Phe Leu Leu
  5                      10                      15                      20

ttt tct gtt gtc act ttg tat ctc ttc tcc cat tcc cat ccc act ccc      272
Phe Ser Val Val Thr Leu Tyr Leu Phe Ser His Ser His Pro Thr Pro
                      25                      30                      35

att agc atc ttc tct gat gtg ttt aat atg tat cct tgg ata tat atg      320
Ile Ser Ile Phe Ser Asp Val Phe Asn Met Tyr Pro Trp Ile Tyr Met
                      40                      45                      50

tat tct tac atg gtg ttt tct gta aat tta tat aaa tag tattacatga      369

```

Tyr Ser Tyr Met Val Phe Ser Val Asn Leu Tyr Lys \*  
 55 60 65

taattctcat tctgacccct tcttcattta aaactatggt tttcagttct gttgggtgttg 429  
 tgtttatatg gtgcttttag ccactgcatt gtatttttat tgctctgtct actgcgtttt 489  
 atttgctgt tcccctaagt gacagacacc ttatttggtc tccctgtacc acaaacaatg 549  
 ctctgtgggt atagtggctc acacttatag gctcagatct ttggggagga tgacgcagaa 609  
 agatcgcttg agcccaggag tttcaaacca aaccgggcaa tgagacccaa acctcatctc 669  
 tgccacaaat taaaaactta attgagcaca ttggcattgt gctccccccc canctncttc 729  
 acagactggg gaagaaaaac cattcacc 757

<210> 25  
 <211> 884  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (137)..(715)

<400> 25  
 ggacttcccg ggtcgccctg ggctgctcgt ctggtgctc gtgctccggc tgccttggcg 60  
 ggtgccgggc cagctggacc ccagcactgg ccggcggttc tcggagcaca aactctgcgc 120  
 ggacgacgaa tgcagc atg tta atg tac cgc ggt gag gct ctt gaa gat 169  
 Met Leu Met Tyr Arg Gly Glu Ala Leu Glu Asp  
 1 5 10

ttc aca ggc ccg gat tgt cgt ttt gtg aat ttt aaa aaa ggt gat cct 217  
 Phe Thr Gly Pro Asp Cys Arg Phe Val Asn Phe Lys Lys Gly Asp Pro  
 15 20 25

gta tat gtt tac tat aaa ctg gca aga gga tgg cct gaa gtt tgg gct 265  
 Val Tyr Val Tyr Tyr Lys Leu Ala Arg Gly Trp Pro Glu Val Trp Ala  
 30 35 40

gga agt gtt gga cgc act ttt gga tat ttt cca aaa gat tta atc cag 313  
 Gly Ser Val Gly Arg Thr Phe Gly Tyr Phe Pro Lys Asp Leu Ile Gln  
 45 50 55

gta gtt cat gaa tat acc aaa gaa gag cta caa gtt cca aca gat gag 361  
 Val Val His Glu Tyr Thr Lys Glu Glu Leu Gln Val Pro Thr Asp Glu  
 60 65 70 75

acg gat ttt gtt tgt ttt gat gga gga aga gat gat ttt cat aat tat 409  
 Thr Asp Phe Val Cys Phe Asp Gly Gly Arg Asp Asp Phe His Asn Tyr  
 80 85 90

aat gta gaa gaa ctt tta ggg ttt ttg gaa ctg tac aat tct gca gct 457  
 Asn Val Glu Glu Leu Leu Gly Phe Leu Glu Leu Tyr Asn Ser Ala Ala  
 95 100 105

aca gat tct gag aaa gct gta gaa caa act tta cag gat atg gaa aaa 505  
 Thr Asp Ser Glu Lys Ala Val Glu Gln Thr Leu Gln Asp Met Glu Lys

110	115	120	
aac cct gaa tta tct aat gaa agg gaa cct gaa cct gaa cca gta gaa			553
Asn Pro Glu Leu Ser Asn Glu Arg Glu Pro Glu Pro Glu Pro Val Glu			
125	130	135	
gcc aac tca gag gaa agt gat agt gta ttc tca gaa aac act gag gat			601
Ala Asn Ser Glu Glu Ser Asp Ser Val Phe Ser Glu Asn Thr Glu Asp			
140	145	150	155
ctt cag gaa cag ttt aca act tca aag cac cac tcc cat ggc aac agg			649
Leu Gln Glu Gln Phe Thr Thr Ser Lys His His Ser His Gly Asn Arg			
	160	165	170
caa gca aat tat gct tca gga gag cag gct tca ttt gaa tct ttt gaa			697
Gln Ala Asn Tyr Ala Ser Gly Glu Gln Ala Ser Phe Glu Ser Phe Glu			
	175	180	185
gaa atg ctg caa gaa taa aataaa agtgcgccgaa agtggaacc accaaccgg			751
Glu Met Leu Gln Glu *			
190			
cataagtctt aggtctccaa aggaccggaa aagaatgatg gctattaact tttgaaaaaa			811
aaaagactct tgaattggaa aaccaaattg gcttacagcc gaagcacttt tattttgatg			871
atggaccacc cga			884
<210> 26			
<211> 1070			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (111)..(305)			
<400> 26			
cgcaattccc gggctcgaccc acgcgtccgg ggtggaaaaa gtttgagaga aggagggagg			60
aaaagggtgtc ctggctagca ccatgtggat tctcttgaga tgagaagaaa atg ccc			116
		Met Pro	
		1	
ggc tac gtc ccc ctt ctg ctg ctc ctg ctt ctc ctg agg tgt tca caa			164
Gly Tyr Val Pro Leu Leu Leu Leu Leu Leu Leu Arg Cys Ser Gln			
5	10	15	
cgg ggt gga gga gtt aat ttt ggt gag aag gat gca aaa gtc ccc ggg			212
Arg Gly Gly Gly Val Asn Phe Gly Glu Lys Asp Ala Lys Val Pro Gly			
20	25	30	
acc tgg aga gat gga gtc agg gtc cct gga gaa gga gcc tct tgg gac			260
Thr Trp Arg Asp Gly Val Arg Val Pro Gly Glu Gly Ala Ser Trp Asp			
35	40	45	50
tca gac agg gcc agt cct gag cga agg tac gga ata ggt gag tga acc			308
Ser Asp Arg Ala Ser Pro Glu Arg Arg Tyr Gly Ile Gly Glu *			
55	60	65	
ttgggaactc cggaccctgt tatctaccct caatcacctg ccacaggag gcagggaccc			368

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cagcgtcttt ctcatatccc cttttaagga aatgctctgc ttttgatttt gcgcatttta 428
tttaagaatc tttgtttcaa ctttcctgga gaaatgaaaa atttggcact cctctaatacc 488
cagcgtctttg ggaggtgag aaggagtggg atcccttgag ccaggaggtt tgagacaagc 548
ctgggcgaca taatgagaca ccatctctac aaataccaga aaaatcatcc aggcgtggta 608
gcccattgct gtattctaata ctactcggga ggctgaagtg ggaggatcac ttgatgccat 668
gaggccaagg tgcattgagc cctgaatggg ctaacgaact ttaacctgat tcacagaaaa 728
gaacctgggg ccaataagag agtatggaca caacaaacat aggcgggccc cttataaga 788
tacaaagttt ataccctgt tggaaaaaaa ttattttttt tagtggcacc agatcactct 848
gatcccgaga ttttacagca gcgtcagggc aaacctcttc taagcactcc cttcacccac 908
gtcgtatctt caacttccta tgatacatca accagtaaata accgccgtcc taacatcgaa 968
ctgaatgcta gttactactt ctacagctgc taacaccttc ataatatcga ctccgtctct 1028
tttacattag actttgtagg tcaagcttta atctgcatct cc 1070

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```

<210> 27
<211> 917
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (254) ..(466)

```

```

<400> 27
ccctgcaggt accggtccgg aattcccggg tcgacccacg cgtccgggat tagtttaaat 60
tatcataaaa gtgcttgaaa atctttaact tgcattgaaa tttggaattc tgaaaaattc 120
ataaataccc tgccagtatc tatgaaagga aaagctgcag atccgactat ataccaataa 180
tccatttttc taaaagttca gagaaactct gtagctcatt attcctggga tataaggtaa 240
tcctggctgg gtt atg aaa ttt ctt ctc atg tct ctt ccc tat aga cat 289
Met Lys Phe Leu Leu Met Ser Leu Pro Tyr Arg His
1 5 10
ctc ttt tgt atc act cag gct att ctt tct gaa ata gct gaa ggt att 337
Leu Phe Cys Ile Thr Gln Ala Ile Leu Ser Glu Ile Ala Glu Gly Ile
15 20 25
aga aac gat cca ttc aaa ttt tat ctt tat tct gtt ctt gcc ctt ttc 385
Arg Asn Asp Pro Phe Lys Phe Tyr Leu Tyr Ser Val Leu Ala Leu Phe
30 35 40
ctc cac tat tat atg tat gtt ttt gtt tca agg ttc agt atc tac tac 433
Leu His Tyr Tyr Met Tyr Val Phe Val Ser Arg Phe Ser Ile Tyr Tyr
45 50 55 60
tta aag tta ctt aga att ttt aag ttt tcc taa tataaaca agcatttgaa 484
Leu Lys Leu Leu Arg Ile Phe Lys Phe Ser *

```

65

70

```

agaaactact ttaattgtta tgatgactaa acttgtctca aaccaaaaat atgcgctaaa 544
cactacgtag taagaatgag accagcctgg gcaacatagc aagacccttt ctctacaaaa 604
aaaagtttaa aaattatctg ggcgtgggtgg cacacacctg tggctcctagc tactgggagg 664
cggaaggatt gcttgagccc aggagtttga ggctgcattg ggctgtgatc acacaccgtg 724
gcactccaag ctgggcgata gaaggaagat cgctctctac aaataaatac ataaatacaa 784
tttgaaaaga aacgggagtt gggaaccttg tcaagagggg caactactag agaagccatt 844
ttaactatt attccatacg tgaacaaccc aggccgagat gtccctcccg ctggcaacat 904
gggatgcaaa cac 917

```

```

<210> 28
<211> 703
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (285)..(509)

```

```

<400> 28
atacgactca ctatagggaa tttggccctc gaggccaaga attcggcacg agggctatta 60
catagaaatt ttgtagaatc taataagata aactagaaac atgacatggt cagctgtttt 120
ctctacgaat aaacaaattg gcgctaaaac tggctcttgc atctagattt ctagttatat 180
ctcagttatc ttttccccac atgggatgtg aaagtaatgt tatatgcttt cttatgtacg 240
tacttttgac ttaggtcagt ctccacactg cattaaaatt acta atg aga caa att 296
                               Met Arg Gln Ile
                               1

gca gtt ttc cag agg ttc atg ttt cca ttt ctc ctt cct tgg ctt tcc 344
Ala Val Phe Gln Arg Phe Met Phe Pro Phe Leu Leu Pro Trp Leu Ser
  5              10              15              20

tgc att ttt agc tcc agt caa aat tct att tat tat gta tca act ttt 392
Cys Ile Phe Ser Ser Ser Gln Asn Ser Ile Tyr Tyr Val Ser Thr Phe
          25              30              35

ata aaa tgc ttg gct ttg aaa agt ata att aaa aga caa aga tct gaa 440
Ile Lys Cys Leu Ala Leu Lys Ser Ile Ile Lys Arg Gln Arg Ser Glu
          40              45              50

att aat agg ggg ttt tta gct atc tat cat gca tta aga aat caa gtg 488
Ile Asn Arg Gly Phe Leu Ala Ile Tyr His Ala Leu Arg Asn Gln Val
          55              60              65

acc agg tgt ggt ggc ctg taa tc ctagcacttt gggaggctga agtgggagga 541
Thr Arg Cys Gly Gly Leu *
          70              75

ccacttgagc tcaggagtgc aagaccagcc tgggcaacat agcaagaccc tgtctctact 601

```

aaaaataaaa aaaattgacc agggggggggg tgcattgctg tagttccagc tacttgggac 661  
gctaaagggg gaagactgct ttaaccccc ggggcgggag ac 703

<210> 29  
<211> 373  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (75) .. (287)

<400> 29  
actcgcccggt aattaccggg gcgacccacg cgctccggaga actgtttgtg gaaaacattg 60  
gttccttaaca ggac atg cat agc agg aca aga atc aga ttg tgt ctg tgt 110  
Met His Ser Arg Thr Arg Ile Arg Leu Cys Leu Cys  
1 5 10  
aat gcc aag aag agt tgc cag aag tac tta tca tct ttg aaa tta tcc 158  
Asn Ala Lys Lys Ser Cys Gln Lys Tyr Leu Ser Ser Leu Lys Leu Ser  
15 20 25  
act ttg tta tcc cct ttg ctg ttt ttg cct ttt tat acc cca tct ctt 206  
Thr Leu Leu Ser Pro Leu Leu Phe Leu Pro Phe Tyr Thr Pro Ser Leu  
30 35 40  
aaa gga tgg ggc att ttt gtt ttg agt ttt tat ttt atg tta att ata 254  
Lys Gly Trp Gly Ile Phe Val Leu Ser Phe Tyr Phe Met Leu Ile Ile  
45 50 55 60  
gcc gac tgt aac ctg ttc aaa ata ata att tag gagctctt ctagagttgg 305  
Ala Asp Cys Asn Leu Phe Lys Ile Ile Ile \*  
65 70  
gaatgctgag aattttttaa aattactaaa acttgaata gctttttcaa atgccaaagc 365  
agatttgg 373

<210> 30  
<211> 665  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (408) .. (566)

<400> 30  
gtaccgctcc ggaattcccc ggtcgaccca cgcgtccgag gacgcgtggg cggacgcgtg 60  
ggcggaacgcg tgggctgacg ttcttgtgat gttttcccat gcataaacat gccacatcca 120  
tggtcttggg tcatcttttt tgccctttca tggagtcata aattttccca actgaagtct 180  
tgtatattct gttagattaa ttccctatttc tagttgctgt aaatgatata ttatgtttta 240

```

ttacatttct aataggatat ggtggttggtg aaatgttaac cctctcatta gatctactag      300
tttacctggtt gattctattg tgttttctat gtaaagtatt ttgtcagcta taaataataa      360
cattttatatt tctctttcct tgcaatacct atgctcattt attttttt  atg ttt acc      416
                                     Met Phe Thr
                                     1
cat tgg tta ggg cct cct gta tac att aaa cag ttc ata gtc atg ata      464
His Trp Leu Gly Pro Pro Val Tyr Ile Lys Gln Phe Ile Val Met Ile
      5              10              15

gtg agt att ctt aca ctg ttc cca gta tta cag gga atg ctt aga aat      512
Val Ser Ile Leu Thr Leu Phe Pro Val Leu Gln Gly Met Leu Arg Asn
      20              25              30              35

ttt ctt tat tta aac att atg ttt gtt gta gcc ttg tta aag gct att      560
Phe Leu Tyr Leu Asn Ile Met Phe Val Val Ala Leu Leu Lys Ala Ile
              40              45              50

tta taa tttttactag aaatatatttg acatttattg ggattttttt ctatctctaa      616
Leu *

tctattgaga taggcacatt ccttttgtct cactccatta taaagggag      665

```

```

<210> 31
<211> 756
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (61)..(669)

```

```

<400> 31
gcacatatta catgattacg ccaagcttgg cagcaggggcc tgattcacag acgctacagg      60

atg gag cgg ggc gca gga gcc aag ctg ctg ccg ctg ctg ctg ctt ctg      108
Met Glu Arg Gly Ala Gly Ala Lys Leu Leu Pro Leu Leu Leu Leu Leu
      1              5              10              15

cgg gcg act ggt ttc aca tgt gca cag gca gat ggc cgg aac ggc tac      156
Arg Ala Thr Gly Phe Thr Cys Ala Gln Ala Asp Gly Arg Asn Gly Tyr
              20              25              30

acg gcg gtc atc gaa gtg acc agc ggg ggt ccc tgg ggc gac tgg gcc      204
Thr Ala Val Ile Glu Val Thr Ser Gly Gly Pro Trp Gly Asp Trp Ala
              35              40              45

tgg cct gag atg tgt ccc gat gga ttc ttc gcc agc ggg ttc tcg ctc      252
Trp Pro Glu Met Cys Pro Asp Gly Phe Phe Ala Ser Gly Phe Ser Leu
              50              55              60

aag gtt gag cct ccc caa ggc att cct ggc gac gac act gca ctg aat      300
Lys Val Glu Pro Pro Gln Gly Ile Pro Gly Asp Asp Thr Ala Leu Asn
      65              70              75              80

ggg atc agg ctg cac tgc gcg cgc ggg aac gtc cta ggc aat acg cac      348
Gly Ile Arg Leu His Cys Ala Arg Gly Asn Val Leu Gly Asn Thr His

```



	85	90	95	
gtg gta gag tcc cag tct gga agc tgg ggc gaa tgg agt gag ccg ctg				396
Val Val Glu Ser Gln Ser Gly Ser Trp Gly Glu Trp Ser Glu Pro Leu				
	100	105	110	
tgg tgt cgc ggc ggc gcc tac cta gtg gct ttc tcg ctt cgc gtg gag				444
Trp Cys Arg Gly Gly Ala Tyr Leu Val Ala Phe Ser Leu Arg Val Glu				
	115	120	125	
gca ccc acg acc ctc ggt gac aac aca gca gcg aac aac gtg cgc ttc				492
Ala Pro Thr Thr Leu Gly Asp Asn Thr Ala Ala Asn Asn Val Arg Phe				
	130	135	140	
cgc tgt tca gac ggc gag gaa ctg cag ggg cct ggg ctg agc tgg gga				540
Arg Cys Ser Asp Gly Glu Glu Leu Gln Gly Pro Gly Leu Ser Trp Gly				
	145	150	155	160
gac ttt gga gac tgg agt gac cat tgc ccc aag ggc gcg tgc ggc ctg				588
Asp Phe Gly Asp Trp Ser Asp His Cys Pro Lys Gly Ala Cys Gly Leu				
	165	170	175	
cag acc aag atc cag gga cct aga ggc ctc ggc gat gac act gcg ctg				636
Gln Thr Lys Ile Gln Gly Pro Arg Gly Leu Gly Asp Asp Thr Ala Leu				
	180	185	190	
aac gac gcg cgc tta ttc tgc tgc cgc agt tga acggcgcc gtcgcccgcg				687
Asn Asp Ala Arg Leu Phe Cys Cys Arg Ser *				
	195	200		
ctctctcccg ggccaggagg ctagtccac ctcttgctat taaagcttct ctgagttgaa				747
aaaaaaaa				756

<210> 32  
 <211> 545  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(336)

<400> 32	
atg agg caa gtg gcg aga gtg atc gtg ttc ctg acc ctg agt act ttg	48
Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu	
1 5 10 15	
agc ctt gct aag acc acc cag ccc atc tcc atg gac tca tat gaa gga	96
Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly	
20 25 30	
caa gaa gtg aac ata acc tgt agc cac aac aac att gct aca aat gat	144
Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp	
35 40 45	
tat atc acg tgg tac caa cag ttt ccc agc caa gga cca cga ttt att	192
Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile	
50 55 60	
att caa gga tac aag aca aaa gtt aca aac gaa gtg gcc tcc ctg ttt	240

```

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
 65              70              75              80

atc cct gcc gac aga aag tcc agc act ctg agc ctg ccc egg gtt tcc      288
Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
              85              90              95

ctg agc gac act gct gtg tac tac tgc ctc gtg ggt gac aca cag tga      336
Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Thr Gln *
              100              105              110

gacagatggg cctgcacctg tgccgttttc ctctgtgggg tgggagtcac agcctagaaa      396

gaagtccaaa agtgctttct aaaattttta ttttcaaaag gtattagcaa atttatgtat      456

tcttctacta tttgcaaaat caatcttatt tattttttaa ataggtattt cacttatgtg      516

atctaaaatt aaaaaagtat aaaagggaa                                      545

<210> 33
<211> 493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (31)..(414)

<400> 33
attgagggct gtgttataac tatctattcg      atg atg aag ata ccc cac caa      51
Met Met Lys Ile Pro His Gln
              1              5

acc caa aaa aag aga tct ctc gag gat ccg aat tgc cgg ccg cgt cga      99
Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro Arg Arg
              10              15              20

ccg cgc ggg gaa ggg gag acg tgg ggt aga gtg acc atg acg aaa tta      147
Pro Arg Gly Glu Gly Glu Thr Trp Gly Arg Val Thr Met Thr Lys Leu
              25              30              35

gcg cag tgg ctt tgg gga cta gcg atc ctg ggc tcc acc tgg gtg gcc      195
Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val Ala
              40              45              50              55

ctg acc acg gga gcc ttg ggc ctg gag ctg ccc ttg tcc tgc cag gaa      243
Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln Glu
              60              65              70

gtc ctg tgg cca ctg ccc gcc tac ttg ctg gtg tcc gcc ggc tgc tat      291
Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys Tyr
              75              80              85

gcc ctg ggc act gtg ggc tat cgt gtg gcc act ttt cat gac tgc gag      339
Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys Glu
              90              95              100

gac gcc gca cgc gag ctg cag agc cag ata cag gag gcc cga gcc gac      387
Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala Asp
              105              110              115.

```

tta gcc cgc agg ggg ctg cgc ttc tga cagcc taacccatt cctgtgcgga 439  
 Leu Ala Arg Arg Gly Leu Arg Phe \*  
 120 125

cagcccttcc tccatttcc cattaaagag ccagtttatt ttctaaaaaa aaaa 493

<210> 34  
 <211> 1900  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (314)..(709)

<220>  
 <221> misc\_feature  
 <222> (1)...(1900)  
 <223> n = a,t,c or g

<400> 34  
 atttggccct cgaggccaag aattcggcac gagcataagg ttgtagtagc aggagccctc 60  
 tatcttttgt tcgggnncat ggaaggggtc ctcanagcnn nngagactca gactgatctt 120  
 gcttacttgg cctttatccc cttggctttc ctagaccctg gcttgcgag ctggatgcag 180  
 acaacatccc cccaccaccc aagagggagg gtagctcttc cgccaccagg ggcaagcaca 240  
 tttgtatcgg catttcacca acacgcttat tttggcagtg gcagcatcca ttgtgtttat 300  
 catctggaca acc atg aag ttc aga ata gtg aca tgt cag tcg gac tgg 349  
 Met Lys Phe Arg Ile Val Thr Cys Gln Ser Asp Trp  
 1 5 10  
 cgg gag ctg tgg gta gac gat gcc atc tgg cgc ttg ctg ttc tcc atg 397  
 Arg Glu Leu Trp Val Asp Asp Ala Ile Trp Arg Leu Leu Phe Ser Met  
 15 20 25  
 atc ctc ttt gtc atc atg gtt ctc tgg cga cca tct gca aac aac cag 445  
 Ile Leu Phe Val Ile Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln  
 30 35 40  
 agg ttt gcc ttt tca cca ttg tct gag gaa gag gag gag gat gaa caa 493  
 Arg Phe Ala Phe Ser Pro Leu Ser Glu Glu Glu Glu Glu Asp Glu Gln  
 45 50 55 60  
 aag gag cct atg ctg aaa gaa agc ttt gaa gga atg aaa atg aga agt 541  
 Lys Glu Pro Met Leu Lys Glu Ser Phe Glu Gly Met Lys Met Arg Ser  
 65 70 75  
 acc aaa caa gaa ccc aat gga aat agt aaa gtt aac aaa gca cag gaa 589  
 Thr Lys Gln Glu Pro Asn Gly Asn Ser Lys Val Asn Lys Ala Gln Glu  
 80 85 90  
 gat gat ttg aag tgg gta gaa gag aat gtt cct tct tct gtg aca gat 637  
 Asp Asp Leu Lys Trp Val Glu Glu Asn Val Pro Ser Ser Val Thr Asp  
 95 100 105  
 gta gca ctt cca gcc ctt ctg gat tca gat gag gaa cga atg atc aca 685  
 Val Ala Leu Pro Ala Leu Leu Asp Ser Asp Glu Glu Arg Met Ile Thr

110	115	120	
cac ttt gaa agg tcc aaa atg gag taaggaatgg gaagatttgc agttaagat			739
His Phe Glu Arg Ser Lys Met Glu			
125	130		
ggctaccatc agggaagaga tcagcatctg tgtcagtcct ctgtacggct ccatgggatt			799
aaaggaagca atgacatcct gatctgttcc ttgatctttg ggcatcggag ttggcgagag			859
gtgtcagaac aaagagaaca tcttactgaa aacaagttca taagatgaga aaaatctacg			919
agcttcttat ttacaacact gctgccccct ttctcccag actctgacat ggatgttcat			979
gcaacttaag tgtgtgtgtc ctgaactttc tgtaatgttt cattttttaa atctgacaaa			1039
ctaaaaagtt taacgtcttc taaaagattg tcatcaacac cataatatgt aatctccagg			1099
agcaactgcc tgtaattttt atttatttag ggagttacat aggtgatggg ggaaattgtt			1159
aactaccttt cattttcctg ggaagtcaag gttacatctt gcagagggtg ttttgagaaa			1219
aaagggccct tctgagttaa ggagccatag ttctatcaat gatcaaaaga aaaaaaaaaa			1279
aaagagaaac tgttacagta tgattcagat catttaaaaa agcaaaatca agtgcaattt			1339
tgtttacaaa tgggtgtatat taaagatttt tctatttcag atgtacttta aagagaaata			1399
ttagcttaac tcttttgaca tctgctattg tgacacatcc cattgctggc aatgtggtgc			1459
acactccgaa acttttaact actgttttgt aagcctccaa ggggtggcatt gcagggctct			1519
taggcaatgt tttgtttgcc tttatgcaga gaggtgctcc aagtgtgtg attgagcacc			1579
gtgctagagg aactgtaatg cttcagaagt ttagcttat acaaaggaaa caggctctgc			1639
tggcttaatt taaacagtta ttgcatgaag tagcgtggag gccctggact gctgctcggt			1699
ctttaggatg gactgttctg gtatctggta ttggtttaga gactgttaat aaggacatc			1759
acaaggtgat gggattcatt tgaagcactc tatttctggt ttaatggttt tatccaattt			1819
tgccctccca agatttttgt tctacataaa aagttcatgc cactttttaa tataaaaaaa			1879
tttaacaaaa aaaaaaaaaa a			1900

<210> 35  
 <211> 1105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (238) ..(591)

<400> 35	
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ggtagccgagc tcggatccac tagtccagtg tgggtggaatt cggcgtctct ggggcagggtg	120
ttggctctgg tgctgggtgg cgctctgtgg ggtggcacgc agccgctgct gaagcggggc	180

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tccgccggcc tgcagcgggt tcatgagccg acctgggccc agcagttgct acaggag      237
atg aag acc ctc ttc ttg aat act gag tac ctg atg ccc ttt ctc ctc      285
Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro Phe Leu Leu
  1             5             10             15

aac cag ggg gga tcc ctt ctc tat tac ctc acc ttg gca tcg aca gat      333
Asn Gln Gly Gly Ser Leu Leu Tyr Tyr Leu Thr Leu Ala Ser Thr Asp
             20             25             30

ctg acc ctg gct gtg ccc atc tgt aac tct ctg gct atc atc ttc aca      381
Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu Ala Ile Ile Phe Thr
             35             40             45

ctg att gtt ggg aag gcc ctt gga gaa gat att ggt gga aaa cga gca      429
Leu Ile Val Gly Lys Ala Leu Gly Glu Asp Ile Gly Gly Lys Arg Ala
             50             55             60

gtt gct ggc atg gtg ctc acc gtg ata gga att tca ctc tgc atc aca      477
Val Ala Gly Met Val Leu Thr Val Ile Gly Ile Ser Leu Cys Ile Thr
             65             70             75             80

agc tca gtt cca tgg act gca gaa ctc cag ctg cat gga aag ggc cag      525
Ser Ser Val Pro Trp Thr Ala Glu Leu Gln Leu His Gly Lys Gly Gln
             85             90             95

ctg cag act ttg agc cag aaa tgc aaa cgg gag gcc tct ggg act cag      573
Leu Gln Thr Leu Ser Gln Lys Cys Lys Arg Glu Ala Ser Gly Thr Gln
             100             105             110

tca gag cgc ttt ggc tga atgagg ggtggaaccg agggaagaag gtagagagct      627
Ser Glu Arg Phe Gly *
             115

gtgagcccca gccccacctg actccagcac acctggcgag tagtagctgt caataaatct      687

atggtaaaca gacaagagga ggtggaaggc catacagaat ggagccgtga gtatggccag      747

cctccagctc tcagccagga ggtccccaac cccaaggaag gaagaaactg gaaattagga      807

actgcttcct catttaacaa ggtgcttctt ttcattgtgat gaggcctgt gaagaaggga      867

caggatatac agacgggggc agctggagac agttatgatg agtgccggct ttgtgtctga      927

gcattctgct cccatggaca tccccaacaa cagcagggac caacctatgt cactgtcaaa      987

gggcagctga gagaggcctg agccccaggg acccctcacc tgatgggaat gagagtgtgg      1047

ggagcttgct tcttggtgta atggtctgct ggggtctggc atagaaagca gatggctt      1105

<210> 36
<211> 1379
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (439) .. (720)

<400> 36
tttcgtgccca tggcggcgctc tctgagtagg tagccggccc cgccttcca tggatttccc      60

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gaccctcgcc tcgaattcat ttctgtctcc acatgcaccc tctaaccctg acccctgcta 120  
caaccccaga ggccggactc ctggattcat ctccctagct tccctgggcc tgccttagcc 180  
gccagtcgca gccgaggcga agagagcgaa ggaggggaagt gggggcggct agctggggct 240  
agaaggccag gagagggcgg ggtgggcggc cgtttgggggt gggggtcagg gtgactcact 300  
cgtctgcatt cagggcaggt gttggctctg gtgctgggtg ccgctctgtg ggggtggcacg 360  
cagccgctgc tgaagcgggc ctccgccggc ctgcagcggg ttcattgagcc gacctgggcc 420  
cagcagttgc tacaggag atg aag acc ctc ttc ttg aat act gag tac ctg 471  
Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu  
1 5 10  
atg ccc ttt ctc ctc aac cag tgt gga tcc ctt ctc tat tac ctc acc 519  
Met Pro Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr  
15 20 25  
ttg gca tgc aca gat ctg acc ctg gct gtg ccc atc tgt aac tct ctg 567  
Leu Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu  
30 35 40  
gct atc atc ttc aca ctg att gtt ggg aag gcc ctt gga gaa gat att 615  
Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp Ile  
45 50 55  
ggg gga aaa cga gca gtt gct ggc atg gtg ctc acc gtg ata gga att 663  
Gly Gly Lys Arg Ala Val Ala Gly Met Val Leu Thr Val Ile Gly Ile  
60 65 70 75  
tca ctc tgc atc aca agc tca gtg agt aag acc cag ggg caa cag tct 711  
Ser Leu Cys Ile Thr Ser Ser Val Ser Lys Thr Gln Gly Gln Gln Ser  
80 85 90  
acc ctt tga gtgggcc gaaccactt ccagctctgc tgcctccagg aagcccctgg 767  
Thr Leu \*  
gccatgaagt gctggcagtg agcggatgga cctagcactt cccctctctg gccttagctt 827  
cctcctctct tatggggata acagctacct catggatcac aataagagaa caagagtgaa 887  
agagttttgt aaccttcaag tgcgtttcag ctgcggggat ttagcacagg agactctacg 947  
ctcaccctca gcaacctttc tgccccagca gctctcttcc tgctaacatc tcaggctccc 1007  
agcccagcca ccattactgt ggctgatct ggactatcat ggtggcaggt tccatggact 1067  
gcagaactcc agctgcatgg aaagggccag ctgcagactt tgagccagaa atgcaaacgg 1127  
gaggcctctg ggactcagtc agagcgcttt ggctgaatga ggggtggaac cgaggggaaga 1187  
aggtgcgtcg gagtggcaga tgcaggaaat gagctgtcta ttagccttgc ctgccccacc 1247  
catgaggtag gcagaaatcc tcaactgccag cccctcttaa acaggtagag agctgtgagc 1307  
cccagcccca cctgactcca gcacacctgg cgagtagtag ctgtcaataa atctatggta 1367  
aacagacaaa aa 1379

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<210> 37
<211> 2084
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (215) .. (1672)

<400> 37
aagctggtac gcctgcaggt accggtcogt aattccoggg tcgacccacg cgtccgggtcc      60
cccacggaga cgcgccaagg tagccccgcg cgtgtccgta ggcgcgctct ctggaagacg      120
cgggtgggggg tgcgcagggc tgcaccctca caccaattgc cccggcgaag gccgagccca      180
gaaagtgagt gcgcgtgagt gtgcgcgcgc ccgc      atg cgg ggg cgt ggc agt      232
                                   Met Arg Gly Arg Gly Ser
                                   1           5

caa cag caa caa ccc aca cgc cgg cag ggc cag aaa ctc cca tct ccc      280
Gln Gln Gln Gln Pro Thr Arg Arg Gln Gly Gln Lys Leu Pro Ser Pro
              10              15              20

tca cca gcc gga aag tac gag tcg gct cag cct gga ggg acc caa cca      328
Ser Pro Ala Gly Lys Tyr Glu Ser Ala Gln Pro Gly Gly Thr Gln Pro
              25              30              35

gag cct ggc ctg gga gcc agg atg gcc atc cac aaa gcc ttg gtg atg      376
Glu Pro Gly Leu Gly Ala Arg Met Ala Ile His Lys Ala Leu Val Met
              40              45              50

tgc ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag ggc      424
Cys Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly
              55              60              65              70

cat gtc cca ccc ggc tgc agc caa ggc ctc aac ccc ctg tac tac aac      472
His Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn
              75              80              85

ctg tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct      520
Leu Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala
              90              95              100

ggg gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc      568
Gly Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala
              105              110              115

agc ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc      616
Ser Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr
              120              125              130

cag gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt      664
Gln Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe
              135              140              145              150

gcc tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct cgg cgc ttc      712
Ala Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe
              155              160              165

ctc ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac      760
Leu Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His

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170	175	180	
gtc ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc Val Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly			808
185	190	195	
tgg gtg atc ttc act gtg gct ctg ctg ctg acc ctg gta gag gtc atc Trp Val Ile Phe Thr Val Ala Leu Leu Leu Thr Leu Val Glu Val Ile			856
200	205	210	
atc aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag Ile Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu			904
215	220	225	230
ggc ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc Gly Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro			952
235	240	245	
tgt gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg Cys Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met			1000
250	255	260	
ctg ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc Leu Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly			1048
265	270	275	
cgc tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca Arg Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr			1096
280	285	290	
gcc acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac Ala Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr			1144
295	300	305	310
ggc aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc Gly Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala			1192
315	320	325	
atc gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc Ile Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile			1240
330	335	340	
ccc gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag Pro Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln			1288
345	350	355	
ggg gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa Gly Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys			1336
360	365	370	
gag cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg Glu Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met			1384
375	380	385	390
gat gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac Asp Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr			1432
395	400	405	
aat ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg Asn Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu			1480
410	415	420	
atg cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg Met His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg			1528



425	430	435	
gcc acc gcc aac agc cag gtg atg ggc agt gcc aac tcg acc ctg cgg			1576
Ala Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg			
440	445	450	
gct gaa gac atg tac tcg gcc cag agc cac cag gcg gcc aca ccg ccg			1624
Ala Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro			
455	460	465	470
aaa gac ggc aag aac tct cag gtc ttt aga aac ccc tac gtg tgg gac			1672
Lys Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp			
475	480	485	
tgagtcagcg gtggcgagga gaggcggctcg gatttgggga gggccctgag gacctggccc			1732
cgggcaaggg actctccagg ctctctctcc ccctggcagg ccagcaaca tgtgccccag			1792
atgtggaagg gcctccctct ctgccagtgt ttgggtgggt gtcattgggtg tccccaccca			1852
ctcctcagtg tttgtggagt cgaggagcca accccagcct cctgccagga tcacctgggc			1912
ggtcacactc cagccaaata gtgttctcgg ggtgggtggct gggcagcgcc tatgtttctc			1972
tggagattcc tgcaacctca agagacttcc caggcgctca ggctggatc ttgctctctc			2032
gtgaggaaca agggtgccta ataaatacat ttctgcttta ttaaaaaaaaa aa			2084

<210> 38  
 <211> 484  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (39)..(392)

<400> 38			
atttggccct cgaggccaag aattcggcac gagcttat	atg gtt aaa aca gac		53
	Met Val Lys Thr Asp		
	1	5	
gca cac cta aaa aac cct ccc ttt gct ccc ttt agg gtt tat aca ttg			101
Ala His Leu Lys Asn Pro Pro Phe Ala Pro Phe Arg Val Tyr Thr Leu			
10	15	20	
acc cta tca ttg tta ttg aaa ttg tca cat tac tct tgt ctt tgg gtt			149
Thr Leu Ser Leu Leu Leu Lys Leu Ser His Tyr Ser Cys Leu Trp Val			
25	30	35	
aaa aaa gac ttt aaa gac tcc tcg ttt tac aat agc aat aat aat agc			197
Lys Lys Asp Phe Lys Asp Ser Ser Phe Tyr Asn Ser Asn Asn Asn Ser			
40	45	50	
aat agc aat cat tgt aaa tct tta ttg agc act cac tat atg cca ggc			245
Asn Ser Asn His Cys Lys Ser Leu Ser Thr His Tyr Met Pro Gly			
55	60	65	
gct gta att agt aat tta tgc ctt atc tca tgt aaa gtt tcc agc agc			293
Ala Val Ile Ser Asn Leu Cys Leu Ile Ser Cys Lys Val Ser Ser Ser			
70	75	80	85

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cct att aag cag aca cat ggc att tcc atg tta cag atg aag aga ctg      341
Pro Ile Lys Gln Thr His Gly Ile Ser Met Leu Gln Met Lys Arg Leu
          90                      95                      100

aaa cac aca tta gct cgc ctt gcc cca ggg aca cat ggt ggg agc cag      389
Lys His Thr Leu Ala Arg Leu Ala Pro Gly Thr His Gly Gly Ser Gln
          105                      110                      115

aac tagg agttgagccc aggcatactg atgcctgggtg cacttgagacg ctgctgtaca      446
Asn

gccactccag gtgtggatga gcaggaaaca cattgaag                          484

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<210> 39
<211> 2259
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (182)..(1078)

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<400> 39
ggcggagttt taatcgaggg ctctctaattg taagccttgc gaaccgcccc ggaaatcccg      60
ggtcgaccca cgcgtccggg ttccacctgg cggtggctc tcagtcacct cgtgtgtagtc      120
gcggagctgt gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc      180
g      atg ggg aca aag gcg caa gtc gag agg aaa ctg ttg tgc ctc ttc      226
      Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe
          1          5          10          15

ata ttg gcg atc ctg ttg tgc tcc ctg gca ttg ggc agt gtt aca gtg      274
Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val
          20          25          30

cac tct tct gaa cct gaa gtc aga att cct gag aat aat cct gtg aag      322
His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys
          35          40          45

ttg tcc tgt gcc tac tcg ggc ttt tct tct ccc cgt gtg gag tgg aag      370
Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys
          50          55          60

ttt gac caa gga gac acc acc aga ctc gtt tgc tat aat aac aag atc      418
Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile
          65          70          75

aca gct tcc tat gag gac cgg gtg acc ttc ttg cca act ggt atc acc      466
Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr
          80          85          90          95

ttc aag tcc gtg aca cgg gaa gac act ggg aca tac act tgt atg gtc      514
Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val
          100          105          110

tct gag gaa ggc ggc aac agc tat ggg gag gtc aag gtc aag ctc atc      562
Ser Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile

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115	120	125	
gtg ctt gtg cct cca tcc aag cct aca gtt aac atc ccc tcc tct gcc			610
Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala			
130	135	140	
acc att ggg aac cgg gca gtg ctg aca tgc tca gaa caa gat ggt tcc			658
Thr Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser			
145	150	155	
cca cct tct gaa tac acc tgg ttc aaa gat ggg ata gtg atg cct acg			706
Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr			
160	165	170	175
aat ccc aaa agc acc cgt gcc ttc agc aac tct tcc tat gtc ctg aat			754
Asn Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn			
180	185	190	
ccc aca aca gga gag ctg gtc ttt gat ccc ctg tca gcc tct gat act			802
Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr			
195	200	205	
gga gaa tac agc tgt gag gca cgg aat ggg tat ggg aca ccc atg act			850
Gly Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr			
210	215	220	
tca aat gct gtg cgc atg gaa gct gtg gag cgg aat gtg ggg gtc atc			898
Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile			
225	230	235	
gtg gca gcc gtc ctt gta acc ctg att ctc ctg gga atc ttg gtt ttt			946
Val Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe			
240	245	250	255
ggc atc tgg ttt gcc tat agc cga ggc cac ttt gac aga aca aag aaa			994
Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys			
260	265	270	
ggg act tcg agt aag aag gtg att tac agc cag cct agt gcc cga agt			1042
Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser			
275	280	285	
gaa gga gaa ttc aaa cag acc tcg tca ttc ctg gtg tgag cctggtcggc			1092
Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val			
290	295		
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ctgtagtttc acaggatgcc ttatttgtct tctacacccc acagggcccc ctacttcttc			1212
ggatgtgttt ttaataatgt cagctatgtg ccccatcctc cttcatgccc tccctccctt			1272
tcctaccact gctgagtggc ctggaacttg tttaaagtgt ttattcccca tttctttgag			1332
ggatcaggaa ggaatcctgg gtatgccatt gacttccctt ctaagtagac agcaaaaatg			1392
gcgggggtcg caggaatctg cactcaactg cccacctggc tggcagggat ctttgaatag			1452
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tagagcggga attagaggct agagcggctg aaatggttgt ttggtgatga cactggggtc			1572
cttccatctc tggggccccc tctcttctgt cttcccatgg gaagtgccac tgggatccct			1632

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 gaaagctgga gctggtggct taggcatca ccctccctt ggctggaact actggacaga 2052  
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 <212> DNA  
 <213> Homo sapiens

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 <222> (1)..(777)

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 1 5 10 15  
 ttg gcg atc ctt cct gag aat aat cct gtg aag ttg tcc tgt gcc tac 96  
 Leu Ala Ile Leu Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr  
 20 25 30  
 tcg ggc ttt tct tct ccc cgt gca gct tcc tat gag gac cgg gtg acc 144  
 Ser Gly Phe Ser Ser Pro Arg Ala Ala Ser Tyr Glu Asp Arg Val Thr  
 35 40 45  
 ttc ttg cca act ggt atc acc ttc aag tcc gtg aca cgg gaa gac act 192  
 Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr  
 50 55 60  
 ggg aca tac act tgt atg gtc ttt gag gaa ggc ggc aac agc tat ggg 240  
 Gly Thr Tyr Thr Cys Met Val Phe Glu Glu Gly Gly Asn Ser Tyr Gly  
 65 70 75 80  
 gag gtc aag gtc aag ctc atc gtg ctt gtg cct cca tcc aag cct aca 288  
 Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr  
 85 90 95  
 gtt aac atc ccc tcc tct gcc acc att ggg aac cgg gca gtg ctg aca 336  
 Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val Leu Thr  
 100 105 110  
 tgc tca gaa caa gat ggt tcc cca cct tct gaa tac acc tgg ttc aaa 384

Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys  
 115 120 125

gat ggg ata gtg atg cct acg aat ccc aaa agc acc cgt gcc ttc agc 432  
 Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr Arg Ala Phe Ser  
 130 135 140

aac tct tcc tat gtc ctg aat ccc aca aca gga gag ctg gtc ttt gat 480  
 Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp  
 145 150 155 160

ccc ctg tca gcc tct gat act gga gaa tac agc tgt gag gca cgg aat 528  
 Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn  
 165 170 175

ggg tat ggg aca ccc atg act tca aat gct gtg cgc atg gaa gct gtg 576  
 Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val  
 180 185 190

gag cgg aat gtg ggg gtc atc gtg gca gcc gtc ctt gta acc ctg att 624  
 Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu Val Thr Leu Ile  
 195 200 205

ctc ctg gga atc ttg gtt ttt ggc atc tgg ttt gcc tat agc cga ggc 672  
 Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly  
 210 215 220

cac ttt gac aga aca aag aaa ggg act tcg agt aag aag gtg att tac 720  
 His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr  
 225 230 235 240

agc cag cct agt gcc cga agt gaa gga gaa ttc aaa cag acc tcg tca 768  
 Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser  
 245 250 255

ttc ctg gtg 777  
 Phe Leu Val

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 <213> Homo sapiens

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 <222> (515) .. (1333)

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 gccagctgcc tctacactgc cctattcgac ttccaatcag ccagctgcgt ctacactgcc 180  
 ctattcgact tccaatcagc cagctgcctc tacactgccc tattcgtctt ccaatcagcc 240  
 agctgcgtct aactgccct attcgacttc caatcagcca gctgcctcta cactgcccta 300  
 ttcgacttcc aatcagccag ctgcgtctac actgccttat tcgacttcca atcagccagc 360

72

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ctc ttc acg gaa cct aat gaa ata tcc cag tat tta cca ata aag gaa 1252
Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr Leu Pro Ile Lys Glu
      235              240              245

gca gtt tgt gag aag cta ata ttt cca gaa aga att gat cct aac cca 1300
Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg Ile Asp Pro Asn Pro
      250              255              260

gca gac tca caa aaa agt aca caa gtg gaa taa aatgtgat acaacatata 1351
Ala Asp Ser Gln Lys Ser Thr Gln Val Glu *
      265              270

ctcactatgg aatctgactg gacaccttgg ctatttgtaa ggggttattt ttattatgag 1411

aattaattgc cttgtttatg tacagatttt ctgtagcctt aaaggaaaaa aaaataaaga 1471

tcgttacagg cagggttcac tcaactgctg tttgtactgt ctgtcttcac attcatattc 1531

cagatttata ttttctggag ttaaatttgg atgatttcta aattatcaca aagtgggacc 1591

tcagcagtag tgatgtgtgt gtctcatgag cagtgcacac agtctgcatt catcatgaaa 1651

cactatcttc taccaggagg aggttaatgt aa 1683

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<210> 42
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (351)..(1058)

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cactgctcat gatgtgttac accaggtagc tttctgcttg gacgtgatgt gttctagcaa 180

cctttaagat ttcagtgtct gaaaccatgg ttacttgttg ctttacttca ggccccacat 240

ttgtgggggc ttcttgttta atttcagggt ttgtacacat gagagcttct agcttaaatt 300

caaaatctgt tgctacaggt aatttttgat tgatttcagc gtgtgtacac atg gag 356
                        Met Glu
                        1

tct tct tgc ttg gat ata gga tct gta cct atg gga act tcc tgt ttg 404
Ser Ser Cys Leu Asp Ile Gly Ser Val Pro Met Gly Thr Ser Cys Leu
      5              10              15

gat tca tgg cct gta cac ata att tct tgc cta gat tca ggg tct gtc 452
Asp Ser Trp Pro Val His Ile Ile Ser Cys Leu Asp Ser Gly Ser Val
      20              25              30

cgt att aaa act tct tgc ctg gat tca ggg cct gta tac atg gga act 500
Arg Ile Lys Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met Gly Thr
      35              40              45              50

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tct tgc ctg gat tca ggg cct gta tac atg gga act tct tgc ctg ggt Ser Cys Leu Asp Ser Gly Pro Val Tyr Met Gly Thr Ser Cys Leu Gly 55 60 65	548
tca gag cct gta tac atg gga act tct tgc ctg ggt tca gag tct gta Ser Glu Pro Val Tyr Met Gly Thr Ser Cys Leu Gly Ser Glu Ser Val 70 75 80	596
cac atg gga act tct tgc ctg ggt tca gag tct gta cac atg gga act His Met Gly Thr Ser Cys Leu Gly Ser Glu Ser Val His Met Gly Thr 85 90 95	644
tct tgc ctg gct tca ggg cct gta cac atg gga act tct tgc ctg ggt Ser Cys Leu Ala Ser Gly Pro Val His Met Gly Thr Ser Cys Leu Gly 100 105 110	692
tca ggg cct gta cac atg gga act tct tgc ctg ggt tca ggg tct gaa Ser Gly Pro Val His Met Gly Thr Ser Cys Leu Gly Ser Gly Ser Glu 115 120 125 130	740
cac atg gga act tct cgc ctg gat tca ggg cct gta cac gtg gga act His Met Gly Thr Ser Arg Leu Asp Ser Gly Pro Val His Val Gly Thr 135 140 145	788
tct tgc ctg ggt tca ggg tct gaa cac gtg gga act tct tgc ctg ggt Ser Cys Leu Gly Ser Gly Ser Glu His Val Gly Thr Ser Cys Leu Gly 150 155 160	836
tca gaa tat gta tac acg gga act tct cgc ctg gat tca ggg cct gta Ser Glu Tyr Val Tyr Thr Gly Thr Ser Arg Leu Asp Ser Gly Pro Val 165 170 175	884
cac atg gga act tct tgc ctg gat tca gca tct gaa cac atg gga act His Met Gly Thr Ser Cys Leu Asp Ser Ala Ser Glu His Met Gly Thr 180 185 190	932
tct tcc ctg gat tgc gcg tct gaa ctc gtg gat att act tgt ttg tcc Ser Ser Leu Asp Ser Ala Ser Glu Leu Val Asp Ile Thr Cys Leu Ser 195 200 205 210	980
aaa gtt att aca cct ttg ggt ttt tgg aaa aac cat gga gat ttt tgt Lys Val Ile Thr Pro Leu Gly Phe Trp Lys Asn His Gly Asp Phe Cys 215 220 225	1028
cct ggt aaa aga tat gat gcc att cct tta t aaaaaagagc tttgtttggt Pro Gly Lys Arg Tyr Asp Ala Ile Pro Leu 230 235	1079
cccagaggta atatctcttc taattttttc tcaccttgat acaagtaaag aactttcgat	1139
atatggtctg acacagctaa tatgatgtta ctttttttgt caaagttctc ttttacagag	1199
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tcctggccca gtgtcttttag agcaaatcgt gtaaacacag ctagccctga ggggatgaag	1559



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aacatatttc tgcttggtg ctcttgtgt gacttgatgt aatgaaaaat cctggatatc 1619
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<210> 43
<211> 2253
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (533)..(1204)

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cctcagtggg ttcccaggat acacaaacca ctcttgaca gctaggcagg tgctggtgac 180
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atgtgtgggg tcttcttggt taatttcagg gttgtacac atgagagctt ctagcttaaa 480
ttcaaaatct gttgctacag gtaatttttg attgatttca gcgtgtgtac ac atg 535
Met
1

gag tct tct tgc ttg gat ata gga tct gta cat atg gga act tcc tgt 583
Glu Ser Ser Cys Leu Asp Ile Gly Ser Val His Met Gly Thr Ser Cys
5 10 15

ttg gat tca tgg cct gta cac ata att tct tgc cta gat tca ggg tct 631
Leu Asp Ser Trp Pro Val His Ile Ile Ser Cys Leu Asp Ser Gly Ser
20 25 30

gtc cgt att aaa act tct tgc ctg gat tca ggg cct gta tac atg gga 679
Val Arg Ile Lys Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met Gly
35 40 45

act tct tgc ctg gat tca ggg cct gta tac atg gga act tct tgc ctg 727
Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met Gly Thr Ser Cys Leu
50 55 60 65

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ggt tca gag cct gta tac atg gga act tct tgc ctg ggt tca gag tct 775  
 Gly Ser Glu Pro Val Tyr Met Gly Thr Ser Cys Leu Gly Ser Glu Ser  
                     70                    75                    80

gta tac atg gga act tct tgc ctg ggt tca gag tct gta tac atg gga 823  
 Val Tyr Met Gly Thr Ser Cys Leu Gly Ser Glu Ser Val Tyr Met Gly  
                     85                    90                    95

act tct tgc ctg gct tca ggg cct gta cac atg gga act tct tgc ctg 871  
 Thr Ser Cys Leu Ala Ser Gly Pro Val His Met Gly Thr Ser Cys Leu  
                     100                    105                    110

ggt tca ggg tct gaa cac atg gga act tct cgc ctg gat tca ggg cct 919  
 Gly Ser Gly Ser Glu His Met Gly Thr Ser Arg Leu Asp Ser Gly Pro  
                     115                    120                    125

gta cac gtg gga act tct tgc ctg ggt tca ggg tct gaa cac atg gga 967  
 Val His Val Gly Thr Ser Cys Leu Gly Ser Gly Ser Glu His Met Gly  
                     130                    135                    140                    145

act tct tgc ctg ggt tca gaa tct gta tac acg gga act tct cgc ctg 1015  
 Thr Ser Cys Leu Gly Ser Glu Ser Val Tyr Thr Gly Thr Ser Arg Leu  
                     150                    155                    160

gat tca ggg cct gta cac atg gga act tct tgc ctg gat tca gca tct 1063  
 Asp Ser Gly Pro Val His Met Gly Thr Ser Cys Leu Asp Ser Ala Ser  
                     165                    170                    175

gaa cac atg gga act tct tcc ctg gat tgc gcg tct gaa ctc gtg gat 1111  
 Glu His Met Gly Thr Ser Ser Leu Asp Ser Ala Ser Glu Leu Val Asp  
                     180                    185                    190

att act tgt ttg tcc aaa gtt att aca cct ttg ggt ttt tgg aaa aac 1159  
 Ile Thr Cys Leu Ser Lys Val Ile Thr Pro Leu Gly Phe Trp Lys Asn  
                     195                    200                    205

cat gga gat ttt tgt cct ggt aaa aga tat gat gcc att cct tta taa 1207  
 His Gly Asp Phe Cys Pro Gly Lys Arg Tyr Asp Ala Ile Pro Leu  
                     210                    215                    220

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aagtaaagaa ctttcgatat atggtctgac acagctaata tgatgttacc ttttttgtca 1327

aagttctctt ttacagaggt gtaggacgat aagcatttgt acctaaagct ttcaaacatg 1387

ccctctggga ttatgtcgtt gccaaaggagg caggccagaa gaggaaggtc ggccacacag 1447

aggcccagac tctcacagag cttctctctg cagagcatga cgggtgtccag gctctctagg 1507

cagagctcgc taattgaaaa gtagggacaa gtgtcataga ttaggtaatc agtgtcttcc 1567

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ctgacttttc ttctgcaagc tcc      atg ttt tca cat ctt ccc ttt gac tgt Met Phe Ser His Leu Pro Phe Asp Cys	170
1  5	
gtc ctg ctg ctg ctg ctg cta cta ctt aca agg tcc tca gaa gtg gaa Val Leu Leu Leu Leu Leu Leu Leu Leu Thr Arg Ser Ser Glu Val Glu	218
10  15  20  25	
tac aga gcg gag gtc ggt cag aat gcc tat ctg ccc tgc ttc tac acc Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro Cys Phe Tyr Thr	266
30  35  40	
cca gcc gcc cca ggg aac ctc gtg ccc gtc tgc tgg ggc aaa gga gcc Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp Gly Lys Gly Ala	314
45  50  55	
tgt cct gtg ttt gaa tgt ggc aac gtg gtg ctc agg act gat gaa agg Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg Thr Asp Glu Arg	362
60  65  70	
gat gtg aat tat tgg aca tcc aga tac tgg cta aat ggg gat ttc cgc Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn Gly Asp Phe Arg	410
75  80  85	
aaa gga gat gtg tcc ctg acc ata ggg aat gtg act cta gca gac agt Lys Gly Asp Val Ser Leu Thr Ile Gly Asn Val Thr Leu Ala Asp Ser	458
90  95  100  105	
ggg atc tac tgc tgc cgg atc caa atc cca ggc ata atg aat gat gaa Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile Met Asn Asp Glu	506
110  115  120	
aaa ttt aac ctg aag ttg gtc atc aaa cca gcc aag gtc acc cct gca Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala Lys Val Thr Pro Ala	554

125	130	135	
ccg act ctg cag aga gac ttc act gca gcc ttt cca agg atg ctt acc			602
Pro Thr Leu Gln Arg Asp Phe Thr Ala Ala Phe Pro Arg Met Leu Thr			
140	145	150	
acc agg gga cat ggc cca gca gag aca cag aca ctg ggg agc ctc cct			650
Thr Arg Gly His Gly Pro Ala Glu Thr Gln Thr Leu Gly Ser Leu Pro			
155	160	165	
gat ata aat cta aca caa ata tcc aca ttg gcc aat gag tta cgg gac			698
Asp Ile Asn Leu Thr Gln Ile Ser Thr Leu Ala Asn Glu Leu Arg Asp			
170	175	180	185
tct aga ttg gcc aat gac tta cgg gac tct gga gca acc atc aga ata			746
Ser Arg Leu Ala Asn Asp Leu Arg Asp Ser Gly Ala Thr Ile Arg Ile			
190	195	200	
ggc atc tac atc gga gca ggg atc tgt gct ggg ctg gct ctg gct ctt			794
Gly Ile Tyr Ile Gly Ala Gly Ile Cys Ala Gly Leu Ala Leu Ala Leu			
205	210	215	
atc ttc ggc gct tta att ttc aaa tgg tat tct cat agc aaa gag aag			842
Ile Phe Gly Ala Leu Ile Phe Lys Trp Tyr Ser His Ser Lys Glu Lys			
220	225	230	
ata cag aat tta agc ctc atc tct ttg gcc aac ctc cct ccc tca gga			890
Ile Gln Asn Leu Ser Leu Ile Ser Leu Ala Asn Leu Pro Pro Ser Gly			
235	240	245	
ttg gca aat gca gta gca gag gga att cgc tca gaa gaa aac atc tat			938
Leu Ala Asn Ala Val Ala Glu Gly Ile Arg Ser Glu Glu Asn Ile Tyr			
250	255	260	265
acc att gaa gag aac gta tat gaa gtg gag gag ccc aat gag tat tat			986
Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Glu Pro Asn Glu Tyr Tyr			
270	275	280	
tgc tat gtc agc agc agg cag caa ccc tca caa cct ttg ggt tgt cgc			1034
Cys Tyr Val Ser Ser Arg Gln Gln Pro Ser Gln Pro Leu Gly Cys Arg			
285	290	295	
ttt gca atg cca tag atccaaccac cttatTTTTg agcttggtgt tttgtctttt			1089
Phe Ala Met Pro			
300			
tcagaaacta tgagctgtgt cacctgactg gttttggagg ttctgtccac tgctatggag			1149
cagagttttc ccattttcag aagataatga ctcacatggg aattgaactg ggacctgcac			1209
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<400> 45  
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 aggtgccgac gccaccgccc agccc atg atc ctg gaa cag tac gtg gtg gtg 412  
 Met Ile Leu Glu Gln Tyr Val Val Val  
 1 5  
 tcc aac tat aag aag cag gag aac tcg gag ctg agc ctc cag gcc ggg 460  
 Ser Asn Tyr Lys Lys Gln Glu Asn Ser Glu Leu Ser Leu Gln Ala Gly  
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 Glu Val Val Asp Val Ile Glu Lys Asn Glu Ser Gly Trp Trp Phe Val  
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 agc act tct gag gag cag ggc tgg gtc cct gcc acc tac ctg gag gcc 556  
 Ser Thr Ser Glu Glu Gln Gly Trp Val Pro Ala Thr Tyr Leu Glu Ala  
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 cag aat ggt act cgg gat gac tcc gac atc aac acc tct aag act gga 604  
 Gln Asn Gly Thr Arg Asp Asp Ser Asp Ile Asn Thr Ser Lys Thr Gly  
 60 65 70  
 gaa gtg tcc aag aga cgc aag gcc cat ctg cgg cgc ctg gat cgc cgg 652  
 Glu Val Ser Lys Arg Arg Lys Ala His Leu Arg Arg Leu Asp Arg Arg  
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 Trp Thr Leu Gly Gly Met Val Asn Arg Gln His Ser Arg Glu Glu Lys  
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 tat gtc acc gtg cag cct tac acc agc caa agc aag gac gag att ggc 748  
 Tyr Val Thr Val Gln Pro Tyr Thr Ser Gln Ser Lys Asp Glu Ile Gly  
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Trp	Trp	Tyr	Ile	Arg	Tyr	Leu	Gly	Lys	Glu	Gly	Trp	Ala	Pro	Ala	Ser		
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Tyr	Leu	Lys	Lys	Ala	Lys	Asp	Asp	Leu	Pro	Thr	Arg	Lys	Lys	Asn	Leu		
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Glu	Gly	His	Glu	Ala	Pro	Ile	Ala	Lys	Lys	Glu	Ile	Ser	Leu	Pro	Ile		
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Gln	Arg	Ala	Gln	Ile	Ser	Ser	Pro	Asn	Leu	Arg	Thr	Arg	Pro	Pro	Pro		
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Pro	Ser	Val	Glu	Val	Glu	Tyr	Tyr	Thr	Ile	Ala	Glu	Phe	Gln	Ser	Cys		
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Glu	Ser	Ser	Glu	Asp	Val	Ala	Leu	Glu	Glu	Glu	Thr	Ile	Tyr	Glu	Asn		
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Lys	Pro	Arg	Ser	Ala	Ser	Asp	Ala	Gly	Ile	Arg	Gly	Thr	Pro	Lys	Val		
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Arg	Ala	Lys	Lys	Asp	Ala	Asp	Ala	Asn	Ala	Gly	Leu	Thr	Ser	Cys	Pro		
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Arg	Pro	Thr	Gly	Gln	Leu	Arg	Gly	Gly	Leu	Lys	Gly	Ser	Lys	Ser	Glu		
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Ser	Arg	Arg	Ser	Ser	Ser	Asp	Leu	Ile	Thr	Leu	Pro	Ala	Thr	Thr	Pro	
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Pro	Cys	Pro	Thr	Lys	Lys	Glu	Trp	Glu	Gly	Pro	Ala	Thr	Ser	Tyr	Met	
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Thr	Cys	Ser	Ala	Tyr	Gln	Lys	Val	Gln	Asp	Ser	Glu	Ile	Ser	Phe	Pro	
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Ala	Gly	Val	Glu	Val	Gln	Val	Leu	Glu	Lys	Gln	Glu	Ser	Gly	Trp	Trp	
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Tyr	Val	Arg	Phe	Gly	Glu	Leu	Glu	Gly	Trp	Ala	Pro	Ser	His	Tyr	Leu	
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Val	Leu	Asp	Glu	Asn	Glu	Gln	Pro	Asp	Pro	Ser	Gly	Lys	Glu	Leu	Asp	
730					735					740					745	
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Thr	Val	Pro	Ala	Lys	Gly	Arg	Gln	Asn	Gly	Lys	Ser	Asp	Ser	Leu		
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gag	aag	atc	gag	agg	cgc	gtc	caa	gca	ctg	aac	acc	gtc	aac	cag	agc	2716
Glu	Lys	Ile	Glu	Arg	Arg	Val	Gln	Ala	Leu	Asn	Thr	Val	Asn	Gln	Ser	
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Lys	Lys	Ala	Thr	Pro	Pro	Ile	Pro	Ser	Lys	Pro	Pro	Gly	Gly	Phe	Gly	
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Lys	Thr	Ser	Gly	Thr	Pro	Ala	Val	Lys	Met	Arg	Asn	Gly	Val	Arg	Gln	
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gtg	gcg	gtc	agg	ccc	cag	tcg	gtg	ttt	gtg	tcc	ccg	cca	ccc	aag	gac	2860
Val	Ala	Val	Arg	Pro	Gln	Ser	Val	Phe	Val	Ser	Pro	Pro	Pro	Lys	Asp	
810					815					820					825	
aac	aac	ctg	tcc	tgc	gcc	ctg	cgg	agg	aat	gag	tca	ctc	acg	gcc	act	2908
Asn	Asn	Leu	Ser	Cys	Ala	Leu	Arg	Arg	Asn	Glu	Ser	Leu	Thr	Ala	Thr	
				830					835					840		
gat	ggc	ctc	cga	ggc	gtc	cga	cgg	aac	tcc	tcc	ttt	agc	act	gct	cgc	2956
Asp	Gly	Leu	Arg	Gly	Val	Arg	Arg	Asn	Ser	Ser	Phe	Ser	Thr	Ala	Arg	
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Ser	Ala	Ala	Ala	Glu	Ala	Lys	Gly	Arg	Leu	Ala	Glu	Arg	Ala	Ala	Ser	
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cag	ggt	tca	gac	tca	ccc	cta	ctg	ccc	gcc	cag	cgc	aac	agc	atc	ccc	3052
Gln	Gly	Ser	Asp	Ser	Pro	Leu	Leu	Pro	Ala	Gln	Arg	Asn	Ser	Ile	Pro	
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gtg	tcc	cct	gtg	cgc	ccc	aag	ccc	atc	gag	aag	tct	cag	ttc	atc	cac	3100



Val Ser Pro Val Arg Pro Lys Pro Ile Glu Lys Ser Gln Phe Ile His	
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Asn Asn Leu Lys Asp Val Tyr Val Ser Ile Ala Asp Tyr Glu Gly Asp	
910 915 920	
gag gag aca gca ggc ttc cag gag ggg gtg tcc atg gag gtt ctg gag	3196
Glu Glu Thr Ala Gly Phe Gln Glu Gly Val Ser Met Glu Val Leu Glu	
925 930 935	
agg aac cct aat ggc tgg tgg tac tgc cag atc ctg gat ggt gtg aag	3244
Arg Asn Pro Asn Gly Trp Trp Tyr Cys Gln Ile Leu Asp Gly Val Lys	
940 945 950	
ccc ttc aaa ggc tgg gtg cct tcc aac tac ctt gag aaa aag aac tag	3292
Pro Phe Lys Gly Trp Val Pro Ser Asn Tyr Leu Glu Lys Lys Asn *	
955 960 965	
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tgattctgtc agt atg tgt cat tgg caa aat agc ttt ctc tgc caa agc 229
Met Cys His Trp Gln Asn Ser Phe Leu Cys Gln Ser
1 5 10
ttt ctg acc ttt ggc tcc atc tta gct ttg tta gca gga aag gcc tgc 277
Phe Leu Thr Phe Gly Ser Ile Leu Ala Leu Leu Ala Gly Lys Ala Cys
15 20 25
tac cca gag tca gag tca atc aga gaa ttg ttc atg tgg tcc tta gaa 325
Tyr Pro Glu Ser Glu Ser Ile Arg Glu Leu Phe Met Trp Ser Leu Glu
30 35 40

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ctt tac tcc tta ccc ttt tat ctt ttc ttt aaa ctt tcg cct cta aat      373
Leu Tyr Ser Leu Pro Phe Tyr Leu Phe Phe Lys Leu Ser Pro Leu Asn
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ctg cca ggg aaa ttg gga ctt ata gaa acc ttg tca act tgt ttg ggt      421
Leu Pro Gly Lys Leu Gly Leu Ile Glu Thr Leu Ser Thr Cys Leu Gly
                      65                      70                      75

caa aaa tta gat cct gtg tta gaa act ctg caa aga gtg aga tcc atg      469
Gln Lys Leu Asp Pro Val Leu Glu Thr Leu Gln Arg Val Arg Ser Met
                      80                      85                      90

gca tca ttg atc gcc aac ttc ttt gtt cct ttc atc cag aag aaa ggt      517
Ala Ser Leu Ile Ala Asn Phe Phe Val Pro Phe Ile Gln Lys Lys Gly
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cag ctc att acg taa gaaacttttc atcaggaaaa gcagacaacc gataaaaaac      572
Gln Leu Ile Thr *
110

agaaactaag tattctgcaa ggaaacctgg tttaaggaga atgtattgaa actggatatg      632

cctgttcctt ttactctc cctttggcat ttctttttt tttctgtaag ataatcatag      692

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Leu Ala Tyr Cys Thr Gly Ser Val Ala Ser Tyr Glu Leu Thr Gln Pro
                      15                      20                      25

ccc tca gtg tcc gtg tcc cca ggc aag aca gcc agc atc acc tgc tct      148
Pro Ser Val Ser Val Ser Pro Gly Lys Thr Ala Ser Ile Thr Cys Ser
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gga gat aaa ttg ggg gat aaa tat gct tcc tgg tat cag cag aag gca      196
Gly Asp Lys Leu Gly Asp Lys Tyr Ala Ser Trp Tyr Gln Gln Lys Ala
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ggc cag tcc ccc gtg ctg gtc atc tat cga cat agc aag cgg ccc tca      244
Gly Gln Ser Pro Val Leu Val Ile Tyr Arg His Ser Lys Arg Pro Ser
                      60                      65                      70

ggg atc cct gag cga ttc tct ggc tcc aat tct ggg aac aca gcc act      292
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
                      75                      80                      85                      90

```

ctg acc atc agt ggg acc cag gtc atg gat gag gct gac tat tac tgt 340  
 Leu Thr Ile Ser Gly Thr Gln Val Met Asp Glu Ala Asp Tyr Tyr Cys  
 95 100 105  
 cag gcg tgg gac agc agc atc gtg gtg ttc ggc gga ggg acc aag ttg 388  
 Gln Ala Trp Asp Ser Ser Ile Val Val Phe Gly Gly Gly Thr Lys Leu  
 110 115 120  
 acc gtc cta ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg 436  
 Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro  
 125 130 135  
 ccc tcc tct gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc 484  
 Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
 140 145 150  
 ata agt gac ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat 532  
 Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
 155 160 165 170  
 agc agc ccc gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa 580  
 Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln  
 175 180 185  
 agc aac aac aag tac gcg gcc agc agc tat ctg agc ctg acg cct gag 628  
 Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu  
 190 195 200  
 cag tgg aag tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg 676  
 Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
 205 210 215  
 agc acc gtg gag aag aca gtg gcc cct aca gaa tgt tca taggttctca 725  
 Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
 220 225 230  
 accctcaccc cccaccacgg gagactagag ctgcaggatc ccaggggagg ggtctctcct 785  
 cccaccccaa gcatcaagcc cttctccctg cactcaataa accctcaata aatattctca 845  
 ttgtcaatga ggtc 859

<210> 48  
 <211> 1612  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (43) .. (1464)

<400> 48  
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 Met Gly Ser Thr  
 1  
 gcc atc ctc gcc ctc ctc ctg gct gtt ctg caa gga gtc tgt gct gag 102  
 Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly Val Cys Ala Glu  
 5 10 15 20

gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc ggg gag tct	150
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser	
25 30 35	
gtg aag att tcc tgt aag ggc tct gga tac agc ttt agc gac tac tgg	198
Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Ser Asp Tyr Trp	
40 45 50	
gtc gcc tgg gtg cgc cag tcg ccc gac aaa ggc ctg gcg tgg atg ggg	246
Val Ala Trp Val Arg Gln Ser Pro Asp Lys Gly Leu Ala Trp Met Gly	
55 60 65	
atc atc tat cct ggt gac tct gat acc agg tac agc ccg tcc ttc caa	294
Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln	
70 75 80	
ggc cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac ctg	342
Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu	
85 90 95 100	
cag tgg agt agc ctg aag gac tcg gac acc gcc atg tat tat tgt gcg	390
Gln Trp Ser Ser Leu Lys Asp Ser Asp Thr Ala Met Tyr Tyr Cys Ala	
105 110 115	
aga ggt gcc cga gga acc gcg ccc tcc tac cac tac tac ggt tta gac	438
Arg Gly Ala Arg Gly Thr Ala Pro Ser Tyr His Tyr Tyr Gly Leu Asp	
120 125 130	
gtc tgg ggc aga ggg acc tcg gtc acc gtc tcc tca gcc tcc acc aag	486
Val Trp Gly Arg Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys	
135 140 145	
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg	534
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly	
150 155 160	
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg	582
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro	
165 170 175 180	
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc	630
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr	
185 190 195	
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg	678
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val	
200 205 210	
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac	726
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn	
215 220 225	
gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc	774
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro	
230 235 240	
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa	822
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu	
245 250 255 260	
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac	870
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	
265 270 275	

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac	918
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	
280 285 290	
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc	966
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly	
295 300 305	
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac	1014
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn	
310 315 320	
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg	1062
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	
325 330 335 340	
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca	1110
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	
345 350 355	
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa	1158
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	
360 365 370	
cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac	1206
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn	
375 380 385	
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc	1254
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	
390 395 400	
gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc	1302
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
405 410 415 420	
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag	1350
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
425 430 435	
ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc	1398
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
440 445 450	
tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc	1446
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	
455 460 465	
tcc ctg tcc ccg ggt aaa tgagtg cgacggccgg caagcccccg ctccccggg	1500
Ser Leu Ser Pro Gly Lys	
470	
ctctcgcggt cgcacgagga tgcttgccac gtaccccgtc tacatacttc ccaggcaccc	1560
agcatggaaa taaagcacc accactgccc tgggcccctg caaaaaaaaa aa	1612

&lt;210&gt; 49

&lt;211&gt; 664

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> CDS  
 <222> (205) .. (348)

<400> 49  
 gtcgagggtcc ggaattcccg ggtcgaccca cgcgtccgac caggaatata aagatgagtt 60  
 tgagcatcat cctttcggga aatgtaaata cctaaagcaa aggattctag ggcaactgtt 120  
 tttcttcccc attatcaact ccataaagag tcttttctga cttctttttc aattgtcccc 180  
 tcctggcctt ttaataacat agat atg ctg ggt atc tgt tta tgt tct ata 231  
 Met Leu Gly Ile Cys Leu Cys Ser Ile  
 1 5  
 tgt gta ctt aga ctt tgt tta gaa aag agt aag att ttt cca cct cca 279  
 Cys Val Leu Arg Leu Cys Leu Glu Lys Ser Lys Ile Phe Pro Pro Pro  
 10 15 20 25  
 aga acc agt gat cac tcc ctt gag ggc tct gtc acc cct gtg gag aat 327  
 Arg Thr Ser Asp His Ser Leu Glu Gly Ser Val Thr Pro Val Glu Asn  
 30 35 40  
 gca gca cgg tca ggc atg taa aa gggctcttta ccgggtcttc tttcaggtgg 380  
 Ala Ala Arg Ser Gly Met \*  
 45  
 gggacttaga ttagtagata atccttcttg ggccacgggc ctcatgactg gtcagtagtg 440  
 ttgccagatt tcacaaactg tatatataga atgtccagtt aaacttgaat ttcagacaaa 500  
 caaatccttt ttttaagtaaa agtatgtcct atgcatatt tagacatcgt ttgttgatc 560  
 tggcaatgct acttgtaagg atcctactct tctgaggata gaaagtgcac tttccattaa 620  
 gtaagaattt tcattaacag gaagaacgtg agcctccatt taat 664

<210> 50  
 <211> 1001  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (257) .. (805)

<400> 50  
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 cccaccttac tttatctgaa cgcgcctaag ctgctgcagc tggcaccggt ttgcgctcgg 120  
 cgaagagggc tgggggaggg agatgacggt ggtcttttcc ctgcttgga cctgagagc 180  
 accatctccc tttttctcgc cactccaagg ttgcagacga agcatagatc tggttggagt 240  
 tggaggggtga gagaaa atg aat tct aat tta cct gca gag aac tta tcc 289  
 Met Asn Ser Asn Leu Pro Ala Glu Asn Leu Ser  
 1 5 10  
 att gca gtc aat atg acc aag act ttg cct aca gca gta acg cat gga 337  
 Ile Ala Val Asn Met Thr Lys Thr Leu Pro Thr Ala Val Thr His Gly

	15	20	25	
ttt aat tcc act aat gac cca cct tca atg tca att aca agg ctt ttt				385
Phe Asn Ser Thr Asn Asp Pro Pro Ser Met Ser Ile Thr Arg Leu Phe				
	30	35	40	
tca gcc tta ctg gaa tgc ttt ggc att gtc ctt tgt ggc tac ata gca				433
Ser Ala Leu Leu Glu Cys Phe Gly Ile Val Leu Cys Gly Tyr Ile Ala				
	45	50	55	
gga agg gcc aat gtc ata aca tca acc cag gcc aaa gga cta gga aat				481
Gly Arg Ala Asn Val Ile Thr Ser Thr Gln Ala Lys Gly Leu Gly Asn				
	60	65	70	75
ttt gtc tcc aga ttt gca ctt cca gct tta tta ttc aaa aac atg gtt				529
Phe Val Ser Arg Phe Ala Leu Pro Ala Leu Leu Phe Lys Asn Met Val				
	80	85	90	
gta ctt aat ttt tcc aat gtg gac tgg gcc ttc cta tat agt atc tta				577
Val Leu Asn Phe Ser Asn Val Asp Trp Ala Phe Leu Tyr Ser Ile Leu				
	95	100	105	
att gcc aaa gct tct gta ttt ttc att gta tgt gta tta acc tta ttg				625
Ile Ala Lys Ala Ser Val Phe Phe Ile Val Cys Val Leu Thr Leu Leu				
	110	115	120	
gtt gcc agt cct gat agt cga ttt agc aaa gct gga cta ttc cct att				673
Val Ala Ser Pro Asp Ser Arg Phe Ser Lys Ala Gly Leu Phe Pro Ile				
	125	130	135	
ttt gct aca caa agt aat gac ttt gca ttg gga tac cct ata ggt aag				721
Phe Ala Thr Gln Ser Asn Asp Phe Ala Leu Gly Tyr Pro Ile Gly Lys				
	140	145	150	155
tta att ttt att ttt caa gtg ttt aaa aaa ttc aat ttt aat tta ttt				769
Leu Ile Phe Ile Phe Gln Val Phe Lys Lys Phe Asn Phe Asn Leu Phe				
	160	165	170	
agg cat ttg tta gta aca gat tct tac tct cat atc taag aagtttttca				819
Arg His Leu Leu Val Thr Asp Ser Tyr Ser His Ile				
	175	180		
ttttttttctc aaatatgtct taggatgaat catagttttt cctaaacttc agagtttgag				879
gatacctttaa acatctacct aaaataaacg ggcataattct aataaccccc tgtgaacagg				939
cccaaattgg aattttttttc ttcccgggaa gcacatatga aaagaagctt atatttttta				999
ga				1001

<210> 51  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (182) .. (499)

<400> 51  
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tattatgagc agaggaaata aacatgcaga tggcttggtt tccttcgcat aacttgtaga 120

ggggtaggta gcataaaaga cagccgttct caagaggcaa ccatgcgcct cactacttac 180

c atg ttc ctg cgg ggc atc ccc tcc cgt agg gag tct ctg aaa aca 226  
Met Phe Leu Arg Gly Ile Pro Ser Arg Arg Glu Ser Leu Lys Thr  
1 5 10 15

aac aca cac aga agt tgg cgg tgg gca cca cat tct cct ctt gac cta. 274  
Asn Thr His Arg Ser Trp Arg Trp Ala Pro His Ser Pro Leu Asp Leu  
20 25 30

acc atc agg aat ttg ctg tgc cat ctg ttc ata aaa ctt agc cag gcc 322  
Thr Ile Arg Asn Leu Leu Cys His Leu Phe Ile Lys Leu Ser Gln Ala  
35 40 45

cag aaa gct tgt ccc aac cac atg cta aga gcc aag cag atg gaa cag 370  
Gln Lys Ala Cys Pro Asn His Met Leu Arg Ala Lys Gln Met Glu Gln  
50 55 60

aag ctc ccc caa gct gct ggc tcc cac tat ggc tgg gat gaa gca aga 418  
Lys Leu Pro Gln Ala Ala Gly Ser His Tyr Gly Trp Asp Glu Ala Arg  
65 70 75

acc tgg gcc cac aca ggc tgc aag gca gcg gac gcg tgg gtc gac ccg 466  
Thr Trp Ala His Thr Gly Cys Lys Ala Ala Asp Ala Trp Val Asp Pro  
80 85 90 95

gga gtt ccg gag cag gac ctt cca gcg ttc aat 499  
Gly Val Pro Glu Gln Asp Leu Pro Ala Phe Asn  
100 105

<210> 52  
<211> 738  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (52)..(393)

<400> 52  
atttgccct cgaggccaag aattcggcac gagcgggaac cacgcacggt t atg agc 57  
Met Ser  
1

tca tgg ttt ctg agg gcc ggg cat ggc ctc atc tgg gtc ctc ttc ttc 105  
Ser Trp Phe Leu Arg Ala Gly His Gly Leu Ile Trp Val Leu Phe Phe  
5 10 15

agg att ggt cag gct gca gtc gga gtg tca gct ggg cct ggg ggg tca 153  
Arg Ile Gly Gln Ala Ala Val Gly Val Ser Ala Gly Pro Gly Gly Ser  
20 25 30

ccc aag gcc cac ctg ggg aga gtg gct tcc cag cac cct cat ggg gca 201  
Pro Lys Ala His Leu Gly Arg Val Ala Ser Gln His Pro His Gly Ala  
35 40 45 50

gag agc agg gcc tgc ctc ctt gca cgt ggc ttg cct aag gcc ctg agc 249

Glu Ser Arg Ala Cys Leu Leu Ala Arg Gly Leu Pro Lys Ala Leu Ser  
55 60 65

tcc atg ctg gct gtt gac tgc agg cca cgc tca ggg cct ctc cat cgg 297  
Ser Met Leu Ala Val Asp Cys Arg Pro Arg Ser Gly Pro Leu His Arg  
70 75 80

gcg gct cac atc atg gca gca agc ctc atc agc aag cca gtg aga ggg 345  
Ala Ala His Ile Met Ala Ala Ser Leu Ile Ser Lys Pro Val Arg Gly  
85 90 95

tgc cta tcc gag gat gat att cca tca cct ctg tca gat tct gct tac 393  
Cys Leu Ser Glu Asp Ile Pro Ser Pro Leu Ser Asp Ser Ala Tyr  
100 105 110

tagtcagtcc ccaggcccag gccactcgca aggggaggac attacaggag gcgtgagtat 453

aggtggtgtg atctgtgggg accggcgcat aggctgccc ccacatgggg ttaaaccta 513

taaaacttcg aagctgaatt taattatatt cgaacactag gaaataaata aggatcgctg 573

tttctggcct tcccagaaca ctatagggtg ggattggata ctatattccc ccttaatttt 633

gtaaaagggg aaagcatgcc ctttcgatgc caacaattca cggggcctta cagggaaacc 693

ttccaacccc ccacgggagg gcttttactt cccatccggt gcgcg 738

<210> 53  
<211> 748  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (461) .. (616)

<400> 53  
atttggccct cgaggccaag aattcggcac gagctctggc agacgagcat aagaatccac 60

attttaaaca agcattccag gtgattctga tgcaagggtga tttgggggtct tgaagcctca 120

cacttacaga aactgctctc ttttgcattt atgaacctgg ctgttgaagg cttcagatca 180

catgcttggg gatggtagat actagtgggg atcatctgac tccagactgg gaatcttctc 240

gttacaggat gaccccaatc acttaggttt acttctggat cttgataatt ccttgatagt 300

cctcttttac tgatgtctct tacggccctt aagaaggcag agaaggggtt aactgaggcc 360

acagaataga gagagtgaag gaactgaagg gtcattttac agagtgactg ggggtgtggcc 420

cagtcctcca gtaggtgccc agagccagtc caaaattaga atg ggg tgg gat tca 475  
Met Gly Trp Asp Ser  
1 5

aaa ctg ctt ttc cta ttc act tgc ctt tca tgt gta acc aca tgc agt 523  
Lys Leu Leu Phe Leu Phe Thr Cys Leu Ser Cys Val Thr Thr Cys Ser  
10 15 20

gtg tca aca tgc ttt cag gcg cca tta ggc agc agc agt ttt gct ccc 571  
Val Ser Thr Cys Phe Gln Ala Pro Leu Gly Ser Ser Ser Phe Ala Pro

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                25                30                35
tct ggg ttc atg gac gct tgg tat tcc tgt tat gtg ttg gct tag aat      619
Ser Gly Phe Met Asp Ala Trp Tyr Ser Cys Tyr Val Leu Ala *
          40                45                50

agctctgctc tctggggctc tgagcattgt ccattaactc tttcagcacc agccctttga    679

gatgctaagg gcttttgaat gaaatgtaat aaccaccacg ccgagcccta tgcagtctca    739

aaaaaaaaa                                                                748

<210> 54
<211> 539
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (48)..(368)

<400> 54
attcagcctc cagagcacca gcactggcac tggcactggc acacgct  atg gca aat      56
                                     Met Ala Asn
                                     1

gaa gtg caa gac ctg ctc tcc cct cgg aaa ggg gga cat cct cct gca      104
Glu Val Gln Asp Leu Leu Ser Pro Arg Lys Gly Gly His Pro Pro Ala
          5                10                15

gta aaa gct gga gga atg aga att tcc aaa aaa caa gaa att ggc acc      152
Val Lys Ala Gly Gly Met Arg Ile Ser Lys Lys Gln Glu Ile Gly Thr
          20                25                30                35

ttg gaa aga cat acc aaa aaa aca gga ttc gag aaa aca agt gcc att      200
Leu Glu Arg His Thr Lys Lys Thr Gly Phe Glu Lys Thr Ser Ala Ile
          40                45                50

gca aat gtt gcc aaa ata cag aca ccg gat gcc ctg aat gac gca ctg      248
Ala Asn Val Ala Lys Ile Gln Thr Pro Asp Ala Leu Asn Asp Ala Leu
          55                60                65

gag aag ctc aac tat aaa ttt cca gca aca gtg cac atg gcg cat caa      296
Glu Lys Leu Asn Tyr Lys Phe Pro Ala Thr Val His Met Ala His Gln
          70                75                80

aaa ccc aca cct gct ctg gaa aag gtt gtt cca ctg aaa agg atc tac      344
Lys Pro Thr Pro Ala Leu Glu Lys Val Val Pro Leu Lys Arg Ile Tyr
          85                90                95

att att cag cag cct cga aaa tgt taagcctgga tttaaaacac agccgtctgg    398
Ile Ile Gln Gln Pro Arg Lys Cys
          100                105

ccagctgcct cgaatatctg acagcttagc aaaaagggcc aaagctttcc ataggcgtgc    458

tgcacttgct tggtaaatta agcagctttt gtatcttccc ctttgacttt aggtaataaa    518

gcatccaaac ttgtaaattct g                                              539

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<210> 55
<211> 558
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (212) .. (499)

<400> 55
gccctgaaga acctctacat gaggtaggtg gagattaact tggaagacct actgggagtg      60
ctggcttccg ccacatcct ccagttcagt ggctgtttc aaaggtgcgt ggatgtgatg      120
atagccagac tcaagccaag caccatcaag aaattctacg aggccggctg caaggttatt      180
tacctttagt gaattccatc ttctgaaaac a   atg ctt ttg tgg gtc ttc ttg      232
                                   Met Leu Leu Trp Val Phe Leu
                                   1               5

caa ctg aac tac aag att cag gca att ccg act tat gaa acc gtg atg      280
Gln Leu Asn Tyr Lys Ile Gln Ala Ile Pro Thr Tyr Glu Thr Val Met
              10               15               20

aca ttt ttt aag agc ttt cct gag aac tgt tgc ttt ctg gac cgg gac      328
Thr Phe Phe Lys Ser Phe Pro Glu Asn Cys Cys Phe Leu Asp Arg Asp
              25               30               35

ata gga cag agc ttg agg ccg ctc ttc ctc tgc ttg cgt ctg cac ggc      376
Ile Gly Gln Ser Leu Arg Pro Leu Phe Leu Cys Leu Arg Leu His Gly
              40               45               50               55

atc acc aaa ggc aag gat ctg agg tgc tgc ggc acc tta act tct tcc      424
Ile Thr Lys Gly Lys Asp Leu Arg Cys Cys Gly Thr Leu Thr Ser Ser
              60               65               70

cag agt cat ggc tcg acc agg tta cag tca acc att acc acg cac tgg      472
Gln Ser His Gly Ser Thr Arg Leu Gln Ser Thr Ile Thr Thr His Trp
              75               80               85

aga atg ggg gcg aca tgg tcc acc tga aagat cttaacaccc aggetgtgag      524
Arg Met Gly Ala Thr Trp Ser Thr *
              90               95

atttgggctg ctctttaacc aggagaatac aact      558

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<210> 56
<211> 1340
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (1098)

<220>
<221> misc_feature
<222> (1) ... (1340)
<223> n = a,t,c or g

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<400> 56  
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 Met Leu Tyr Trp Val Val Ile His Phe Gly Ala Arg Gly Pro Gly Gly  
 1 5 10 15

cgc cga aaa cgg cga acg aca aac ggg gag ggc cgg aat gcg gca agg 96  
 Arg Arg Lys Arg Arg Thr Thr Asn Gly Glu Gly Arg Asn Ala Ala Arg  
 20 25 30

cac gcc ggg aaa gag gga aac ccg cga aag ccc acg ggc aac gcc caa 144  
 His Ala Gly Lys Glu Gly Asn Pro Arg Lys Pro Thr Gly Asn Ala Gln  
 35 40 45

acc ccc atg gac cca agg aaa cgt aaa aag gga agt ctg acc ccg gga 192  
 Thr Pro Met Asp Pro Arg Lys Arg Lys Lys Gly Ser Leu Thr Pro Gly  
 50 55 60

cca aat aga cgc caa cag gaa agc gag ggc gca agg aga caa tcg cga 240  
 Pro Asn Arg Arg Gln Gln Glu Ser Glu Gly Ala Arg Arg Gln Ser Arg  
 65 70 75 80

cgg gga gag aac ggg agc gaa gca gcc cag agc ccc agc cgg gga acg 288  
 Arg Gly Glu Asn Gly Ser Glu Ala Ala Gln Ser Pro Ser Arg Gly Thr  
 85 90 95

gaa cgg aag gca acc aag agg gtg aaa aga aag caa gac gtc acc ggg 336  
 Glu Arg Lys Ala Thr Lys Arg Val Lys Arg Lys Gln Asp Val Thr Gly  
 100 105 110

aat gac cca cat agc cct tct ttg tct tcg gga ggt ccc atc cat aaa 384  
 Asn Asp Pro His Ser Pro Ser Leu Ser Ser Gly Gly Pro Ile His Lys  
 115 120 125

gcc aac act tcc gga aga tta aag gtg tcg gac agg ggg aca gct gag 432  
 Ala Asn Thr Ser Gly Arg Leu Lys Val Ser Asp Arg Gly Thr Ala Glu  
 130 135 140

agg aga gga gga ttt ctt gcc agg tgg aga gtc ttc acc gtc tgt tgg 480  
 Arg Arg Gly Gly Phe Leu Ala Arg Trp Arg Val Phe Thr Val Cys Trp  
 145 150 155 160

gtg cag gcc tgt gtc tgt cct gga aag atg cta gca atg ggg gcg ctg 528  
 Val Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu  
 165 170 175

gca gga ttc tgg atc ctc tgc ctc ctc act tat ggt tac ctg tcc tgg 576  
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser Trp  
 180 185 190

ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta cta gct caa gct 624  
 Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala Gln Ala  
 195 200 205

gga gag aaa cta gag ccc agc aca act tcc acc tcc cag ccc cat ctc 672  
 Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln Pro His Leu  
 210 215 220

att ttc atc cta gcg gat gat cag gga ttt aga gat gtg ggt tac cac 720  
 Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp Val Gly Tyr His  
 225 230 235 240

gga tct gag att aaa aca cct act ctt gac aag ctc gct gcc gaa gga 768  
 Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu Ala Ala Glu Gly

	245	250	255	
gtt aaa ctg gag aac tac tat gtc cag cct att tgc aca cca tcc agg				816
Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys Thr Pro Ser Arg				
	260	265	270	
agt cag ttt att act gga aag tat cag ata cac acc gga ctt caa cat				864
Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr Gly Leu Gln His				
	275	280	285	
tct atc ata aga cct acc caa ccc aac tgt tta cct ctg gac aat gcc				912
Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro Leu Asp Asn Ala				
	290	295	300	
acc cta cct cag aaa ctg aag gag gtt gga tat tca acg cat atg gtc				960
Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser Thr His Met Val				
	305	310	315	320
gga aaa tgg cac ttg ggt ttt tac aga aaa gaa tgc atg ccc acc aga				1008
Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Met Pro Thr Arg				
	325	330	335	
aga gga ttt gat acc ttt ttt ggt tcc ctt ttg gga agt ggg gat tac				1056
Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr				
	340	345	350	
tat aca cac tac aaa tgg gac agt ccc tgg gat gtg tgg cta tgacttg				1105
Tyr Thr His Tyr Lys Trp Asp Ser Pro Trp Asp Val Trp Leu				
	355	360	365	
tatganaacg accatgctgc ctgggactat gacaatggca tataacttcac acagatgtac				1165
actcagagag gacagccaat cctagctttc cataacccca caaggcctaa aattttaaaa				1225
atggccatcc aagcgggtca tttcccactg ggaggtccct gggagggatt tcgaacactt				1285
accggggcct tattcaacat taaggggggg gaggattggg cccccccccc ccccc				1340

<210> 57  
 <211> 1786  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1044) .. (1382)

<400> 57	
tagggagaag tgccaacata tttgcagttt attttcaaatt ggttcagagg ctgtctgtgt	60
acatgagaag acaaagataa ggcaaatgca gcaaaattgt aataattggt gaatccaggt	120
gaagggacta tggctggtct ttgtactttt ttttccaact tttctgtagg tttaaaattt	180
tcaaaataaa aaatgggaaa tacttttaaaa attgtaatca aagacattag tacagaaact	240
ttcataatgt attttatttt tacagtaaaa ttaatttatg taaattgata gaattttact	300
aatttcactc ccaagttaca ttaaaaggct tacatatggt tgataatagc atatgtaaac	360
tagaactctg aatgatatcc attggtcata atacgtacta tgtagcggta atgggtgactt	420

ttgtgattgc acaagtctag agatgcccc aatgacattg acttagacat ctggttattc	480
taaggctgaa actgaagttg aatagaaggt tttagtcaaa tactgagatg aaaactgagg	540
cagtcctggc gggggggagt gagggtgtgt gtatatatac acacatagac atcatgcttc	600
taaacattta cagaaagaaa gggtagatta tctacaaaa aataagaatc agactgatat	660
gagatcttac aaacctaacc ccttctctt tctaaaactc cagattctca tatttctgac	720
ttctattttg atattttacac ttcatattt accaggagtc ttcaacattt tgttcaaaac	780
agtactcttg gttttcttcc tccaagacta ctccttactc atatcagcaa atagcagctc	840
ttttcaagtg ctcagtgtaa aaacctacaa ttaatccttg atttctcttt cagtcagcct	900
atactaaatc aatttcattt aaaatatctc ggctactact ctgcatctcc actgctacca	960
tgggcctctc cagtcacatt ctccaagagc actctatctc atttaaaaga caaaatctct	1020
gcagtggcct gtgatgctcc tta atg gcc tac ata atc cag ccc tca agc	1070
Met Ala Tyr Ile Ile Gln Pro Ser Ser	
1 5	
acc tcc gtg atc tct gta aaa ctt tcc ctt ggt cac tgt gct tca gcc	1118
Thr Ser Val Ile Ser Val Lys Leu Ser Leu Gly His Cys Ala Ser Ala	
10 15 20 25	
aca tta acc agc ttg cat att tct cac att cac caa gct tgt tcc tgc	1166
Thr Leu Thr Ser Leu His Ile Ser His Ile His Gln Ala Cys Ser Cys	
30 35 40	
ctt ggg gcc ttt gta ctt acc atg ttc tgt tct gag aat act ctg cct	1214
Leu Gly Ala Phe Val Leu Thr Met Phe Cys Ser Glu Asn Thr Leu Pro	
45 50 55	
caa gat atc cta caa cta tct tac tgt att cag ctc tct gct caa gta	1262
Gln Asp Ile Leu Gln Leu Ser Tyr Cys Ile Gln Leu Ser Ala Gln Val	
60 65 70	
tta act gat gaa acc tgt cat ccc tac tcc act cca tgt tct gct tta	1310
Leu Thr Asp Glu Thr Cys His Pro Tyr Ser Thr Pro Cys Ser Ala Leu	
75 80 85	
ctt aac agc aat tgc aca tat ggc ccc ctg aat aat ata cat tta gtc	1358
Leu Asn Ser Asn Cys Thr Tyr Gly Pro Leu Asn Asn Ile His Leu Val	
90 95 100 105	
act tat ttt tac tta tct gct aat taaaatgtag actttttcta ttctgtttac	1412
Thr Tyr Phe Tyr Leu Ser Ala Asn	
110	
tgctgtattc ccagcatggt ttatccgaat gtgcagtggg ttcttttctt ctcccttate	1472
gtgggaagtg atgtgcacaa atacacataa tggagcctga atgtcatatt gctttcatac	1532
ctgtgtgaat tttggtgaaga aaggaaaagt agcgattgac aggtaatata attacattaa	1592
gtcactctca tagttagctg tttattgctt tctgtctctt attctcagtc cccaggacca	1652
aatgttgacc actaccttcc cccacatata attaggttat ttaccgaacg ccatgcaggt	1712
ggctgttaaa aggaagatat atacttacaa tataaacaca acttttccct gttgtcttcc	1772

tgtctcacac gaaa

1786

<210> 58  
 <211> 665  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (370)..(510)

<400> 58  
 tttagatagc cctgcggtac cggtcgga ttcccggtc gaccacgcg tccgcatttt 60  
 tttgtgttgt cagtaatttc cttataaaga tagtaatttt ctctaaatca aatcttatca 120  
 tgacttctaa cattctgtaa aataatttga gagtactagt taactaattc acaaacttta 180  
 aattagtagt ttattttcag ttaagcacac aagaaagaaa tatacagtct atctataatg 240  
 aaatcttagt tgactagatg ggttgtggtg tcttaaaaat tcccataact gatcacatgg 300  
 cttttaaaat aggaagtctg agattttttt gttttcctca actatatcct ttttaacaag 360  
 ttctatttt atg gat ctt tat gta gtg att ttt tgg tta gta tac ata 408  
                   Met Asp Leu Tyr Val Val Ile Phe Trp Leu Val Tyr Ile  
                   1                  5                  10  
 ttc tct act tac ata atc aca tat ata aaa ggt aat gtg gga ctg tgt 456  
 Phe Ser Thr Tyr Ile Ile Thr Tyr Ile Lys Gly Asn Val Gly Leu Cys  
                   15                  20                  25  
 ttt caa atc tta ttt cag cta agt ttt gag aga aga cca aaa tca gta 504  
 Phe Gln Ile Leu Phe Gln Leu Ser Phe Glu Arg Arg Pro Lys Ser Val  
                   30                  35                  40                  45  
 agg taa gctgagaact aagagtagaa agtttaaact agagcagggg ccaagttag 560  
 Arg \*  
 gagcagccac aacttttctt gcacatcaac ttagttgtaa caatttagtt tgaaagaaaa 620  
 tctggaacat aatactcagt ttgtaaaatt gaagttggta gaatt 665

<210> 59  
 <211> 968  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (231)..(581)

<400> 59  
 ccccaaacac ttagctggct ccccatgact taagtgtgtt ctcttgtgtc ctatggaatc 60  
 cagttctgaa gaggtggggg aggacaactg tgggaaaagc cctggggggc cctcccaagg 120



```

ccccatcagt gctctgagta ggctgtcatc agaacaaagg gctccactgc tgacaagggtt      180
tgagaactgc tggcttgagg tgagaacccc tttaacctct gcgggacagc   atg tct      236
                                     Met Ser
                                     1

ttc cct atc cac ctt cga ttc ttt tct ctt ttt ttt ctt cat tgg ctc      284
Phe Pro Ile His Leu Arg Phe Phe Ser Leu Phe Phe Leu His Trp Leu
          5                      10                      15

ctt ctt agt gga ttc tct tct cta ctg ccc tgg gct tca gcc ttt gtg      332
Leu Leu Ser Gly Phe Ser Ser Leu Leu Pro Trp Ala Ser Ala Phe Val
          20                      25                      30

cag tac tct cga tgc cct gaa cac aca cct tcc ctt tgc cca ggc ggt      380
Gln Tyr Ser Arg Cys Pro Glu His Thr Pro Ser Leu Cys Pro Gly Gly
          35                      40                      45                      50

gca aac aat cca ctt ctt caa gct cca aca caa atg ctg cct cct tta      428
Ala Asn Asn Pro Leu Leu Gln Ala Pro Thr Gln Met Leu Pro Pro Leu
          55                      60                      65

gga tgc ctg ctc tgt gct ctc cct gcc tcc cct agc cca tac ctc tgc      476
Gly Cys Leu Leu Cys Ala Leu Pro Ala Ser Pro Ser Pro Tyr Leu Cys
          70                      75                      80

tgg cac ctt ctg tac cat gcc ttc aga aac ctt ctt atc ccc ctc atc      524
Trp His Leu Leu Tyr His Ala Phe Arg Asn Leu Leu Ile Pro Leu Ile
          85                      90                      95

tct ggg gcc ccc tgt gga tct ggc ata ccc aag ttc agt aaa tgt cta      572
Ser Gly Ala Pro Cys Gly Ser Gly Ile Pro Lys Phe Ser Lys Cys Leu
          100                      105                      110

tca gta agc tgatggt acatgcattt tctaaaatag agctgggact tcccatgggg      628
Ser Val Ser
115

cccacatctg acctggcagc ccatgtattc cggccattag ggatgggaag ccatgaggac      688
ctggccttct gcccgaccca ggcagccatt caaggtgagc aatggccact tccaagactc      748
aagtgcacct ggaccctgcc caacaggccc ccccaggaaa aacaggctgt ccctggcggc      808
agtaagtagc aggcggccca aggtttcttg agctcttggt tttggcccaa cccccacc      868
caaaatactg ggtaggaca ggggacttgt agctccccct cagtgcacct tggccctggg      928
gccaagcccc ctggattggg attcggggaa cgctccagtc      968

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<210> 60  
 <211> 762  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (522) .. (635)

<220>

<400> 60		
ggcccaaaaa aaaaaataacc ccccgctggt ttgtggggtg tnttcttntg nggggaagac		60
agggtttccc ttttttttgc ccccggggtg gaaggccaaa gggcaatttc ccccaggaac		120
ccctgcccct cccggggggcc aagggtattc tcccacctc agcctcttga gtagttaaga		180
aggacaggtt taagcgccca tgccaagcta attttggtat ttgtatagaa gacgaggtct		240
cattatcttc cctaggcttt tcttgaaagt cctgagctca agttaatctg cctgcctcag		300
cctcccaaag tattgggatt acagatgtaa gccaccacac ttggccaatt atggtaattt		360
tgtaagttaa agtatacttg taaagctttg ttccttcag gtaattggct tgaatttgat		420
tttgtagtg aaggatgaag tcaaggacca ttggggttgc tctgtaaaat gaggagctgt		480
ttgggaaata ggtcttaaca ctaatgtgat tcaagaagga a	atg gca gac aca	533
	Met Ala Asp Thr	
	1	
gca gaa aac tca aga tat aat gtg cat att ccc cac aga tgg acc atc		581
Ala Glu Asn Ser Arg Tyr Asn Val His Ile Pro His Arg Trp Thr Ile		
5 10 15 20		
aac aag ttt ttc att tta atg cag tca tct ctt tcc tat tca tgt ctc		629
Asn Lys Phe Phe Ile Leu Met Gln Ser Ser Leu Ser Tyr Ser Cys Leu		
25 30 35		
tat tat taaatctctg gtattgggt tctcaaaga atagccttct gagctctatg		685
Tyr Tyr		
ggctgatctc atcactaact cctatagcag ttaggataat cactctcgtg ccgaattctt		745
ggcctcgagg gccaaat		762

[illegible]

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<210> 62
<211> 800
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (126)..(341)
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<220>
<221> misc_feature
<222> (1)...(800)
<223> n = a, t, c or g
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[illegible]

50	55	60	
ttt gta aaa gta ttc cat gac cta gtc cta t agagcaggtg aatattggag			362
Phe Val Lys Val Phe His Asp Leu Val Leu			
65	70		
attgttttct ctgtaacttt actatcatct acctatcttc gtatttttggg gagagatcat			422
gaaacctctct atcaaactct ctttatgcag taagttataa caaattagca ctggcttata			482
aagatatatc aaattagagt aaaatgcaac tgaaaatata ataaatcatt cggtaattaa			542
tgtttttctta aattcttggg gnaagtacaa gagaagaaat tggagatgtg cagactttaa			602
atgacctaaa cagtcttaca caggagtttt tgcagtatgg taagaaggag gtggctactt			662
atgtttttcaa aaagcacatg acctcatgaa aagtatgcaa ggctatactg tcgacggtag			722
aaaaacgaga gacagagaat aatttaaaga accttcccat gttaggcgtg aaaatgaaaa			782
ggcttaaatt taggtgcc			800
<210> 63			
<211> 524			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (249) .. (425)			
<400> 63			
cgggccgcgtc gacaaacaaa acaaatgaaa aattcacatc tcaaatgtc tggggcaggg			60
cattctgact ctgagctcaa catagcttct cccttcaactt agcccttctc agttcaacct			120
aaaagctata cacagaaaag ctgcttaatt tataacattt tttgaaagca ggctactgaa			180
ttactactga cagccacgtg aattttctgcc agggtaagtg gaaaaaagtg accaaaaggg			240
agaaccaa atg agt gtg cag gca tcc agg gga gcg ggt cag cac agc aca			290
Met Ser Val Gln Ala Ser Arg Gly Ala Gly Gln His Ser Thr			
1	5	10	
cta gat gaa aaa ggc tcg gaa aga tct ctg tcg tgt gca gac ggt ttc			338
Leu Asp Glu Lys Gly Ser Glu Arg Ser Leu Ser Cys Ala Asp Gly Phe			
15	20	25	30
cat gtc tgt tta aat gac aac acg aac agc aga aaa ata gag aaa acc			386
His Val Cys Leu Asn Asp Asn Thr Asn Ser Arg Lys Ile Glu Lys Thr			
35	40	45	
agt aaa tca gtt gct tca tct cca tca tac cgc gag gtc tgactacctt			435
Ser Lys Ser Val Ala Ser Ser Pro Ser Tyr Arg Glu Val			
50	55		
tattttcaagg aatcagttga atcagtcgac gcggccgcga attcggatcc tcgagagatc			495
tctttttttg ggtgtggtgg ggtatcttc			524

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<210> 64
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (27)..(347)

<400> 64
tgccggggagg gtttttttga aaccgt atg tcg tac tcc act cca gct tgg cac      53
                               Met Ser Tyr Ser Thr Pro Ala Trp His
                               1             5

gag gga tgt agg tac gag aat aca gaa tac ggg tgt ttt cta tta agc      101
Glu Gly Cys Arg Tyr Glu Asn Thr Glu Tyr Gly Cys Phe Leu Leu Ser
 10             15             20             25

aca cac att aca gag att tgc aaa aat gtt aca atg ctg ctc ttc tca      149
Thr His Ile Thr Glu Ile Cys Lys Asn Val Thr Met Leu Leu Phe Ser
             30             35             40

cta aac ttt ttc ttt tgg aaa ata gtc atg ttt cat aaa aat gta ata      197
Leu Asn Phe Phe Phe Trp Lys Ile Val Met Phe His Lys Asn Val Ile
             45             50             55

ttt ata tta aca tgt aat ggg ttt att att gtt act ttt aaa tgg att      245
Phe Ile Leu Thr Cys Asn Gly Phe Ile Ile Val Thr Phe Lys Trp Ile
             60             65             70

gat aaa ttt att tta aat att tct att tta att tct aac aca gta aat      293
Asp Lys Phe Ile Leu Asn Ile Ser Ile Leu Ile Ser Asn Thr Val Asn
             75             80             85

gtt aat agc cat aat cca cat aaa caa aag ttc ttt ggg gat ctc agt      341
Val Asn Ser His Asn Pro His Lys Gln Lys Phe Phe Gly Asp Leu Ser
 90             95             100             105

aat ttt taacagcgta aaggggtcct gagaccaaaa agtttgagaa ctgctgcaat      397
Asn Phe

caactataaa gagtaagttt gccctgaact gcattaactg gtatactttt tctctgtctt      457

tgatcaataa gggcttaaat atg      480

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<210> 65
<211> 1013
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (82)..(765)

<220>
<221> misc_feature
<222> (1)...(1013)
<223> n = a,t,c or g

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atggaccctg ttgctacca cagctgccat ctgctccagc aactgcatga gcagcgaatc 60

caaggcctgc tttgtgactg t atg ttg gtg gta aaa gga gtc tgc ttt aaa 111
Met Leu Val Val Lys Gly Val Cys Phe Lys
1 5 10

gcg cat aag aat gtc ctg gca gca ttc agc cag tat ttt agg aat gtt 159
Ala His Lys Asn Val Leu Ala Ala Phe Ser Gln Tyr Phe Arg Asn Val
15 20 25

cag cag atg cac agc aga aca aaa cgt tgg atg aat cgc atc cgc atg 207
Gln Gln Met His Ser Arg Thr Lys Arg Trp Met Asn Arg Ile Arg Met
30 35 40

ctt cac cat cag tta atc gtc atc act ccg cag gtg aaa tct caa aac 255
Leu His His Gln Leu Ile Val Ile Thr Pro Gln Val Lys Ser Gln Asn
45 50 55

aag ctc ctg ata ctt cag atg gca gct gca cag aac tgc ctt tca aac 303
Lys Leu Leu Ile Leu Gln Met Ala Ala Ala Gln Asn Cys Leu Ser Asn
60 65 70

agc caa att act att aca aac tca gaa act ttt aca cct gtg aat gac 351
Ser Gln Ile Thr Ile Thr Asn Ser Glu Thr Phe Thr Pro Val Asn Asp
75 80 85 90

tct gcc cca cac cct gag tca gac gcc aca tgc caa caa cct gtc aag 399
Ser Ala Pro His Pro Glu Ser Asp Ala Thr Cys Gln Gln Pro Val Lys
95 100 105

cag atg agg ctc aaa aag gcc att cat ctg aag aag ctc aat ttc ctg 447
Gln Met Arg Leu Lys Lys Ala Ile His Leu Lys Lys Leu Asn Phe Leu
110 115 120

aag tca cag aaa tac gca gag caa gta tct gaa ccc aag tca gat gat 495
Lys Ser Gln Lys Tyr Ala Glu Gln Val Ser Glu Pro Lys Ser Asp Asp
125 130 135

ggt ttg aca aag agg ttg gaa tct gct agt aaa aat acc cta gag aaa 543
Gly Leu Thr Lys Arg Leu Glu Ser Ala Ser Lys Asn Thr Leu Glu Lys
140 145 150

gct agc agc caa agt gct gaa gaa aaa gaa agt gaa gaa gtc gtc agt 591
Ala Ser Ser Gln Ser Ala Glu Glu Lys Glu Ser Glu Glu Val Val Ser
155 160 165 170

tgt gag aat ttt aat tgc att agt gag acg gag agg cct gaa gac ccg 639
Cys Glu Asn Phe Asn Cys Ile Ser Glu Thr Glu Arg Pro Glu Asp Pro
175 180 185

gct gcc ctg gaa gac cag tcc cag aca ctt cag tcc cag aga caa tac 687
Ala Ala Leu Glu Asp Gln Ser Gln Thr Leu Gln Ser Gln Arg Gln Tyr
190 195 200

gcg tgt gaa tta tgc ggg aaa cct ttt aaa cac cca agc aac ttg gag 735
Ala Cys Glu Leu Cys Gly Lys Pro Phe Lys His Pro Ser Asn Leu Glu
205 210 215

ctt cac aaa cgg tct cat aca ggt aac tga t tcagtacca caggcagaag 786
Leu His Lys Arg Ser His Thr Gly Asn *
220 225

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ggaaggacgt aatgcggatg ctcagacacc actggctctt cttgtttttg taagaagttt 846  
 tgctgttggt tgatgtcatt gatgatttta aacgtcgacg cggccgcgaa ttcggatcct 906  
 cgagagatct ctttttttgg gtttggtggg gtatcttcat catcgaatag atagttatat 966  
 acatcatcgc cnnngaattc caaanncncc cccctctttt aanntcg 1013

<210> 66  
 <211> 3283  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (180) .. (1469)

<400> 66  
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 tccccgggtcg acccaacgct cgggagatgc cggaccgctc cttcccagct cctccccgtg 120  
 ctcgctaaca cagcacggcc gcctgcagtc tctctctgag gagatcgccg gggcctaag 179  
 atg tgt cct ggg gca ctg tgg gtg gcc ctg ccc ctg ctg tcc ctg ctg 227  
 Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu  
 1 5 10 15  
 gct ggc tcc cta cag ggg aag cca ctg cag agc tgg gga cga ggg tct 275  
 Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser  
 20 25 30  
 gct ggg gga aac gcc cac agc cca ctg ggg gtg cct gga ggt ggg ctg 323  
 Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu  
 35 40 45  
 cct gag cac acc ttc aac ctg aag atg ttt ctg gag aac gtg aag gtg 371  
 Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val  
 50 55 60  
 gat ttc ctg cgc agc ctt aac ctg agt ggg gtc cct tcg cag gac aaa 419  
 Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys  
 65 70 75 80  
 acc agg gtg gag ccg ccg cag tac atg att gac ctg tac aac agg tac 467  
 Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr  
 85 90 95  
 acg tcc gat aag tcg act acg cca gcg tcc aac att gtg cgg agc ttc 515  
 Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe  
 100 105 110  
 agc atg gaa gat gcc atc tcc ata act gcc aca gag gac ttc ccc ttc 563  
 Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe  
 115 120 125  
 cag aag cac atc ttg ctc ttc aac atc tcc att cct agg cat gag cag 611  
 Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln  
 130 135 140  
 atc acc aga gct gag ctc cga ctc tat gtc tcc tgt caa aat cac gtg 659  
 Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val

145	150	155	160	
gac ccc tct cat	gac ctg aaa gga agc	gtg gtc att tat	gat gtt ctg	707
Asp Pro Ser His	Asp Leu Lys Gly	Ser Val Val Ile	Tyr Asp Val Leu	
	165	170	175	
gat gga aca gat	gcc tgg gat agt gct	aca gag acc aag	acc ttc ctg	755
Asp Gly Thr Asp	Ala Trp Asp Ser	Ala Thr Glu Thr	Lys Thr Phe Leu	
	180	185	190	
gtg tcc cag gac	att cag gat gag ggc	tgg gag acc ttg	gaa gtg tcc	803
Val Ser Gln Asp	Ile Gln Asp Glu	Gly Trp Glu Thr	Leu Glu Val Ser	
	195	200	205	
agc gcc gtg aag	cgc tgg gtc cgg tcc	gac tcc acc aag	agc aaa aat	851
Ser Ala Val Lys	Arg Trp Val Arg	Ser Asp Ser Thr	Lys Ser Lys Asn	
	210	215	220	
aag ctg gaa gtg	act gtg gag agc cac	agg aag ggc tgc	gac acg ctg	899
Lys Leu Glu Val	Thr Val Glu Ser	His Arg Lys Gly	Cys Asp Thr Leu	
	225	230	235	240
gac atc agt gtc	ccc cca ggt tcc aga	aac ctg ccc ttc	ttt gtt gtc	947
Asp Ile Ser Val	Pro Pro Gly Ser	Arg Asn Leu Pro	Phe Phe Val Val	
	245	250	255	
ttc tcc aat gac	cac agc agt ggg acc	aag gag acc agg	ctg gag ctg	995
Phe Ser Asn Asp	His Ser Ser Gly	Thr Lys Glu Thr	Arg Leu Glu Leu	
	260	265	270	
agg gag atg atc	agc cat gaa caa gag	agc gtg ctc aag	aag ctg tcc	1043
Arg Glu Met Ile	Ser His Glu Gln	Glu Ser Val Leu	Lys Lys Leu Ser	
	275	280	285	
aag gac ggc tcc	aca gag gca ggt gag	agc agt cac gag	gag gac acg	1091
Lys Asp Gly Ser	Thr Glu Ala Gly	Glu Ser Ser His	Glu Glu Asp Thr	
	290	295	300	
gat ggc cac gtg	gct gcg ggg tcg act	tta gcc agg cgg	aaa agg agc	1139
Asp Gly His Val	Ala Ala Gly Ser	Thr Leu Ala Arg	Arg Lys Arg Ser	
	305	310	315	320
gcc ggg gct ggc	agc cac tgt caa aag	acc tcc ctg cgg	gta aac ttc	1187
Ala Gly Ala Gly	Ser His Cys Gln	Lys Thr Ser Leu	Arg Val Asn Phe	
	325	330	335	
gag gac atc ggc	tgg gac agc tgg atc	att gca ccc aag	gag tat gaa	1235
Glu Asp Ile Gly	Trp Asp Ser Trp	Ile Ile Ala Pro	Lys Glu Tyr Glu	
	340	345	350	
gcc tac gag tgt	aag ggc ggc tgc ttc	ttc ccc ttg gct	gac gat gtg	1283
Ala Tyr Glu Cys	Lys Gly Gly Cys	Phe Phe Pro Leu	Ala Asp Asp Val	
	355	360	365	
acg ccg acg aaa	cac gct atc gtg cag	acc ctg gtg cat	ctc aag ttc	1331
Thr Pro Thr Lys	His Ala Ile Val	Gln Thr Leu Val	His Leu Lys Phe	
	370	375	380	
ccc aca aag gtg	ggc aag gcc tgc tgt	gtg ccc acc aaa	ctg agc ccc	1379
Pro Thr Lys Val	Gly Lys Ala Cys	Cys Val Pro Thr	Lys Leu Ser Pro	
	385	390	395	400
atc tcc gtc ctc	tac aag gat gac atg	ggg gtg ccc acc	ctc aag tac	1427
Ile Ser Val Leu	Tyr Lys Asp Asp	Met Gly Val Pro	Thr Leu Lys Tyr	



405	410	415	
cat tac gag ggc atg agc gtg gca gag tgt ggg tgc agg tag tatctgc			1476
His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg *			
420	425	430	
ctgcgggggct ggggaggcag gccaaagggg ctccacatga gaggtcctgc atgcccttgg			1536
gcacaacaag gactgattca atctgcatgc cagcctggag gaggaagggg agcctgctct			1596
ccctccccac accccaccca aagcatcac cgctgagctc aactgccagg gaaggctaag			1656
gaaatgggga tttgagcaca acaggaaagc ctgggagggt tgttgggatg caaggagggtg			1716
atgaaaagga gacaggggga aaaataatcc atagtcagca gaaaacaaca gcagtgcagcc			1776
agaggagcac aggcgggcag gtcactgcag agactgatgg aagttagaga ggtggaggag			1836
gccagctcgc tccaaaaccc ttggggagta gagggaagga gcaggcccg tgtcacaccc			1896
atcattgtat gttatttccc acaaccaggt tggaggggca tggcttccaa tttagagaca			1956
taaaacacag gcagatcaag tagcattgat caatggcatg attccaactc agatttgtgg			2016
gacaccaaag ccaggatct tcccaagtgc cctgctgcag tttagcaggt cctctccagc			2076
taaagagcag tgagacattg ggagcccagg agtggtgagg ccaggccagg ctgaggccca			2136
tcagtcacag gtgtgactgg gctgcttgtc acacacaggg cgtggtcttg ccactgttgc			2196
cagtgtcac tcagcgcca aatgcttttt aatatgaccc ctgaggcact gaaaaataac			2256
cccaggccaa ctgcaggata gagagagagg tcaggacagc agccctgtgg gctgcatgat			2316
acactgtggc tggagttatt gtgacccct ggtgcagtgc tcccacggcc agtgggtgcac			2376
acagggccat tcaactgtcca tagactgaaa ccatgtgacc atttgagagg gccgggcaca			2436
ctttcccctg agggatgggg cagcctgtgg ccagcacctc tgcagttact ctgcatagcc			2496
agctcaccag catgccatgc ccagggtgcc cccagtgac aacctcatgg gagacgggcc			2556
tggatttgaa tttgttgaa ttaaattgtc tctggctttg gtctttgaaa catatctatt			2616
tttattcctt ggtgacatgt ccttaagtga caagactcca gccttcctgg gcgaggcctc			2676
tccagcctcg gaagagctgc agtccttacc ggcgatcact ggctctgcct gcatttgccg			2736
gctctcttga gtcacgtgca tcccagcacc ccgcctgggc tcggactgtg ggaccagact			2796
cagcctcccc gaacacaagg gaagataagg cttccatttg ctctgtgttt caccctctcc			2856
tctgtctctc caggccacac atggaacggg gcggtatgag gaagagtctg aaagtggatga			2916
agagtgcacc tatggccctc tgacctccag ccagagcagg gcctagggga ggcttagaga			2976
ggccagggcc tctccccgtg gttgaagctc ccatttattt aagaaaaagt ggggggtggg			3036
gaaaacgtta tgttaaattg ttacatggaa ccaatgaaca actttaacac acaatacaaa			3096
cgaaacattc ttgtttaatt actggcgtaa tagaaaatat gaattcctgc tacatgccgg			3156
gcagtgtagt gttacaatgc tattccaagt tgggtgttga gcatcttctt tcagtcctgg			3216

tggtgtgctt ctgtgcctgc ttgaaaatct cactaggaaa taaagtcaaa tgtctaaaaa 3276  
 aaaaaaa 3283

<210> 67  
 <211> 1327  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (187) .. (354)

<220>  
 <221> misc\_feature  
 <222> (1) ... (1327)  
 <223> n = a,t,c or g

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 ggaaatccca gccattacca tgaacaaaat ggtaagttac ttctactaga actttactga 120  
 ctttaagcta gagagaaaga gaaagagaga ggtaaaacaa aaatcaaaaa ggaaaaggct 180  
 cagatc atg ttc ggc atg atc aag agg agg gtc aga aga gct gtt ttt 228  
 Met Phe Gly Met Ile Lys Arg Arg Val Arg Arg Ala Val Phe  
 1 5 10  
 gtg ggc cgc acc gtg ctc tgt gga tct tgt aac tct ggg att att atg 276  
 Val Gly Arg Thr Val Leu Cys Gly Ser Cys Asn Ser Gly Ile Ile Met  
 15 20 25 30  
 cac cgt ggc aag act cca ccc ctg aag atg gtc tgc cga ttt gaa gaa 324  
 His Arg Gly Lys Thr Pro Pro Leu Lys Met Val Cys Arg Phe Glu Glu  
 35 40 45  
 tca ttt tct tgc tta ttt tta aac tct taa a gacagggaaa aagactgaag 375  
 Ser Phe Ser Cys Leu Phe Leu Asn Ser \*  
 50 55  
 gagcctaaat gctgtggttt cctcaaacca ttattgttgt aaatcctatg ggtcctgaag 435  
 taactcacta ttctgaagt ttcaaactgc ctcacgactc agaagccttg gcagttgaaa 495  
 gggaaattat tagcttcttc cttgaaacgt tgtcactaag gttaaagggg gacaaaagg 555  
 ggtgaatgtg gggaatttca aaagtaaact acctttttta tagaaaatcc atagctcttt 615  
 acagaacttt gaggttttca aatacttagt tggggtgaaa acacattatt ttacaccagt 675  
 aggccttaca gaaattaaat attacaataa tggattccat tatctatggc cacattacca 735  
 gaagcctgga cgtttacctt ggggcacgtt cgctttatat gctaggagtg cctgcggaat 795  
 tgatccttgg gcttgacgga aacgagcga ttagctccg ctatcgcgga aaaacgcctg 855  
 cgcggcgccc cgcgccacc cgcgtgcctt taatgcgggc gctcacgcgc gtcctctcgc 915  
 cgccgcgtag acgcgtgccc ttccgcgggg aaatcgcccc cgggctcccc cgtcactccc 975

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tccgtnttgt gcgggtgggt cgcgtctctg tccgtgtccg gcggaacatg tccgcccggg 1035
gggggtcccg cgccgggaact ngcggcgctg gcttgccggc gttcgtcatc cagccacgcc 1095
gtgcgntaat ggacgcgcg catcgctcac cacgcgcac gcngcngcnc cgcttactgt 1155
gcggttcccc ccgccctgc nccgatacag aaagaacccg accccccccg ctatattgtc 1215
gttgtctggc tcgacgtgcc gacgtgttcc gccccccgca agcgtcgggt tgacactacg 1275
ctcgtactt gtggaacgg cggcgcgtgg gtgtccctcc gctcgccgag ct 1327

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<210> 68  
 <211> 580  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (22)..(168)

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<400> 68
ataacagggc aagtcacagc c atg gga ttc ctt ttc ctt ctg gat tct gcc 51
                        Met Gly Phe Leu Phe Leu Leu Asp Ser Ala
                        1 5 10

ctc atg cag act tgg gtt aca gta ata gat gta agt ctg cat cat gta 99
Leu Met Gln Thr Trp Val Thr Val Ile Asp Val Ser Leu His His Val
                        15 20 25

gag atc aaa gcc cca aga ata agg ctc atg tgg tcc cta ccc ttg agg 147
Glu Ile Lys Ala Pro Arg Ile Arg Leu Met Trp Ser Leu Pro Leu Arg
                        30 35 40

aga caa aaa tat acg atg tag at ggacagctgc attatgcaca cagatccatt 200
Arg Gln Lys Tyr Thr Met *
                        45

tcaatataac atggtgggct actctgggaa cactcctgct ccacaaggag cagtataaaa 260
aaataaatta atcaaatttt aaaaaagcaa catggtagat cctgggcgct tagagagtac 320
tgctcaagtg ctatgagaac acttgggcag agatatctac ccagacatgg gagtgcgtg 380
gttgagaaat ctgacctac actgctaaca cctctgtctg gagaagttgc tggaggcttc 440
caagatgggg cctgtgggat aaacaaactt taccgaatgg aaaagatgaa aaggaattgg 500
aggccaagag aacagcaagt acaaagacac agagttttta gtacttcctc gtgccgaatt 560
cttggcctcg agggccaaat 580

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<210> 69  
 <211> 1391  
 <212> DNA  
 <213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; (162) .. (482)

&lt;400&gt; 69

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aattcggcac gagcagcagc catggccacc tgcattgccag tcttcctgtgt attgctgcgt      60
atgagcgccc ttccttggat gtggatttcc atgacatggc ctttctcacc ttccttactt      120
cctgtcctgc tatgtattgt gtccctaccat gaattcactc c      atg cta gcc aca      173
                                   Met Leu Ala Thr
                                   1

ttg gcc tgt atg gct att cct tgg aca cac cta gga tgt tct tgc ctc      221
Leu Ala Cys Met Ala Ile Pro Trp Thr His Leu Gly Cys Ser Cys Leu
5                               10                               15                               20

tta gct tgc cta cct ttc tct cat cat ttg ggc ctc agc gag gat atc      269
Leu Ala Cys Leu Pro Phe Ser His His Leu Gly Leu Ser Glu Asp Ile
                               25                               30                               35

atc tcc tca gag aag cct tct gtg acc atg cta tct aaa ata ctc cag      317
Ile Ser Ser Glu Lys Pro Ser Val Thr Met Leu Ser Lys Ile Leu Gln
                               40                               45                               50

cac ttc agt cac cct tta tcc cat tac tct gct ttt tca gaa aca ttg      365
His Phe Ser His Pro Leu Ser His Tyr Ser Ala Phe Ser Glu Thr Leu
                               55                               60                               65

gtg ctc cct gaa aca tat ttg ttt act tgc tta gtg tct ttt ctc ccg      413
Val Leu Pro Glu Thr Tyr Leu Phe Thr Cys Leu Val Ser Phe Leu Pro
                               70                               75                               80

cac tac cat gta agc ttc ttg agg gtt agg gac ctt gtt agg gat aac      461
His Tyr His Val Ser Phe Leu Arg Val Arg Asp Leu Val Arg Asp Asn
85                               90                               95                               100

cac tgt atc ctt aga gtg tga ca catagtaggt tctcaatata tatttttgaa      514
His Cys Ile Leu Arg Val *
                               105

actctaccct gatgcaaaag agatatcaaa taattatagt ttttgcatta taaatgtctt      574
tggtgaaaac cctggcaciaa aactaataat aaagaaataa acagataatg gtgagttctg      634
ggcctgcaaa cctaactctt taaagcagtc acagtaaagtg tgtcattgga tccatagaac      694
ttgggaagtc agcatatctt attgggaaaa gcatgaactt caaagtaaaa cttatgggtca      754
aatctcatta ctgggtgcgtt ctttaagtcac ttaacctttg agccacaagg tacacaaatg      814
tgaaattaga ggaataatag tgactccata agacctcaa gaaaaggaaa taaggtattg      874
tagcccgatg atccttatca catggctaac aaattagggg gtctaaaatt ctggtatggg      934
catacccgga aacacgtcac gcatgtaggg gcctactaag aaaagagggt ccttgagtcg      994
ggaccaggga cgttatgcga aatggcgagg actggaggcc gcggggatgg gccacgtcga      1054
gcattcgccg gcatcgggga ttgggggaac ccggggcggtt cgtgcgcggg gggcggggaa      1114
ggggggcgcg tgagcgaaga gggagcatcg gcggctacgg cgcgcaaccg ggcgagcagc      1174
accggcagtg gcgcaatata cgcggagcag ctcccatgta acggcgaggt ttgtgcgcat      1234

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ccggcggaag tagggcggaag accacgtcgg tgcgcgggaa actcgcgcgc actcgcggc 1294  
 gacaacggca cgggcaccgc cggactaggg ggccaccgcg cgggtgcacct gctggctcgt 1354  
 cggcgagaac gcgggcggat aattcgcgga ccgagcc 1391

<210> 70  
 <211> 684  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (122) .. (262)

<400> 70  
 atgactctca ttgattacac ctgtctctac aacgactcat ctatagggaag agctggtacg 60  
 cctgcacgta ccggtttcta attccccggg cgaccacgc gtccgctgta atgaattaaa 120  
 g atg cat aca cct cat cta cca aat atc ata gtg tat ttt atc cta 166  
 Met His Thr Pro His Leu Pro Asn Ile Ile Val Tyr Phe Ile Leu  
 1 5 10 15  
 ctc tac ata tgc tca caa tac tta tat tta ctt aca att agg cat aat 214  
 Leu Tyr Ile Cys Ser Gln Tyr Leu Tyr Leu Leu Thr Ile Arg His Asn  
 20 25 30  
 cat cta aca caa agc cta ttt tat aat aaa tta ttg agt gtc ttg taa 262  
 His Leu Thr Gln Ser Leu Phe Tyr Asn Lys Leu Leu Ser Val Leu \*  
 35 40 45  
 tttattgaat gctgtacgtt gtgacaaaat tgcaatgggt tggcaccatc ataaatttgg 322  
 aaaatcattt agtggaaacct tcataagttg ggaactgttt gtatacctat aagtgggaatt 382  
 attcggtcac agagtatgcg tatcttcaac ttgagtagat ttgcaaatgg ttttccaaag 442  
 tggctatacc aggttatatc aatttacatt ctaaccagca gtgtttaaga gttctggtgc 502  
 tccacatctc aaacatatat atatatgtgt atagaggagg agagagaggg agagcgagag 562  
 ccacagagag cgcattgttt catatgtccc tgctaactct ttcttgcaga atgactgac 622  
 attttttcta attgatatgt aagatttctt tgtatatctc caaatcaata acctttatgg 682  
 gt 684

<210> 71  
 <211> 545  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (187) .. (396)

<400> 71

ctagagagcg tggggaattc caggattgcc cacttgggac cctgactatg aagggtaag 60  
 atagcccatt ctgccccagc actcagagcc ctattaccaa ggcccctact ccaagaatcc 120  
 accatcaaaa ccggggccct gccagtgcct tcccagtgtt caggcctagg gaagaatagc 180  
 cccatt atg cct gtt act cct gat cct tct gca gtc tct ctc ttt gtg 228  
 Met Pro Val Thr Pro Asp Pro Ser Ala Val Ser Leu Phe Val  
 1 5 10  
 acc cca tgg cct ttg ctg cta tgt ctg ccc tgg ccc cac aga gtg cca 276  
 Thr Pro Trp Pro Leu Leu Leu Cys Leu Pro Trp Pro His Arg Val Pro  
 15 20 25 30  
 ggt cag agc cac cct ggc cta cat agc agg gcc ccg gtt cac agg cta 324  
 Gly Gln Ser His Pro Gly Leu His Ser Arg Ala Pro Val His Arg Leu  
 35 40 45  
 aaa cct ggg cct cct gcc agg ctg caa ctc cca gct gca cac cgc aac 372  
 Lys Pro Gly Pro Pro Ala Arg Leu Gln Leu Pro Ala Ala His Arg Asn  
 50 55 60  
 ctg aga cat ctc agc ata ttc tag gaactagtaa tggggacgct tccgactcgc 426  
 Leu Arg His Leu Ser Ile Phe \*  
 65 70  
 tggggaaggg agatgagggc ctctagctct ccattgccag tctctcatca tcaaagtcac 486  
 ttaaggcccc agcgacccca ggggttcagca gcacctgtt catcatgagc aagaggggtg 545

<210> 72  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (34)..(243)

<400> 72  
 tccctagtcc agtgtggtgg aattcaaaac atc atg tca tgg tat act tgt cag 54  
 Met Ser Trp Tyr Thr Cys Gln  
 1 5  
 tgt ctc ttc ttt ctc agc aac aca tta agg aat ggt gct act tct tgc 102  
 Cys Leu Phe Phe Leu Ser Asn Thr Leu Arg Asn Gly Ala Thr Ser Cys  
 10 15 20  
 cat tgg tat tgt agc cct gat gac atg cag atg gtt gat ttc agc tca 150  
 His Trp Tyr Cys Ser Pro Asp Asp Met Gln Met Val Asp Phe Ser Ser  
 25 30 35  
 aca tac gaa agg att ttc agg cca ttt gtg ttc aag ata aaa ggg cct 198  
 Thr Tyr Glu Arg Ile Phe Arg Pro Phe Val Phe Lys Ile Lys Gly Pro  
 40 45 50 55  
 gac agc ttt agg ata gac atg agc ccc atc cct gaa gac att taa tca 246  
 Asp Ser Phe Arg Ile Asp Met Ser Pro Ile Pro Glu Asp Ile \*  
 60 65 70  
 caatctagac aagctcttgt tgtaaagag ctcaagtatc agatttggaa gtgaatgatc 306

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ttttacattt ttgtcaagct tgaggttcgt gaacttggat ccaacctctt attttttgca      366
gataagaaaa caaggatcac accagttgag agatttctcc gaagtcagac atctcattag      426
agctagagag gccagactag catgtctccc atgatccagt ctgaa                      471

<210> 73
<211> 856
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)..(567)

<220>
<221> misc_feature
<222> (1)...(856)
<223> n = a,t,c or g

<400> 73
aggaggtttc tncattgaac gccttcggtg ccggtccgga attcccgggt cgacccacgc      60
gtccggcggc gctgcgcgtg cgttgttgag tgttcgggac gccggcctgc aggcgcc      117
atg gtc ttc ctc acc gcg cag ctc tgg ctg cgg aat cgc gtc acc gac      165
Met Val Phe Leu Thr Ala Gln Leu Trp Leu Arg Asn Arg Val Thr Asp
  1             5             10             15

cgc tac ttt cgg atc cag gag gtg ctg aag cac gcc agg cac ttc cgg      213
Arg Tyr Phe Arg Ile Gln Glu Val Leu Lys His Ala Arg His Phe Arg
             20             25             30

gga agg aaa aat cgc tgc tac agg ttg gcg gtc aga acc gtg att cga      261
Gly Arg Lys Asn Arg Cys Tyr Arg Leu Ala Val Arg Thr Val Ile Arg
             35             40             45

gcc ttt gtg aaa tgc acc aaa gcc cga tac ctg aag aaa aag aac atg      309
Ala Phe Val Lys Cys Thr Lys Ala Arg Tyr Leu Lys Lys Lys Asn Met
             50             55             60

agg acc ctc tgg att aat cga att aca gct gct agc cag gaa cat gga      357
Arg Thr Leu Trp Ile Asn Arg Ile Thr Ala Ala Ser Gln Glu His Gly
             65             70             75             80

ctg aag tat cca gcg ctc att ggg aat tta gtt aag tgc cag gtg gag      405
Leu Lys Tyr Pro Ala Leu Ile Gly Asn Leu Val Lys Cys Gln Val Glu
             85             90             95

ctc aac agg aaa gtc cta gcg gat ctg gcc atc tac gag cca aag act      453
Leu Asn Arg Lys Val Leu Ala Asp Leu Ala Ile Tyr Glu Pro Lys Thr
             100            105            110

ttc aaa tct ttg gct gcc ttg gcc agt agg agg cga cac gaa gga ttt      501
Phe Lys Ser Leu Ala Ala Leu Ala Ser Arg Arg Arg His Glu Gly Phe
             115            120            125

gct gct gcc ttg ggg gat ggg aag gaa cct gaa ggc att ttt tcc aga      549
Ala Ala Ala Leu Gly Asp Gly Lys Glu Pro Glu Gly Ile Phe Ser Arg
             130            135            140

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gtg gtg cag tac cac tga ggactg ttgctgtatt gattaggaaa agagacagag 603  
 Val Val Gln Tyr His \*  
 145 150

taatttgacag ttgttttgat ttatactttt gtttatctac aacccaataa cagacatgag 663  
 ggatggccct gtctctctgg gacagagcct caaagatgat gtccatgttt tgtgtgaatg 723  
 aaactcaaac actcttcagt ttttagagtc attttctggg atcgagcgac cacaccgagg 783  
 agcacaccct gcttccaagg ctgctgcctt ctgacacagt ggggggatcc ccaccaccc 843  
 tggtccct caa 856

<210> 74  
 <211> 1155  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (251) .. (1084)

<400> 74  
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 aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg acgtaagctc ggctcacagt 120  
 cgcaggagag ttctggggta cacgggcaaa ggggcttgag aaggcccgga ggcgaagccg 180  
 aagagaagca actgtgcccc ggagaagaga agctcgccca ttccagactg ggaaccagct 240  
 ttcagtgaag atg gca ggg cca gaa ctg ttg ctc gac tcc aac atc cgc 289  
 Met Ala Gly Pro Glu Leu Leu Leu Asp Ser Asn Ile Arg  
 1 5 10

ctc tgg gtg gtc cta ccc atc gtt atc atc act ttc ttc gta ggc atg 337  
 Leu Trp Val Val Leu Pro Ile Val Ile Ile Thr Phe Phe Val Gly Met  
 15 20 25

atc cgc cac tac gtg tcc atc ctg ctg cag agc gac aag aag ctc acc 385  
 Ile Arg His Tyr Val Ser Ile Leu Leu Gln Ser Asp Lys Lys Leu Thr  
 30 35 40 45

cag gaa caa gta tct gac agt caa gtc cta att cga agc aga gtc ctc 433  
 Gln Glu Gln Val Ser Asp Ser Gln Val Leu Ile Arg Ser Arg Val Leu  
 50 55 60

agg gaa aat gga aaa tac att ccc aaa cag tct ttc ttg aca cga aaa 481  
 Arg Glu Asn Gly Lys Tyr Ile Pro Lys Gln Ser Phe Leu Thr Arg Lys  
 65 70 75

tat tat ttc aac aac cca gag gat gga ttt ttc aaa aaa act aaa cgg 529  
 Tyr Tyr Phe Asn Asn Pro Glu Asp Gly Phe Phe Lys Lys Thr Lys Arg  
 80 85 90

aag gta gtg cca cct tct cct atg act gat cct act atg ttg aca gac 577  
 Lys Val Val Pro Pro Ser Pro Met Thr Asp Pro Thr Met Leu Thr Asp  
 95 100 105

atg atg aaa ggg aat gta aca aat gtc ctc cct atg att ctt att ggt 625



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Met Met Lys Gly Asn Val Thr Asn Val Leu Pro Met Ile Leu Ile Gly
110                      115                      120                      125

gga tgg atc aac atg aca ttc tca ggc ttt gtc aca acc aag gtc cca      673
Gly Trp Ile Asn Met Thr Phe Ser Gly Phe Val Thr Thr Lys Val Pro
                      130                      135                      140

ttt cca ctg acc ctc cgt ttt aag cct atg tta cag caa gga atc gag      721
Phe Pro Leu Thr Leu Arg Phe Lys Pro Met Leu Gln Gln Gly Ile Glu
                      145                      150                      155

cta ctc aca tta gat gca tcc tgg gtg agt tct gca tcc tgg tac ttc      769
Leu Leu Thr Leu Asp Ala Ser Trp Val Ser Ser Ala Ser Trp Tyr Phe
                      160                      165                      170

ctc aat gta ttt ggg ctt cgg agc att tac tct ctg att ctg ggc caa      817
Leu Asn Val Phe Gly Leu Arg Ser Ile Tyr Ser Leu Ile Leu Gly Gln
                      175                      180                      185

gat aat gcc gct gac caa tca cga atg atg cag gag cag atg acg gga      865
Asp Asn Ala Ala Asp Gln Ser Arg Met Met Gln Glu Gln Met Thr Gly
190                      195                      200                      205

gca gcc atg gcc atg ccc gca gac aca aac aaa gct ttc aag aca gag      913
Ala Ala Met Ala Met Pro Ala Asp Thr Asn Lys Ala Phe Lys Thr Glu
                      210                      215                      220

tgg gaa gct ttg gag ctg acg gat cac cag tgg gca cta gat gat gtc      961
Trp Glu Ala Leu Glu Leu Thr Asp His Gln Trp Ala Leu Asp Asp Val
                      225                      230                      235

gaa gaa gag ctc atg ggc caa aga cct cca ctt cga agg cat gtt caa      1009
Glu Glu Glu Leu Met Gly Gln Arg Pro Pro Leu Arg Arg His Val Gln
240                      245                      250

aaa gga att aca gac ctc tat ttt ttg aag acc gag cag gga tta gct      1057
Lys Gly Ile Thr Asp Leu Tyr Phe Leu Lys Thr Glu Gln Gly Leu Ala
255                      260                      265

gtg tca gga act tgg agt tgc act taa ccttg taactttggt tggagctggc      1109
Val Ser Gly Thr Trp Ser Cys Thr *
270                      275

acctcttgaa ataaaaagga ggatgcacga gctgggaaaa aaaaaa      1155

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&lt;210&gt; 75

&lt;211&gt; 749

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (285) .. (440)

&lt;400&gt; 75

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taaaaatggtt gaaaataagg cttactttta ttatttgaat atggtaatta tgtaattatc      60
cttttaatat gttaagggtta tattctgtgc cttagagtat gctaagcact ttatacataa      120
ttatcttatt taagcctcgt agaaatctta tgagcaaaat gttactcggg acacttaaag      180

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**PCT/US01/02623**

gcgggtggaat	tcgcacacac	acacgtagta	caaagaaata	ctatcagtga	atggaggcaa	60
gtcattgagt	tctgtaatct	tgatagtcca	gagaaagga	tgaatctgcc	agatcagagg	120
agctcctgat	gtcttcttca	tcagggttaag	gatattttct	tttatatcta	atttaattca	180
tctaagaacg	actcattaaa	ttacgtataa	ttctttacta	cataaatgaa	gttccctctt	240
attcctat	ttt	tttttt	tttaaattagg	a	atg gtt act tat ttt atc aaa	292
					Met Val Thr Tyr Phe Ile Lys	
					1 5	
tgc ttt cat tat gag gtt tct ttt ctt ctt tgg ttt gct gtt gtc agg	340					
Cys Phe His Tyr Glu Val Ser Phe Leu Leu Trp Phe Ala Val Val Arg						
10 15 20						
aat gat gta gac agg cca gtc tcc ctg tca ctc ttc tct tcc tat agt	388					
Asn Asp Val Asp Arg Pro Val Ser Leu Ser Leu Phe Ser Ser Tyr Ser						
25 30 35						
tta ttc tca aca tat cca gac aca tgt ccc ttg ttc aaa ctc ccc acc	436					

Leu Phe Ser Thr Tyr Pro Asp Thr Cys Pro Leu Phe Lys Leu Pro Thr  
 40 45 50 55  
 cac tta ctg tgt tgt tta gag gaa ata taa a tgtccttatt ataactgaca 487  
 His Leu Leu Cys Cys Leu Glu Glu Ile \*  
 60 65  
 aggccctacc ctgttcaatc ttactacttt tctgcctaata ctacttctct ctctctatct 547  
 aactcatcct actcagtcac cttggctttc ttgatgttcc tggaatatac tggacatgtt 607  
 ccctttacag agccttttca gttgctcgtc tccttacctt ggatgtatct ccatcccaca 667  
 tcaccacact tagtttagatc cctcacagac ttcagatctt tactcaaagg tcaccttttt 727  
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 <212> DNA  
 <213> Homo sapiens

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 <222> (280) .. (420)

<400> 77  
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 tttcagaaaa ttaactctca ttgagtggca ttttctgact ccgggaataa aggatttttt 180  
 ttctaagatt gttttcttaa aattagaaga ctgatgttgt attattaaaa acaaccaact 240  
 caccatgctt cagggtagag attcttttgt ctattgcta atg gag gat gtt aga 294  
 Met Glu Asp Val Arg  
 1 5  
 gag aag gtc atg gct gta cct att atg ctg ttc tat ttc agc cta ctc 342  
 Glu Lys Val Met Ala Val Pro Ile Met Leu Phe Tyr Phe Ser Leu Leu  
 10 15 20  
 tat aat tct ctg ctt ttt ttg aat cct att ctt ttg ctg agt acc acc 390  
 Tyr Asn Ser Leu Leu Phe Leu Asn Pro Ile Leu Leu Ser Thr Thr  
 25 30 35  
 cac cta ctt ctg gga gac aag gct gtg tga a agacatcctc agacgtctca 441  
 His Leu Leu Leu Gly Asp Lys Ala Val \*  
 40 45  
 tctgctttct catccatctg cacctggatg ctggg 476

<210> 78  
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 <212> DNA  
 <213> Homo sapiens

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 <222> (370)..(672)

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 tttctagacg tgtgtgtgtg tatgtgtacg catgtgtgtg tatgcacaag tagttttggg 180  
 ttctcttttc ttggtggtgt acagaagggt agtcaaagcc cgactcatga tccctaactc 240  
 gagtctttta atgggattgt gtcctaactg caaaaccgc ctcaccaact ttgttataaa 300  
 ctccccgggt ttatagggtac agtcatctac tgtcccttcc taacagcatg gtgcagaaac 360  
 actccataa atg agt ctt gtg ttg aat cag att gaa tta agt gag aaa 408  
                   Met Ser Leu Val Leu Asn Gln Ile Glu Leu Ser Glu Lys  
                   1                  5                  10  
 gga atg gcg gtg aaa aat gtg gct tta gtc atc aca tgg gcc tac ggg 456  
 Gly Met Ala Val Lys Asn Val Ala Leu Val Ile Thr Trp Ala Tyr Gly  
                   15                  20                  25  
 ttt gtg aaa gta aca ttg agt ctc ctt gtg ttc tgt gtg tac tgc atg 504  
 Phe Val Lys Val Thr Leu Ser Leu Leu Val Phe Cys Val Tyr Cys Met  
                   30                  35                  40                  45  
 tat gtc atc ttg cat cta agg atg tat att acc cat aaa gga gca tgc 552  
 Tyr Val Ile Leu His Leu Arg Met Tyr Ile Thr His Lys Gly Ala Cys  
                   50                  55                  60  
 aga cac atg agt gca tct tgg ctt gcc act aac tgc ctg tgg cct tgg 600  
 Arg His Met Ser Ala Ser Trp Leu Ala Thr Asn Cys Leu Trp Pro Trp  
                   65                  70                  75  
 ggc tgt cac tca act ttt cat ctg gaa att gag aat aat aat act att 648  
 Gly Cys His Ser Thr Phe His Leu Glu Ile Glu Asn Asn Asn Thr Ile  
                   80                  85                  90  
 atc ctt ctg gaa ttg tgt gca taa atgcacaggg cctgggtcat aaaaagtact 702  
 Ile Leu Leu Glu Leu Cys Ala \*  
                   95                  100  
 cagtgagggc caggcgcggt ggcgcacgcc tgtaatccca gcactttggg aggccgaggg 762  
 gtgcagatta cgaggtcaag agatcgagac catcctggct aacacggtga aaccctgtct 822  
 ctactaaaaa tac 835

<210> 79  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (282)..(1193)

<400> 79

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tgcaggagcc tgagttacgg ggagatgttc ttcacgggtgg aaacggcact tacctgacct	180
ggttgttggt gcatgtgccc ccgcaggaca cagcccccta ctcctgccac gtgcagcaca	240
gcagcctggc ccagcccctc gtggtgcccg gggaggccag g atg tgt ggc agg	293
Met Cys Gly Arg	
1	
ttc ctg cgg cgg ctg ctg gcg gag gag agc cgg cgc tcc acc ccc gtg	341
Phe Leu Arg Arg Leu Leu Ala Glu Glu Ser Arg Arg Ser Thr Pro Val	
5 10 15 20	
ggg cgc ctc ttg ctt ccc gtg ctc ctg gga ttc cgc ctt gtg ctg ctg	389
Gly Arg Leu Leu Leu Pro Val Leu Leu Gly Phe Arg Leu Val Leu Leu	
25 30 35	
gct gcc agt ggg cct gga gtc tat ggt gat gag cag agt gaa ttc gtg	437
Ala Ala Ser Gly Pro Gly Val Tyr Gly Asp Glu Gln Ser Glu Phe Val	
40 45 50	
tgt cac acc cag cag ccg ggc tgc aag gct gcc tgc ttc gat gcc ttc	485
Cys His Thr Gln Gln Pro Gly Cys Lys Ala Ala Cys Phe Asp Ala Phe	
55 60 65	
cac ccc ctc tcc ccg ctg cgt ttc tgg gtc ttc cag gtc atc ttg gtg	533
His Pro Leu Ser Pro Leu Arg Phe Trp Val Phe Gln Val Ile Leu Val	
70 75 80	
gct gta ccc agc gcc ctc tat atg ggt ttc act ctg tat cac gtg atc	581
Ala Val Pro Ser Ala Leu Tyr Met Gly Phe Thr Leu Tyr His Val Ile	
85 90 95 100	
tgg cac tgg gaa tta tca gga aag ggg aag gag gag gag acc ctg atc	629
Trp His Trp Glu Leu Ser Gly Lys Gly Lys Glu Glu Glu Thr Leu Ile	
105 110 115	
cag gga cgg gag ggc aac aca gat gtc cca ggg gct gga agc ctc agg	677
Gln Gly Arg Glu Gly Asn Thr Asp Val Pro Gly Ala Gly Ser Leu Arg	
120 125 130	
ctg ctc tgg gct tat gtg gct cag ctg ggg gct cgg ctt gtc ctg gag	725
Leu Leu Trp Ala Tyr Val Ala Gln Leu Gly Ala Arg Leu Val Leu Glu	
135 140 145	
ggg gca gcc ctg ggg ttg cag tac cac ctg tat ggg ttc cag atg ccc	773
Gly Ala Ala Leu Gly Leu Gln Tyr His Leu Tyr Gly Phe Gln Met Pro	
150 155 160	
agc tcc ttt gca tgt cgc cga gaa cct tgc ctt ggt agt ata acc tgc	821
Ser Ser Phe Ala Cys Arg Arg Glu Pro Cys Leu Gly Ser Ile Thr Cys	
165 170 175 180	
aat ctg tcc cgc ccc tct gag aag acc att ttc cta aag acc atg ttt	869
Asn Leu Ser Arg Pro Ser Glu Lys Thr Ile Phe Leu Lys Thr Met Phe	
185 190 195	
gga gtc agc ggt ttc tgt ctc ttg ttt act ttt ttg gag ctt gtg ctt	917
Gly Val Ser Gly Phe Cys Leu Leu Phe Thr Phe Leu Glu Leu Val Leu	
200 205 210	

ctg ggt ttg ggg aga tgg tgg agg acc tgg aag cac aaa tct tcc tct 965  
 Leu Gly Leu Gly Arg Trp Trp Arg Thr Trp Lys His Lys Ser Ser Ser  
           215                                  220                                  225

tct aaa tac ttc cta act tca gag agc acc aga aga cac aag aaa gca 1013  
 Ser Lys Tyr Phe Leu Thr Ser Glu Ser Thr Arg Arg His Lys Lys Ala  
           230                                  235                                  240

acc gat agc ctc cca gtg gtg gaa acc aaa gag caa ttt caa gaa gca 1061  
 Thr Asp Ser Leu Pro Val Val Glu Thr Lys Glu Gln Phe Gln Glu Ala  
           245                                  250                                  255                                  260

gat ggg aaa ttg cct gtc ccc aac aaa tca ggc tgt ttg cag atg agt 1109  
 Asp Gly Lys Leu Pro Val Pro Asn Lys Ser Gly Cys Leu Gln Met Ser  
                                   265                                  270                                  275

ctt cct ttg caa ctt cgt aac ttc ttc cta gcc tct gat tgg ttg ctt 1157  
 Leu Pro Leu Gln Leu Arg Asn Phe Phe Leu Ala Ser Asp Trp Leu Leu  
                                   280                                  285                                  290

tct gca aag cat gaa ctg gcc aaa ggg aaa ctt cta 1193  
 Ser Ala Lys His Glu Leu Ala Lys Gly Lys Leu Leu  
           295                                  300

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 <212> DNA  
 <213> Homo sapiens

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 <222> (247)..(1413)

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 aaaaaaagag atctctcgag gatecgaatt cgcgcccgcg tcgacgccag gtgttgagg 120  
 cctttgctac gcggtccgag gctttcattg cacaccgcg ctaatgccgc cgccacggct 180  
 acagaaacga cctgccaaga cgtcgcgcg acccccgctc cgcggtaccc gccgattgtg 240  
 gcctcc atg aca gcc gac agc aaa gct gca cgg ctg cgg cgg atc gag 288  
           Met Thr Ala Asp Ser Lys Ala Ala Arg Leu Arg Arg Ile Glu  
                   1                                  5                                  10

cgc tgg cag gcg acg gtg cac gct gcg gag tcg gta gac gag aag ctg 336  
 Arg Trp Gln Ala Thr Val His Ala Ala Glu Ser Val Asp Glu Lys Leu  
           15                                  20                                  25                                  30

cga atc ctc acc aag atg cag ttt atg aag tac atg gtt tac ccg cag 384  
 Arg Ile Leu Thr Lys Met Gln Phe Met Lys Tyr Met Val Tyr Pro Gln  
                                   35                                  40                                  45

acc ttc gcg ctg aat gcc gac cgc tgg tac cag tac ttc acc aag acc 432  
 Thr Phe Ala Leu Asn Ala Asp Arg Trp Tyr Gln Tyr Phe Thr Lys Thr  
                   50                                  55                                  60

gtg ttc ctg tcg ggt ctg ccg ccg ccc cca gcg gag ccc gag ccc gag 480  
 Val Phe Leu Ser Gly Leu Pro Pro Pro Pro Ala Glu Pro Glu Pro Glu

65	70	75	
ccc gaa ccc gaa cct gaa cct gcg ctg gac ctc gcg gcg ctg cgt gcg Pro Glu Pro Glu Pro Glu Pro Ala Leu Asp Leu Ala Ala Leu Arg Ala 80 85 90			528
gtc gcc tgc gac tgc ctg ctg cag gag cac ttc tac ctg cgg cgc agg Val Ala Cys Asp Cys Leu Leu Gln Glu His Phe Tyr Leu Arg Arg Arg 95 100 105 110			576
cgg cgc gtg cac cgt tac gag gag agc gag gtc ata tct ttg ccc ttc Arg Arg Val His Arg Tyr Glu Glu Ser Glu Val Ile Ser Leu Pro Phe 115 120 125			624
ctg gat cag ctg gtg tca acc ctc gtg ggc ctc ctc agc cca cac aac Leu Asp Gln Leu Val Ser Thr Leu Val Gly Leu Leu Ser Pro His Asn 130 135 140			672
ccg gcc ctg gcc gct gcc gcc ctc gat tat aga tgc cca gtt cat ttt Pro Ala Leu Ala Ala Ala Ala Leu Asp Tyr Arg Cys Pro Val His Phe 145 150 155			720
tac tgg gtg cgt ggt gaa gaa att att cct cgt ggt cat cga aga ggt Tyr Trp Val Arg Gly Glu Glu Ile Ile Pro Arg Gly His Arg Arg Gly 160 165 170			768
cga att gat gac ttg cga tac cag ata gat gat aaa cca aac aac cag Arg Ile Asp Asp Leu Arg Tyr Gln Ile Asp Asp Lys Pro Asn Asn Gln 175 180 185 190			816
att cga ata tcc aag caa ctc gca gag ttt gtg cca ttg gat tat tct Ile Arg Ile Ser Lys Gln Leu Ala Glu Phe Val Pro Leu Asp Tyr Ser 195 200 205			864
gtt cct ata gaa atc ccc act ata aaa tgt aaa cca gac aaa ctt cca Val Pro Ile Glu Ile Pro Thr Ile Lys Cys Lys Pro Asp Lys Leu Pro 210 215 220			912
tta ttc aaa cgg cag tat gaa aac cac ata ttt gtt ggc tca aaa act Leu Phe Lys Arg Gln Tyr Glu Asn His Ile Phe Val Gly Ser Lys Thr 225 230 235			960
gca gat cct tgc tgt tac ggt cac acc cag ttt cat ctg tta cct gac Ala Asp Pro Cys Cys Tyr Gly His Thr Gln Phe His Leu Leu Pro Asp 240 245 250			1008
aaa tta aga agg gaa agg ctt ttg aga caa aac tgt gct gat cag ata Lys Leu Arg Arg Glu Arg Leu Leu Arg Gln Asn Cys Ala Asp Gln Ile 255 260 265 270			1056
gaa gtt gtt ttt aga gct aat gct att gca agc ctt ttt gct tgg act Glu Val Val Phe Arg Ala Asn Ala Ile Ala Ser Leu Phe Ala Trp Thr 275 280 285			1104
gga gca caa gct atg tat caa gga ttc tgg agt gaa gca gat gtt act Gly Ala Gln Ala Met Tyr Gln Gly Phe Trp Ser Glu Ala Asp Val Thr 290 295 300			1152
cga cct ttt gtc tcc cag gct gtg atc aca gat gga aaa tac ttt tcc Arg Pro Phe Val Ser Gln Ala Val Ile Thr Asp Gly Lys Tyr Phe Ser 305 310 315			1200
ttt ttc tgc tac cag cta aat act ttg gca ctg act aca caa gct gat Phe Phe Cys Tyr Gln Leu Asn Thr Leu Ala Leu Thr Thr Gln Ala Asp			1248

320	325	330	
caa aat aac cct cgt aaa aat ata tgt tgg ggt aca caa agt aag cct			1296
Gln Asn Asn Pro Arg Lys Asn Ile Cys Trp Gly Thr Gln Ser Lys Pro			
335	340	345	350
ctt tat gaa aca att gag gat aat gat gtg aaa ggt ttt aat gat gat			1344
Leu Tyr Glu Thr Ile Glu Asp Asn Asp Val Lys Gly Phe Asn Asp Asp			
355	360	365	
ggt cta ctt cag ata gtt cac ttt cta ctg aat aga cca aaa gaa gaa			1392
Val Leu Leu Gln Ile Val His Phe Leu Leu Asn Arg Pro Lys Glu Glu			
370	375	380	
aaa tca cag ctg ttg gaa aac tg aaaaagcata tttgattgag aactgtggga			1445
Lys Ser Gln Leu Leu Glu Asn			
385			
atattttaa at tttactgaag gaacaataat gatgagattt gtaactgtca actattaaat			1505
acattgattt ttgagacaaa tatttcttat gtcaacctgt tattagatct cttactctgc			1565
tcaaatccat cactgaaaga tttaatttta gttacctttt gttgatttaa aaataattgc			1625
atttgatat tgctaactga taagacaaat tgagttattg agctattaaa tgcacatttt			1685
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gtgtcacgga gcgaatagtc gattgaaact gatgcgttga gtaggtcggc caaggaagta	180
gagactaaag ttaggggtggg ggagatgaag tgcataatg ataatagctt ttggtattta	240
aaggccccgt taagaaaagt aaaatccaaa cgctgggctg ggagaaaaat ctgtgtaatc	300
ccatatatat aaatggatgg gtatttgaaa tatataatac actctcaaag ttttcaataa	360
taagaaaaca ggcacgcaat aaccaggaag atatatggat ggcaaataag cccatgaaaa	420
tattcttaac attattaatt ataagtgaac tgcaatttaa aactgatgag atattatccc	480
tgatctataa aaagagcaaa aatttaaata tgtgaccata ccaactatta atgaggatgt	540
agagtaactg aacttcttca tgcattggtg ttgagaatgt gaaaaaaaaa aacaactttg	600
gaaaataatg tggcagtttt ctaaaaagtt aaatataaac ctaccataag atccaattat	660
tctactcctt ggtgttagta ccaataaaaa tgaaagtatg tgcctacata cagactcata	720



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cacaaatgtg ttcagaagtt ttacttgtga tagcaaaaat taaaaacaag tcgacttttc      780
atcaacagat aaatatgaaa acacattatg atatatgcat acaataaatt ccactctaca      840
ataaaaaaat aatacatttg gtacattcca ctacacga      atg agt ctc aaa aga      893
                                         Met Ser Leu Lys Arg
                                         1              5

att att ctg aga aaa gat tta aga ttt aaa aaa agt atc aca ctg cat      941
Ile Ile Leu Arg Lys Asp Leu Arg Phe Lys Lys Ser Ile Thr Leu His
              10              15              20

gaa caa ttt cat gta ttt aaa ttc tac aaa aag aca caa acc agt agc      989
Glu Gln Phe His Val Phe Lys Phe Tyr Lys Lys Thr Gln Thr Ser Ser
              25              30              35

gtg att gtt gag ggg agg aga aga ggg agg tat tac aaa ggg aca tgt      1037
Val Ile Val Glu Gly Arg Arg Arg Gly Arg Tyr Tyr Lys Gly Thr Cys
              40              45              50

gaa aac ttt ttg gag tgatgcatat atatataatg tatattattat ggtgattatg      1092
Glu Asn Phe Leu Glu
              55

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<210> 82  
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 <212> DNA  
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<220>  
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<220>  
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 <222> (1)...(659)  
 <223> n = a,t,c or g

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aagattgata ctcaaactgg gttttacaaa tgtagcaggt aagaggtagt gactgtcaa      119
atg ttc aaa gtt gtg ttt tgt ttt ggt ttg gtt tgg ttt tgc ttt caa      167
Met Phe Lys Val Val Phe Cys Phe Gly Leu Val Trp Phe Cys Phe Gln
  1              5              10              15

agg gca cac aaa cca atc cga ttt gaa aaa cac aac ttt aca ata aat      215
Arg Ala His Lys Pro Ile Arg Phe Glu Lys His Asn Phe Thr Ile Asn
              20              25              30

gaa gga aac ctg ttc tct atg aat atc cca att gta acg att agg tct      263
Glu Gly Asn Leu Phe Ser Met Asn Ile Pro Ile Val Thr Ile Arg Ser
              35              40              45

cac cac agg aca agt tgc tac cac aaa tta atc aca tgt gaa cag caa      311
His His Arg Thr Ser Cys Tyr His Lys Leu Ile Thr Cys Glu Gln Gln
              50              55              60

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act gtc ttt acg aac ata aag agg cat tct aag ttg tag cagacgcctg 360  
 Thr Val Phe Thr Asn Ile Lys Arg His Ser Lys Leu \*  
 65 70 75

ctctacgaga cattaatgga gtaaaatcct ggagtattac agataaacag ttaaagtgat 420  
 gaacaagggc tttatggttt gtataaacag aaatataaac aattttgtat ttttctcaat 480  
 tatatgtaat taaataacgt ttcagggtaa caaagtattg ggtccctttt tttaccagct 540  
 tattctaaag aggctttgaa taaaggaaat tttgtttctt gcctccaaga aagagccccc 600  
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 <211> 653  
 <212> DNA  
 <213> Homo sapiens

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 <222> (147)..(308)

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 acatcttctc aattccccag atcttggttt agttgtagag gcccaaagta gagctctcta 120  
 aacaaaggct tcctcagtcg tgtaaa atg aat ttg tat ctc ttt gct gtt ctc 173  
 Met Asn Leu Tyr Leu Phe Ala Val Leu  
 1 5

ttc ttt tat gta ttt cta cat ata aaa atc atc ttt att tgt ttt gct 221  
 Phe Phe Tyr Val Phe Leu His Ile Lys Ile Ile Phe Ile Cys Phe Ala  
 10 15 20 25

act aaa tgg cat aat tta ttt tgc aaa ttc agt tat ttt tgt att ttg 269  
 Thr Lys Trp His Asn Leu Phe Ser Lys Phe Ser Tyr Phe Cys Ile Leu  
 30 35 40

cat gtt aag gct cta agc ctt aac tta ggg tct ggg taa atatgaactc 318  
 His Val Lys Ala Leu Ser Leu Asn Leu Gly Ser Gly \*  
 45 50

caagactcct cgaaaatagt gtagaaataa tagcaaaatt aaagatgttt gtattccctg 378  
 tgaatttatt ttttctttca ttcaacacag aatgtgtatc tagtacgtgc taggcattat 438  
 aaatttagca gtgaacaaag atgataaaat ctcagctctc ctggagccaa cgttctagtg 498  
 aaaaatttct ctttcttcta ctttttctgt tgacattcat atgggctaac aatgtacccc 558  
 gagggctggg gattataaag gagaagaaag gtgggggacc cggctcagct ggtaaaatgg 618  
 gaatggaatg acccccttaa cccagaaacc ttctt 653

<210> 84  
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<212> DNA  
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<220>  
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<222> (166) .. (357)

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tccttgctgc agataactgc agtaaaccat gtcttttagct tcatt      atg aag att      174
                                          Met Lys Ile
                                          1

gct tct ttc ttg ctg cag aat aac ggt atg tat tct ctc tca ctg cag      222
Ala Ser Phe Leu Leu Gln Asn Asn Gly Met Tyr Ser Leu Ser Leu Gln
      5              10              15

ctc cca gtg ctc tgt gtc tta aaa tca ttt aaa gcc tat agc ttg ctt      270
Leu Pro Val Leu Cys Val Leu Lys Ser Phe Lys Ala Tyr Ser Leu Leu
      20              25              30              35

tgg gga gtt agt aca ggg gtt aag gaa ggc ttt gcc gga aga aca att      318
Trp Gly Val Ser Thr Gly Val Lys Glu Gly Phe Ala Gly Arg Thr Ile
              40              45              50

gta aat cat gag agt tac tac ttg cgc att gtg tgg tag tctctttaat      367
Val Asn His Glu Ser Tyr Tyr Leu Arg Ile Val Trp *
              55              60

gcataatggt cctttttaat accaaaaatt aattaataaa ggaaatgatt acattgtcca      427
aataactggt aaacatgaca gatctgtttt atgatactgt gtttgacagt taaacattaa      487
gtaaacatgt aattgacttt aagcttgaaa tgttcagaat gctctaacct ttgctacaga      547
atcttttctg cagcaagtta agtattttgt gtgttttttc ccacctgtag cttatcaggc      607
ccggtccaaa gccttctagc agaggggatt gatcctgtca ggggttgctg ccaagacatc      667
ggaaggatgt ttgaccaagg ttttcaaaag ctcaagtgtca catctgccat ttgataaaag      727
aaagattttg gatgcagaac ctggcattta ttggcctttg cggcgctggg atggctcggg      787
tgccctccgg cactctacaa aatgagcccg gtcacactt aattttaaat gggggggcgg      847
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caaccccc                                          915

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<210> 85  
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<212> DNA  
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<221> CDS  
<222> (157) .. (345)

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<211> 1828
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (633)..(1553)
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126

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tgctgctctt caggcaggac ccagatgtgt ccaggcttac ccagacctat gtcacgatct 600  
tcattccagc tcttctgca acctttcttt at atg tta caa gtt aaa tat ttg 653  
Met Leu Gln Val Lys Tyr Leu  
1 5

ctc aac cag gga att gta ctg ccc cag atc gta act gga gtt gca gcc 701  
Leu Asn Gln Gly Ile Val Leu Pro Gln Ile Val Thr Gly Val Ala Ala  
10 15 20

aac ctt gtc aat gcc ctc gcc aac tat ctg ttt ctc cat caa ctg cat 749  
Asn Leu Val Asn Ala Leu Ala Asn Tyr Leu Phe Leu His Gln Leu His  
25 30 35

ctt ggg gtg ata ggc tct gca ctg gca aac ttg att tcc cag tac acc 797  
Leu Gly Val Ile Gly Ser Ala Leu Ala Asn Leu Ile Ser Gln Tyr Thr  
40 45 50 55

ctg gct cta ctc ctc ttt ctc tac atc ctc ggg aaa aaa ctg cat caa 845  
Leu Ala Leu Leu Leu Phe Leu Tyr Ile Leu Gly Lys Lys Leu His Gln  
60 65 70

gct aca tgg gga ggc tgg tcc ctc gag tgc ctg cag gac tgt gcc tcc 893  
Ala Thr Trp Gly Gly Trp Ser Leu Glu Cys Leu Gln Asp Cys Ala Ser  
75 80 85

ttc ctc cgc ctg gcc atc ccc agc atg ctc atg ctg tgc atg gag tgg 941  
Phe Leu Arg Leu Ala Ile Pro Ser Met Leu Met Leu Cys Met Glu Trp  
90 95 100

tgg gcc tat gag gtc ggg agc ttc ctc agt ggc atc ctc ggc atg gtg 989  
Trp Ala Tyr Glu Val Gly Ser Phe Leu Ser Gly Ile Leu Gly Met Val  
105 110 115

gag ctg ggc gct cag tcc atc gtg tat gaa ctg gcc atc att gtg tac 1037  
Glu Leu Gly Ala Gln Ser Ile Val Tyr Glu Leu Ala Ile Ile Val Tyr  
120 125 130 135

atg gtc cct gca ggc ttc agt gtg gct gcc agt gtc cgg gta gga aac 1085  
Met Val Pro Ala Gly Phe Ser Val Ala Ala Ser Val Arg Val Gly Asn  
140 145 150

gct ctg ggt gct gga gac atg gag cag gca cgg aag tcc tct acc gtt 1133  
Ala Leu Gly Ala Gly Asp Met Glu Gln Ala Arg Lys Ser Ser Thr Val  
155 160 165

tcc ctg ctg att aca gtg ctc ttt gct gta gcc ttc agt gtc cta ctg 1181  
Ser Leu Leu Ile Thr Val Leu Phe Ala Val Ala Phe Ser Val Leu Leu  
170 175 180

tta agc tgt aag gat cac gtg ggg tac att ttt act acc gac cga gac 1229  
Leu Ser Cys Lys Asp His Val Gly Tyr Ile Phe Thr Thr Asp Arg Asp  
185 190 195

atc att aat ctg gtg gct cag gtg gtt cca att tat gct gtt tcc cac 1277  
Ile Ile Asn Leu Val Ala Gln Val Val Pro Ile Tyr Ala Val Ser His  
200 205 210 215

ctc ttt gaa gct ctt gct tgc acg agt ggt ggt gtt ctg agg ggg agt 1325  
Leu Phe Glu Ala Leu Ala Cys Thr Ser Gly Gly Val Leu Arg Gly Ser

220	225	230	
gga aat cag aag gtt gga gcc att	gtg aat acc att ggg tac tat gtg	1373	
Gly Asn Gln Lys Val Gly Ala Ile	Val Asn Thr Ile Gly Tyr Tyr Val		
235	240	245	
gct ggc ctc ccc atc ggg atc gcg ctg atg ttt gca acc aca ctt gga	1421		
Ala Gly Leu Pro Ile Gly Ile Ala Leu Met Phe Ala Thr Thr Leu Gly			
250	255	260	
gtg atg ggt ctg tgg tca ggg atc atc atc tgt aca gtc ttt caa gct	1469		
Val Met Gly Leu Trp Ser Gly Ile Ile Ile Cys Thr Val Phe Gln Ala			
265	270	275	
gtg tgt ttt cta ggc ttt att att cag cta aat tgg aaa aaa gcc tgt	1517		
Val Cys Phe Leu Gly Phe Ile Ile Gln Leu Asn Trp Lys Lys Ala Cys			
280	285	290	
295			
cag cag ggt gcc ctg aaa acc ttg aag gaa ttt taa cgaa cgatgttgga	1567		
Gln Gln Gly Ala Leu Lys Thr Leu Lys Glu Phe *			
300	305		
aagacaggcg agcctcagtc agatcagcag atgcgccaag aagaaccttt gccggaacat	1627		
ccacaggacg gcgctaaatt gtccaggaaa cagctggtgc tgcggcgagg gcttctgctc	1687		
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ggccgaatta cgccactctt t	1828		
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ttaacagctg ttaaataatct cagactcacc ccagcctgaa gctaggtttc tgacaataac	180		
atg cat tta act cta agt tta ctt ctg ttc tcc cta cac ttc ccc acg	228		
Met His Leu Thr Leu Ser Leu Leu Leu Phe Ser Leu His Phe Pro Thr			
1 5 10 15			
tat att att cga gtt aat ttt tgt ctt gtt tcc aat tta ttt caa agg	276		
Tyr Ile Ile Arg Val Asn Phe Cys Leu Val Ser Asn Leu Phe Gln Arg			
20 25 30			

atg cga agt aca aaa ctg ctt cgg ctc att gac tta gat ttt tca ttt 324  
 Met Arg Ser Thr Lys Leu Leu Arg Leu Ile Asp Leu Asp Phe Ser Phe  
                   35                  40                  45  
 act ttc tct ctc ttg gat cta cca cca gta aat gaa tat gac atg tat 372  
 Thr Phe Ser Leu Leu Asp Leu Pro Pro Val Asn Glu Tyr Asp Met Tyr  
                   50                  55                  60  
 atc aga aac ttt gga aaa aaa aaa aaa agg ggg ggc cgt ttt aaa gga 420  
 Ile Arg Asn Phe Gly Lys Lys Lys Lys Arg Gly Gly Arg Phe Lys Gly  
                   65                  70                  75                  80  
 tcc agg ttt acg aac gcg ggc tgg caa cgt aaa agt ttt ttt atg ggg 468  
 Ser Arg Phe Thr Asn Ala Gly Trp Gln Arg Lys Ser Phe Phe Met Gly  
                   85                  90                  95  
 ccc cct aaa tcc att cca ggg gcc ggg gtt taa caacgggg ggacgggaaa 519  
 Pro Pro Lys Ser Ile Pro Gly Ala Gly Val \*  
                   100                  105  
 aaanannnnc nntncccccc cccccaccc anaaanccca cncctttttta agccccgcac 579  
 ttttccactc cccccacttt ttaaaaccta atttaaaaaa actcntattc cctcatatcc 639  
 acttataaac acaaataaaa tctttatnca cccacccta atatactctt tacccaaaac 699  
 cccccctttt ttttatcacc caaacttata tccccctttt atcctctcac cncctccact 759  
 ncaaaaatca ttacatttnc cccnaccnacc aaaatccacc tctccccctcc ccaatnnncc 819  
 cactacactn caccctcca ccttccattc ttaacacacc ntctctcccc tctcaaacc 879  
 cccccactct catctcaact aatctacct tctccccact tacacataat ccactttcct 939  
 tactaaattc cccccaattc ttacacact acctcccttc accaaaatca tctcttcccc 999  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (140)..(1363)

<400> 88  
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 cctcctgctg ccaggcacc atg aca gtg agg ggg gat gtg ctg gcc ccg gat 172  
                   Met Thr Val Arg Gly Asp Val Leu Ala Pro Asp  
                   1                  5                  10  
 cca gcg tcg ccc acg acc gca gca gcc tcg ccc agc gtc tcc gtg atc 220  
 Pro Ala Ser Pro Thr Thr Ala Ala Ala Ser Pro Ser Val Ser Val Ile  
                   15                  20                  25  
 ccc gag ggc agc ccc act gcc atg gag cag cct gtg ttc ctg atg aca 268

Pro	Glu	Gly	Ser	Pro	Thr	Ala	Met	Glu	Gln	Pro	Val	Phe	Leu	Met	Thr		
		30					35					40					
act	gcc	gct	cag	gcc	atc	tct	ggc	ttc	ttc	gtg	tgg	acg	gcc	ctg	ctc	316	
Thr	Ala	Ala	Gln	Ala	Ile	Ser	Gly	Phe	Phe	Val	Trp	Thr	Ala	Leu	Leu		
	45				50					55							
atc	aca	tgc	cac	cag	atc	tac	atg	cac	ctg	cgc	tgc	tac	agc	tgc	ccc	364	
Ile	Thr	Cys	His	Gln	Ile	Tyr	Met	His	Leu	Arg	Cys	Tyr	Ser	Cys	Pro		
	60				65				70						75		
aac	gag	cag	cgc	tac	atc	gtg	cgc	atc	ctc	ttc	atc	gtg	ccc	atc	tac	412	
Asn	Glu	Gln	Arg	Tyr	Ile	Val	Arg	Ile	Leu	Phe	Ile	Val	Pro	Ile	Tyr		
			80					85						90			
gcc	ttt	gac	tcc	tgg	ctc	agc	ctc	ctc	ttc	ttc	acc	aac	gac	cag	tac	460	
Ala	Phe	Asp	Ser	Trp	Leu	Ser	Leu	Phe	Phe	Thr	Asn	Asp	Gln	Tyr			
			95				100						105				
tac	gtg	tac	ttc	ggc	acc	gtc	cgc	gac	tgc	tat	gag	gcc	ttg	gtc	atc	508	
Tyr	Val	Tyr	Phe	Gly	Thr	Val	Arg	Asp	Cys	Tyr	Glu	Ala	Leu	Val	Ile		
	110					115						120					
tat	aat	ttc	ctg	agc	ctg	tgc	tat	gag	tac	cta	gga	gga	gaa	agt	tcc	556	
Tyr	Asn	Phe	Leu	Ser	Leu	Cys	Tyr	Glu	Tyr	Leu	Gly	Gly	Glu	Ser	Ser		
	125				130						135						
atc	atg	tcg	gag	atc	aga	gga	aaa	ccc	att	gag	tcc	agc	tgt	atg	tat	604	
Ile	Met	Ser	Glu	Ile	Arg	Gly	Lys	Pro	Ile	Glu	Ser	Ser	Cys	Met	Tyr		
	140				145				150						155		
ggc	acc	tgc	tgc	ctc	tgg	gga	aag	act	tat	tcc	atc	gga	ttt	ctg	agg	652	
Gly	Thr	Cys	Cys	Leu	Trp	Gly	Lys	Thr	Tyr	Ser	Ile	Gly	Phe	Leu	Arg		
				160					165					170			
ttc	tgc	aaa	cag	gcc	acc	ctg	cag	ttc	tgt	gtg	gtg	aag	cca	ctc	atg	700	
Phe	Cys	Lys	Gln	Ala	Thr	Leu	Gln	Phe	Cys	Val	Val	Lys	Pro	Leu	Met		
			175					180					185				
gcg	gtc	agc	act	gtg	gtc	ctc	cag	gcc	ttc	ggc	aag	tac	cgg	gat	ggg	748	
Ala	Val	Ser	Thr	Val	Val	Leu	Gln	Ala	Phe	Gly	Lys	Tyr	Arg	Asp	Gly		
		190					195					200					
gac	ttt	gac	gtc	acc	agt	ggc	tac	ctc	tac	gtg	acc	atc	atc	tac	aac	796	
Asp	Phe	Asp	Val	Thr	Ser	Gly	Tyr	Leu	Tyr	Val	Thr	Ile	Ile	Tyr	Asn		
	205					210					215						
atc	tcc	gtc	agc	ctg	gcc	ctc	tac	gcc	ctc	ttc	ctc	ttc	tac	ttc	gcc	844	
Ile	Ser	Val	Ser	Leu	Ala	Leu	Tyr	Ala	Leu	Phe	Leu	Phe	Tyr	Phe	Ala		
	220				225					230					235		
acc	cgg	gag	ctg	ctc	agc	ccc	tac	agc	ccc	gtc	ctc	aag	ttc	ttc	atg	892	
Thr	Arg	Glu	Leu	Leu	Ser	Pro	Tyr	Ser	Pro	Val	Leu	Lys	Phe	Phe	Met		
				240					245					250			
gtc	aag	tcc	gtc	atc	ttt	ctt	tcc	ttc	tgg	caa	ggc	atg	ctc	ctg	gcc	940	
Val	Lys	Ser	Val	Ile	Phe	Leu	Ser	Phe	Trp	Gln	Gly	Met	Leu	Leu	Ala		
			255					260					265				
atc	ctg	gag	aag	tgt	ggg	gcc	atc	ccc	aaa	atc	cac	tcg	gcc	cgc	gtg	988	
Ile	Leu	Glu	Lys	Cys	Gly	Ala	Ile	Pro	Lys	Ile	His	Ser	Ala	Arg	Val		
		270					275						280				
tcg	gtg	ggc	gag	ggc	acc	gtg	gct	gcc	ggc	tac	cag	gac	ttc	atc	atc	1036	



Ser	Val	Gly	Glu	Gly	Thr	Val	Ala	Ala	Gly	Tyr	Gln	Asp	Phe	Ile	Ile	
285						290					295					
tgt	gtg	gag	atg	ttc	ttt	gca	gcc	ctg	gcc	ctg	cgg	cac	gcc	ttc	acc	1084
Cys	Val	Glu	Met	Phe	Phe	Ala	Ala	Leu	Ala	Leu	Arg	His	Ala	Phe	Thr	
300					305					310					315	
tac	aag	gtc	tat	gct	gac	aag	agg	ctg	gac	gca	caa	ggc	cgc	tgt	gcc	1132
Tyr	Lys	Val	Tyr	Ala	Asp	Lys	Arg	Leu	Asp	Ala	Gln	Gly	Arg	Cys	Ala	
				320					325						330	
ccc	atg	aag	agc	atc	tcc	agc	agc	ctc	aag	gag	acc	atg	aac	ccg	cac	1180
Pro	Met	Lys	Ser	Ile	Ser	Ser	Ser	Leu	Lys	Glu	Thr	Met	Asn	Pro	His	
			335					340					345			
gac	atc	gtg	cag	gac	gcc	atc	cac	aac	ttc	tca	cct	gcc	tac	cag	cag	1228
Asp	Ile	Val	Gln	Asp	Ala	Ile	His	Asn	Phe	Ser	Pro	Ala	Tyr	Gln	Gln	
		350					355					360				
tac	acg	cag	cag	tcc	acc	ctg	gag	cct	ggg	ccc	acc	tgg	cgt	ggg	ggc	1276
Tyr	Thr	Gln	Gln	Ser	Thr	Leu	Glu	Pro	Gly	Pro	Thr	Trp	Arg	Gly	Gly	
	365					370					375					
gcc	cac	ggc	ctc	tcc	cgc	tcc	cac	agc	ctc	agt	ggc	gcc	cgc	gac	aac	1324
Ala	His	Gly	Leu	Ser	Arg	Ser	His	Ser	Leu	Ser	Gly	Ala	Arg	Asp	Asn	
380					385					390					395	
gag	aag	act	ctc	ctg	ctc	agc	tct	gat	gat	gaa	ttc	tag	gtgcgggctg			1373
Glu	Lys	Thr	Leu	Leu	Leu	Ser	Ser	Asp	Asp	Glu	Phe	*				
			400						405							
cagtggcgga	agtgtgtggcg	ccatagccac	ggtcaggctg	tgccccacct	ccagcctcac											1433
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ccacacagtg	gggagctggg	aggtgggggg	aatgggtcca	gactcctctc	ggggccccta											2393

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cctgtgagga gagttggggc ccagccgtct tcttggcctc ctccctttcc tcttggcaga 2933
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tgggcccagg ctgcccggga ggggtgggtg agacacaggc tgaggaccag ccttggccct 3053
gccccgccat ctgctttcac caagctgtct ctccacgtg gcttcccttc tccctccagg 3113
ccaaagtgtc gctgattccc actcccttgg ttttcgctg cccagcgttg ctgtttgcgt 3173
ggaggggtgg ggagctcag tggcagggaa tcagcgttcc gtgggggtcgt ggggacggga 3233
acatgtgccc gaccgtcca tccccctc ctcccttaga tgcataacct accttgtctt 3293
ttttttttta aattttcttt ccaggtagag tagctctttg tacataaaga atacttgaaa 3353
aattaattgt atgatgtatg agaagacaga gtctcctagt tttgtatctt gttgtatgac 3413
tgccatgagt tccaccagaa agccactcta ttttggctc tgtgacattt taaatgcgtg 3473
acagaagtga gcaaataaag tgaggaagaa atctatatat gagataatat agattgtatt 3533
gaaatctcaa aaaaaaaa 3551

```

<210> 89  
 <211> 656  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (116) .. (307)

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<400> 89
accggtccgg aattccccgg tgcaccacg cgtccgacac attccaccct tgagattgct 60
gtaacagtga tctcaacctc tgataaggta agtttataaa cttaatgagg aaaaa atg 118
Met
1
ggg aaa aag gtc act ctt ctg ctg cag aag tgc gct tgg ctt ctc ttg 166
Gly Lys Lys Val Thr Leu Leu Leu Gln Lys Cys Ala Trp Leu Leu Leu
5 10 15

```

gtt tgc tgc cta ttc act ggc att aag tac ctg aac aaa tgt ttt atc 214  
 Val Cys Cys Leu Phe Thr Gly Ile Lys Tyr Leu Asn Lys Cys Phe Ile  
           20                          25                          30

aca gac agg gaa ctg ttg agg gat gtt cac aat gca ttg aac atc ctt 262  
 Thr Asp Arg Glu Leu Leu Arg Asp Val His Asn Ala Leu Asn Ile Leu  
           35                          40                          45

agg cat aat ttt tat gtg aac tgg gca tcc tta aat aca ttc tga ctc 310  
 Arg His Asn Phe Tyr Val Asn Trp Ala Ser Leu Asn Thr Phe \*  
           50                          55                          60

catgatcaga ttaccagaaa gtgcagggtcc cactcactat cttgattcag catctcccat 370  
 ctggccaaaag ttgaatttta cattgagttg gatggtgata aatatgctta gcaaaagtat 430  
 attcgttggt tctgaagttc tctgtgtgta taaacactgg ctgggactag ggaagtgggc 490  
 cccaaataaaa acaatagcaa taatccccc aaactggttggg gaagggcagg ctttattttt 550  
 gtgcactctt aaggggaaat gtaagttaaa ctttccaccc ccccccaaag gtttttgctt 610  
 gtttgagggg ccccaacctt tgggggcccc tcccaatgcc ttaatt 656

<210> 90  
 <211> 646  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (263)..(553)

<400> 90  
 ccggtccgga attcccgggt cgaccacgc gtccgcaact atcttatttc cttatcatgc 60  
 acaagttaaa tgtagactg aggagtaggt gagttatccc caaggaagta aaatgatgtt 120  
 aattttcttg aggtcacatg aattgtgagt agctgaatgc tactgtgaat tctgggcagc 180  
 ccgaccacag agcctgaact cttaaattatt atactgtatt aacttgacat gtttataaaa 240  
 gtaacaatta catgctacct ga atg ccc tca gta gtt ttg aac atg gtg caa 292  
                                   Met Pro Ser Val Val Leu Asn Met Val Gln  
                                   1                          5                          10

ctg ttt atc cct ata cta aaa ttc caa tta ggc tat tct gtt ttg agt 340  
 Leu Phe Ile Pro Ile Leu Lys Phe Gln Leu Gly Tyr Ser Val Leu Ser  
                           15                          20                          25

ctt tgt aat cat gtt tta gaa ttt ttg ttt cct tcc tca ttg tca ggc 388  
 Leu Cys Asn His Val Leu Glu Phe Leu Phe Pro Ser Ser Leu Ser Gly  
                           30                          35                          40

atc ttt tct tcc tcc ctt ccc ctc ctt ctt ccc ttc cct ctt tct ctt 436  
 Ile Phe Ser Ser Ser Leu Pro Leu Leu Leu Pro Phe Pro Leu Ser Leu  
                           45                          50                          55

ccc tct ctt ccc cct tct ctt ttt cct tct ctt aga gtc ttg ctc tgc 484  
 Pro Ser Leu Pro Pro Ser Leu Phe Pro Ser Leu Arg Val Leu Leu Cys  
                           60                          65                          70

```

cac cca cac tgg agt gta gcc tca aac tcc tgg gct gta gcc atc ctc      532
His Pro His Trp Ser Val Ala Ser Asn Ser Trp Ala Val Ala Ile Leu
 75                      80                      85                      90

cta cct cag cct cct gag tag ct gggactgcaa gtgtatacca ctatgcctgg      585
Leu Pro Gln Pro Pro Glu *
                      95

ctaatttaaa aaaatttaaa attttttttt ttttgga aaaacaaagcct cctttgttgc      645
c                                                                646

<210> 91
<211> 1126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (126)..(434)

<220>
<221> misc_feature
<222> (1)...(1126)
<223> n = a,t,c or g

<400> 91
acatccaaca tttgaatgta ttttgactag gtaatttttt tctcctttgt taataaaaat      60

agatttaatt ttttaaagtg catttttctt gcattctcatc aaatatactt tcatacacta      120

taaaa      atg atg ttg ggt cat atg tat cac atg tct gta att cag aaa      167
Met Met Leu Gly His Met Tyr His Met Ser Val Ile Gln Lys
 1                      5                      10

tgc aaa cct ttg gac act gac tca aca tct gga gat att ttt tct ggt      215
Cys Lys Pro Leu Asp Thr Asp Ser Thr Ser Gly Asp Ile Phe Ser Gly
 15                      20                      25                      30

tct tat ggc tgg tgt tct cct aca gct ctc tac gag cag tct tgt gaa      263
Ser Tyr Gly Trp Cys Ser Pro Thr Ala Leu Tyr Glu Gln Ser Cys Glu
 35                      40                      45

gcc cac aag cac cga ggg aac cca tcc ggg ctt tac tat att gat gca      311
Ala His Lys His Arg Gly Asn Pro Ser Gly Leu Tyr Tyr Ile Asp Ala
 50                      55                      60

gat gga agt ggc ccc ctg gga cca ttt ctt gtg tac tgc aat atg aca      359
Asp Gly Ser Gly Pro Leu Gly Pro Phe Leu Val Tyr Cys Asn Met Thr
 65                      70                      75

ggg atg ttg ata atc gtt aga tgc ata gat cag aat aga cca agg aga      407
Gly Met Leu Ile Ile Val Arg Cys Ile Asp Gln Asn Arg Pro Arg Arg
 80                      85                      90

aat tta cct agt tgg cag cat tat taa aacat gcagtttgat agtgtgtact      459
Asn Leu Pro Ser Trp Gln His Tyr *
 95                      100

tgctaagtag aagcattaaa tatgtattta ttaattttgt tgtcaacaaa attttcttgt      519

```

```

atttcttctt tgcctgggtt ggattatagg caagattcaa tgctctgcca aggcattctt 579
ctagctccta cactcctcat aatacatctg ttcattgtgca tcatgataaa atacaaacct 639
ctgattcggg gatttacatg ctttctgtat ttagaaaaaa cagagggtgt taaaaatgct 699
aagaaataac atagatatgt taatgttcta tgtgcatctt aaataattta gtgattttta 759
tgtcatataa ttttttcata accaaagaaa cttgattatt tctcgtgctt tagatattag 819
aatgaacac tgcttgggct gcgcatgggt gctcgcgcct gtaatctcag cactttggga 879
ggccgaggcg ggcggatcgc gagatcgaga gatcgagacc atcctggcca atgtggtgaa 939
accccgcttc tactgaaaaa gcaaaaatta gctgggcatg gtggcgcccg cacctgtagt 999
cccagctact tgggaggctg aggcgggagg atcccttgaa ccanggaggn cgaggttgca 1059
gtgagccagg attgcgcat tgcactccag cctggtgaca gagcaagact gcatctcaaa 1119
aaaaaaa 1126

```

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<210> 92
<211> 904
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (137) .. (322)

```

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<220>
<221> misc_feature
<222> (1) ... (904)
<223> n = a,t,c or g

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<400> 92
cgctccggaa ttcccgggtc gacccacgcg tccgcagggg taagccaccg caccagccc 60
cgtaaatatt tcttgaggat ctactgcgtg ccaggccttg tgctgggttc caggagctga 120
ttcagagagt gcagag atg aaa aaa gga gtg ggg tgt acg tgt gta tcc 169
Met Lys Lys Gly Val Gly Cys Thr Cys Val Ser
1 5 10
gtg tgt cca tgc atg tgt gtg cat ccg tat gtg tgc aca tgt gca tgc 217
Val Cys Pro Cys Met Cys Val His Pro Tyr Val Cys Thr Cys Ala Cys
15 20 25
atg cat gtg tgt gtg tgt ctg tgt gct tgg tgc ctc tct cag cct ggt 265
Met His Val Cys Val Cys Leu Cys Ala Trp Cys Leu Ser Gln Pro Gly
30 35 40
ggc ctg gga ggc ttc tca gaa gag gtc aca tct ctg cca aga cca agg 313
Gly Leu Gly Gly Phe Ser Glu Val Thr Ser Leu Pro Arg Pro Arg
45 50 55
gca ctg taa ggcagcc agatgagagg gaggggaaga gagatgggag ggaggctggg 369
Ala Leu *
60

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ctgaggggtac acagtgtggc tgctgcctgg tgccctgtga gggagcaggg tcccttctag 429  
 ctgggagcaa tggcgcatgc ctgtaatcct agcactttgg gaggtgagg caggagtatc 489  
 gcttgagctc aggagttcga gaccagcctg gacaacatga cgaaacccca tctctacnnn 549  
 nnananaann nnnanaaaag aaaagaaaaa aaaaaaaaga aaaaannaaa agggggccccc 609  
 tttttaaaaa acacaatttt ttcccggggg gtgagaaaaa ttattttttt ttttttgggg 669  
 ccctaaaatt tttttctggg ggccgctttt ttacacggg gggggagggg gaaagnnncg 729  
 ngngggcctt cggtgccgcg ggccgngtgg cgccgggccg ggtcttggtc gttggggggg 789  
 cctgcttctt tttcttttcg ctgtggctcc ggcggttggt ggcgggncgc gttggcccg 849  
 gagttggggg ggccacgact ggtaaattgg tcgggaggag acctctatgg ggctg 904

<210> 93  
 <211> 897  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (188) .. (544)

<400> 93  
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 aaataatagc cttgtcttct taacctgcaa aagtaatttt cctgcataat ttaatgtttt 120  
 catgtggaac aaatgagaat gcttttagaaa gcacattgta cactgtaaac ttctatacaa 180  
 cgtggtg atg tta ttt tta aag aaa ata caa ttc tta aag tgt aac aag 229  
 Met Leu Phe Leu Lys Lys Ile Gln Phe Leu Lys Cys Asn Lys  
 1 5 10  
 gtg ttt aga tcc ctg gat ttt tgc gta gcc cta cct tta ttg ttc tca 277  
 Val Phe Arg Ser Leu Asp Phe Cys Val Ala Leu Pro Leu Leu Phe Ser  
 15 20 25 30  
 tct tct gct gtt tta cag ata act cct gta gat aca ttt tct gat ccc 325  
 Ser Ser Ala Val Leu Gln Ile Thr Pro Val Asp Thr Phe Ser Asp Pro  
 35 40 45  
 cac tta gtt cta acc tta gtt aag ctg ctt atg aac att tta aat att 373  
 His Leu Val Leu Thr Leu Val Lys Leu Leu Met Asn Ile Leu Asn Ile  
 50 55 60  
 gca gtt att agt ctg act ttc cct gga gaa tat gaa gtt tct tta gcc 421  
 Ala Val Ile Ser Leu Thr Phe Pro Gly Glu Tyr Glu Val Ser Leu Ala  
 65 70 75  
 ttt gaa aat att ctc atg tat act cat gca ttc ata atc tgt ttc tgt 469  
 Phe Glu Asn Ile Leu Met Tyr Thr His Ala Phe Ile Ile Cys Phe Cys  
 80 85 90  
 aac aga cag tgg ctt ttt aaa agt aat agt gaa agt aat ctt agt agc 517  
 Asn Arg Gln Trp Leu Phe Lys Ser Asn Ser Glu Ser Asn Leu Ser Ser

95	100	105	110	
aat gtt aat tta ttt gac tct tgc tag ttttc aggtacgcaa aaggaggaga				569
Asn Val Asn Leu Phe Asp Ser Cys *				
115				
tgatttcctt taaaaactca gctttgaata gttcgtgtta tctggtatat ctgaaatatt				629
cagaaatggt aaaacagttt ttgtttgcct ttgctgttaa gtttgaaacc tcttagtgct				689
ttcaattgat aatcctggaa accaacctca gtattgtagt attacataga ttattggagt				749
tttatagtct tgaaaataaa gggctaatag ccatagatat atcgctgaca ctaaaatagc				809
caattgtggt taaaggaaca ttcagggaat ttcaaaaaac ttggaaacgg aaggaactgg				869
ggttgacagt tttggagggg agattccc				897
<210> 94				
<211> 931				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (124)..(456)				
<220>				
<221> misc_feature				
<222> (1)...(931)				
<223> n = a,t,c or g				
<400> 94				
attgatggcg ctgcctgca ggcaccggtc cggaattccc gggtcgaccc acgcgtccgc				60
ctcactctga ccctgatatc ttttctgctg ttaatctgtt ctctgagaaa acatctcaag				120
aag atg cag ctc cat ggc aaa gga tct caa gat ccc agc acc aag ggc				168
Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Gly				
1 5 10 15				
cac ata aaa gct ttg caa act gtg acc tcc ttt ctt ctg tta tgt gcc				216
His Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala				
20 25 30				
att tac ttt ctg tcc atg atc ata tca gtt tgt aat ttt ggg agg ctg				264
Ile Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu				
35 40 45				
gaa aag caa cct gtc ttc atg ttc tgc caa gct att ata ttc agc tat				312
Glu Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr				
50 55 60				
cct tca acc cac cca ttc atc ctg att ttg gga aac aag aag cta aag				360
Pro Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys				
65 70 75				
cag att ttt ctt tca gtt ttg cgg cat gtg agg tac tgg gtg aaa gac				408
Gln Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp				
80 85 90 95				

```

aga agc ctt cgt ctc cat aga ttc aca aga ggg gca ttg tgt gtc ttc      456
Arg Ser Leu Arg Leu His Arg Phe Thr Arg Gly Ala Leu Cys Val Phe
      100                      105                      110

tagcagaaaa caaactgggtg gtgtatgaaa cattttatat ttcttactgg gttttctgta      516
atatatgtat atgaataatt tccacatgta tacctagaaa agtctttttac ctaaagtttag      576
tctacaaaag tacatatata tagatggctg tgggtgtgacc gtgtgtgcac atatgtgaat      636
gtgtatatat cacgcaacag gagtgtcatt catgctgctg gccctgggtg aagtgacaag      696
tacaattaaa ggtggctctg atccttttaa acacctacca aaccctaaat ttgattccaa      756
aaggaccatt ctgcaaagag tttgcaaaga tctgggcccc cttgtgagca ccaaccttta      816
aacatgatgc gccagtctcc caggaggccc tactcattcc cctacataac tatttgatgg      876
ccccaccct accanccccg cttcccccca cctgaaaaaa gcaggccaca gaagc      931

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<210> 95
<211> 1278
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (50)..(1003)

```

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<400> 95
atttggccct cgaggccaag aattcggcac gagggcgggc acgcggggc      atg gct      55
                                   Met Ala
                                   1

ccc tgg gcg gag gcc gag cac tcg gcg ctg aac ccg ctg cgc gcg gtg      103
Pro Trp Ala Glu Ala Glu His Ser Ala Leu Asn Pro Leu Arg Ala Val
      5                      10                      15

tgg ctc acg ctg acc gcc gcc ttc ctg ctg acc cta ctg ctg cag ctc      151
Trp Leu Thr Leu Thr Ala Ala Phe Leu Leu Thr Leu Leu Leu Gln Leu
      20                      25                      30

ctg ccg ccc ggc ctg ctc ccg ggc tgc gcg atc ttc cag gac ctg atc      199
Leu Pro Pro Gly Leu Leu Pro Gly Cys Ala Ile Phe Gln Asp Leu Ile
      35                      40                      45                      50

cgc tat ggg aaa acc aag tgt ggg gag ccg tcg cgc ccc gcc gcc tgc      247
Arg Tyr Gly Lys Thr Lys Cys Gly Glu Pro Ser Arg Pro Ala Ala Cys
      55                      60                      65

cga gcc ttt gat gtc ccc aag aga tat ttt tcc cac ttt tat atc atc      295
Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr Ile Ile
      70                      75                      80

tca gtg ctg tgg aat ggc ttc ctg ctt tgg tgc ctt act caa tct ctg      343
Ser Val Leu Trp Asn Gly Phe Leu Leu Trp Cys Leu Thr Gln Ser Leu
      85                      90                      95

ttc ctg gga gca cct ttt cca agc tgg ctt cat ggt ttg ctc aga att      391
Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu His Gly Leu Leu Arg Ile
      100                      105                      110

```



ctc ggg gcg gca cag ttc cag gga ggg gag ctg gca ctg tct gca ttc Leu Gly Ala Ala Gln Phe Gln Gly Gly Glu Leu Ala Leu Ser Ala Phe 115 120 125 130	439
tta gtg cta gta ttt ctg tgg ctg cac agc tta cga aga ctc ttc gag Leu Val Leu Val Phe Leu Trp Leu His Ser Leu Arg Arg Leu Phe Glu 135 140 145	487
tgc ctc tac gtc agt gtc ttc tcc aat gtc atg att cac gtc gtg cag Cys Leu Tyr Val Ser Val Phe Ser Asn Val Met Ile His Val Val Gln 150 155 160	535
tac tgt ttt gga ctt gtc tat tat gtc ctt gtt ggc cta act gtg ctg Tyr Cys Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu 165 170 175	583
agc caa gtg cca atg gat ggc agg aat gcc tac ata aca ggg aaa aat Ser Gln Val Pro Met Asp Gly Arg Asn Ala Tyr Ile Thr Gly Lys Asn 180 185 190	631
cta ttg atg caa gca cgg tgg ttc cat att ctt ggg atg atg atg ttc Leu Leu Met Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe 195 200 205 210	679
atc tgg tca tct gcc cat cag tat aag tgc cat gtt att ctc ggc aat Ile Trp Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Gly Asn 215 220 225	727
ctc agg aaa aat aaa gca gga gtg gtc att cac tgt aac cac agg atc Leu Arg Lys Asn Lys Ala Gly Val Val Ile His Cys Asn His Arg Ile 230 235 240	775
cca ttt gga gac tgg ttt gaa tat gtt tct tcc cct aac tac tta gca Pro Phe Gly Asp Trp Phe Glu Tyr Val Ser Ser Pro Asn Tyr Leu Ala 245 250 255	823
gag ctg atg atc tac gtt tcc atg gcc gtc acc ttt ggg ttc cac aac Glu Leu Met Ile Tyr Val Ser Met Ala Val Thr Phe Gly Phe His Asn 260 265 270	871
tta act tgg tgg cta gtg gtg aca aat gtc ttc ttt aat cag gcc ctg Leu Thr Trp Trp Leu Val Val Thr Asn Val Phe Phe Asn Gln Ala Leu 275 280 285 290	919
tct gcc ttt ctc agc cac caa ttc tac aaa agc aaa ttt gtc tct tac Ser Ala Phe Leu Ser His Gln Phe Tyr Lys Ser Lys Phe Val Ser Tyr 295 300 305	967
ccg aag cat agg aaa gct ttc cta cca ttt ttg ttt taag ttaacctcag Pro Lys His Arg Lys Ala Phe Leu Pro Phe Leu Phe 310 315	1017
tcatgaagaa tgcaaaccag gtgatggttt caatgcctaa ggacagtga gtctggagtc	1077
caaagtacag tttcagcaaa gctgtttgaa actctccatt ccatttctat accccacaag	1137
ttttcactga atgagcatgg cagtgcact caagaaaatg aatctccaaa gtatcttcaa	1197
agaataaata ctaatggcag atctgcctcg tgccgaattc gaatcgatgg gatcctgcaa	1257
aaagaacaag tagcttgtat t	1278

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<210> 96
<211> 1721
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (162)..(1085)

<400> 96
tggtgttatg ttgagtcggt ttattgaggg cgtagtaata accatctatt cgatgatgaa      60
gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg      120
actttcattt ggtggtgagg actgaacgga gagaactcac c      atg gag ttt ggg      173
                                         Met Glu Phe Gly
                                         1

ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt gtc cag tgt gag      221
Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val Gln Cys Glu
   5              10              15              20

gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag oct ggg ggg tcc      269
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
      25              30              35

ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agt ttt tcg      317
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Ser
      40              45              50

atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca      365
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
      55              60              65

tct att agt ggt agt tcg ggt acc aca tac tac gca gac tcc gtg aag      413
Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
      70              75              80

ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg      461
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
      85              90              95              100

caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt gcg      509
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
      105              110              115

aaa ccg ttt ccg tat ttt gac tac tgg ggc cag gga acc ctg gtc acc      557
Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
      120              125              130

gtc tcg agt ggc gat ggg tcc agt ggc ggt agc ggg ggc gcg tcg act      605
Val Ser Ser Gly Asp Gly Ser Ser Gly Gly Ser Gly Gly Ala Ser Thr
      135              140              145

ggc gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca      653
Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
      150              155              160

ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc      701
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
      165              170              175              180

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agc tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc      749
Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
                185                      190                      195

ctc atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc      797
Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe
                200                      205                      210

agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg      845
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
                215                      220                      225

gag cct gaa gat ttt gca gtg tat tac tgt cag cag acg ggt cgt att      893
Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Gly Arg Ile
                230                      235                      240

ccg ccg acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg      941
Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
                245                      250                      255                      260

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa      989
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
                265                      270                      275

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga      1037
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
                280                      285                      290

gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc cca atc ggg taa      1085
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Pro Ile Gly *
                295                      300                      305

ctcccaggag agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac      1145

cctgacgctg agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca      1205

tcagggcctg agctcgcccg tcacaaagag cttcaacagg ggagagtgtt agagggagaa      1265

gtgcccccac ctgctcctca gttccagcct gacccctcc catccttttg cctctgaccc      1325

tttttccaca ggggacctac cctattgag gtctccagc tcatttttca cctcaccccc      1385

ctcctcctcc ttggctttta ttatgctaatt gttggaggag aatgaataaa taaagtgaat      1445

ctttgcacct gtggtttctc tctttcctca ttttaataatt attatctgtt gttttaccaa      1505

ctactcaatt tctcttataa gggactaaat atgtagtcat cctaaggcgc ataaccattt      1565

ataaaaaatca tccttcattc tattttaccc tatcatctc tgcaagacag tcctccttca      1625

aaccacaag ccttctgtcc tcacagtccc ctgggccatg gtaggagaga cttgcttcc      1685

tgttttcccc tcctcagcaa gccctcatag tcctttt      1721

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<210> 97  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

&lt;222&gt; (162) .. (641)

&lt;400&gt; 97

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gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg      120
actttcattt ggtgggtgagg actgaacgga gagaactcac c      atg gag ttt ggg      173
                                         Met Glu Phe Gly
                                         1

ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt gtc cag tgt gag      221
Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val Gln Cys Glu
   5              10              15              20

gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc      269
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
          25              30              35

ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt gac agc tat gcc      317
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ser Tyr Ala
          40              45              50

atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gat tgg gtc tca      365
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val Ser
          55              60              65

gct gtt agt ggt ggt ggt ggt agc aca tac tac gca gac tcc gtg aag      413
Ala Val Ser Gly Gly Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
          70              75              80

ggc cgg ttc acc atc tcc aga gac aac gcc aag agc acg atg tat ctg      461
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Met Tyr Leu
          85              90              95              100

caa atg aac agt ctg aga gct gag gac acg gcc atg tat tac tgt gca      509
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala
          105              110              115

aaa gat aat tac gat ttt tgg agt ggt acc ttt gac tac tgg ggc cag      557
Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly Gln
          120              125              130

gga acc ctg gtc acc gtc tcc tca gct tcc acc aag ggc cca tcg gtc      605
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          135              140              145

gta gcg ggg gcg cgt cga ctg gcg aaa ttg tgt tga cgca gtctccaggc      655
Val Ala Gly Ala Arg Arg Leu Ala Lys Leu Cys *
          150              155              160

accctgtctt tgtctccagg ggaaagagcc accctctcct gcagggccag tcagagtgtt      715
agcagcagct acttagcctg gtaccagcag aaacctggcc aggctcccag gctctcctc
          775

tatggtgcat ccagcagggc cactggcatc ccagacaggt tcagtggcag tgggtctggg      835
acagacttca ctctcaccat cagcagactg gagcctgaag attttgagt gtattactgt      895
cagcagacgg gtcgtattcc gccgacgttc ggccaaggga ccaaggtgga aatcaaacga      955
actgtggctg caccatctgt ctctatcttc ccgccatctg atgagcagtt gaaatctgga      1015
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg      1075

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aaggtggata acgccctccc aatcgggtaa ctcccaggag agtgtcacag agcaggacag 1135
caaggacagc acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa 1195
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gacccccctcc catcctttgg cctctgaccc tttttccaca ggggacctac ccctattgcg 1375
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tccttt 1741

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<210> 98
<211> 1736
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (162)..(1100)

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gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg 120
actttcattt ggtggtgagg actgaacgga gagaactcac c      atg gag ttt ggg 173
                               Met Glu Phe Gly
                               1

ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt gtc cag tgt gag 221
Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val Gln Cys Glu
5          10          15          20

gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc 269
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
25          30          35

ctg aga ctc tcc tgt gca gcc act gga ttc act ttt agc agc tat gcc 317
Leu Arg Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Ser Ser Tyr Ala
40          45          50

atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca 365
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
55          60          65

gaa att att agt agc ggt ggt acc aca tac tac gca gac tcc gtg aag 413
Glu Ile Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys

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70	75	80	
ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg			461
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu			
85	90	95	100
caa atg aac ggc atg aga gcc gag gac acg gcc ata tat tac tgt gcg			509
Gln Met Asn Gly Met Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala			
	105	110	115
aaa gac ata att agt gat tct tgg cgc tac ttt gac tac tgg ggc cag			557
Lys Asp Ile Ile Ser Asp Ser Trp Arg Tyr Phe Asp Tyr Trp Gly Gln			
	120	125	130
gga gcc ctg gtc acc gtc tcc tca ggg gat ggg tcc agt ggc ggt agc			605
Gly Ala Leu Val Thr Val Ser Ser Gly Asp Gly Ser Ser Gly Gly Ser			
	135	140	145
ggg ggc gcg tcg act ggc gaa att gtg ttg acg cag tct cca ggc acc			653
Gly Gly Ala Ser Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr			
	150	155	160
ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt			701
Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser			
	165	170	175
cag agt gtt agc agc agc tac tta gcc tgg tac cag cag aaa cct ggc			749
Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly			
	185	190	195
cag gct ccc agg ctc ctc atc tat ggt gca tcc agc agg gcc act ggc			797
Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly			
	200	205	210
atc cca gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc			845
Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu			
	215	220	225
acc atc agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag			893
Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln			
	230	235	240
cag acg ggt cgt att ccg ccg acg ttc ggc caa ggg acc aag gtg gaa			941
Gln Thr Gly Arg Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu			
	245	250	255
atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct			989
Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser			
	265	270	275
gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat			1037
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn			
	280	285	290
aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc			1085
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala			
	295	300	305
ctc cca atc ggg taa ctcccaggag agtgtcacag agcaggacag caaggacagc			1140
Leu Pro Ile Gly *			
	310		
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc			1200

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 1260  
 ggagagtgtt agagggagaa gtgccccac ctgctcctca gttccagcct gacccctcc 1320  
 catccttttg cctctgaccc tttttccaca ggggacctac ccctattgcg gtcctccagc 1380  
 tcctctttca cctcaccccc ctctcctcc ttggttttaa ttatgctaatt gttggaggag 1440  
 aatgaataaa taaagtgaat ctttgacact gtggtttctc tctttcctca tttataaatt 1500  
 attatctgtt gttttaccaa ctactcaatt tctcttataa gggactaaat atgtagtcat 1560  
 cctaaggcgc ataaccattt ataaaaatca tccttcattc tattttaccc tatcctcctc 1620  
 tgcaagacag tcctccctca aaccacaaag ccttctgtcc tcacagtccc ctgggccatg 1680  
 gtaggagaga cttgcttcct tgttttcccc tcctcagcaa gccctcatag tccttt 1736

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (162) .. (1253)

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 actttcattt ggtggtgagg actgaacgga gagaactcac c atg gag ttt ggg 173  
 Met Glu Phe Gly  
 1  
 ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt gtc cag tgt gag 221  
 Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val Gln Cys Glu  
 5 10 15 20  
 gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc 269  
 Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser  
 25 30 35  
 ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agt ttt tcg 317  
 Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Ser  
 40 45 50  
 atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca 365  
 Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
 55 60 65  
 tct att agt ggt agt tcg ggt acc aca tac tac gca gac tcc gtg aag 413  
 Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys  
 70 75 80  
 ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg 461  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
 85 90 95 100  
 caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt gcg 509

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
105 110 115	
aaa ccg ttt ccg tat ttt gac tac tgg ggc cag gga acc ctg gtc acc	557
Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr	
120 125 130	
gtc tcg agt ggc gat ggg tcc agt ggc ggt agc gtc acc gtc tcc tca	605
Val Ser Ser Gly Asp Gly Ser Ser Gly Gly Ser Val Thr Val Ser Ser	
135 140 145	
agt gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct gta	653
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val	
150 155 160	
gga gac aga gtc acc atc act tgc cgg gcc agt cag agt att agt agc	701
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser	
165 170 175 180	
tgg ctg gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ttg	749
Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu	
185 190 195	
atc tat aag gca tct agt tta gaa agt ggg gtc cca tca agg ttc agc	797
Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser	
200 205 210	
ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag	845
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln	
215 220 225	
cct gat gat ttt gca act tat tac tgc cag caa tat gtt tat tac ccg	893
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Val Tyr Tyr Pro	
230 235 240	
ctc act ttc ggc gga ggg acc aag gtg gaa atc aaa cga act gtg gct	941
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala	
245 250 255 260	
gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct	989
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser	
265 270 275	
gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag	1037
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu	
280 285 290	
gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc	1085
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser	
295 300 305	
cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc	1133
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu	
310 315 320	
agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa ctc	1181
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Leu	
325 330 335 340	
tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag	1229
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys	
345 350 355	
agc ttc aac agg gga gag tgt tag agggagaagg tgccccacct gtcctcagtc	1283



Ser Phe Asn Arg Gly Glu Cys \*

360

cagcctgccc cctcccatcc ttggcctct gccctttttc cacaggggac ctcccctatt 1343  
 gcggcctcca gctcatcttt acctaccccc cctcccttc cttggcttta attatgctaa 1403  
 tgttgaggga gaatgaataa ataaagtga tctttgcacc tgtggtttct ctctttctc 1463  
 atttaataat tattatctgt tgttttacca actactcaat ttctcttata agggactaaa 1523  
 tatgtagtca tcctaaggcg cataaccatt tataaaaatc atccttcatt ctattttacc 1583  
 ctatcatcct ctgcaagaca gtcctccctc aaaccacaa gccttctgtc ctcacagtcc 1643  
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 gtccttt 1710

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (136) .. (276)

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 attgaacata cacat atg ttc ccc cct tac ttt tct ctt att tta ctt cta 171  
 Met Phe Pro Pro Tyr Phe Ser Leu Ile Leu Leu Leu  
 1 5 10  
 ttc act ttt gct tcg aaa ttc ttt ctg tct ctg aac ctg aaa aaa agc 219  
 Phe Thr Phe Ala Ser Lys Phe Phe Leu Ser Leu Asn Leu Lys Lys Ser  
 15 20 25  
 aac ata gtt aaa gca aga att gag agt aca aag aca gtg ata tca aag 267  
 Asn Ile Val Lys Ala Arg Ile Glu Ser Thr Lys Thr Val Ile Ser Lys  
 30 35 40  
 aga tgt taa tcctcca cacagtctgg ctgcattgag gatattttctc ttgtgtcagt 323  
 Arg Cys \*  
 45  
 agaaaaactgg aaatagctaa gtctattgga actcttcttt ctcaaattct attgaactga 383  
 agagtaggaa atttagaaac agtaagacgt gggagataat ttaactgaat tcactacttt 443  
 tgtgacaagg atatccagag gaactcaggg acttgccc 481

<210> 101  
 <211> 708  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (218) .. (454)

&lt;400&gt; 101

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ccgcgcttca ttgaagtcgt cgcctgcagg taccggagcg gaattcccgg gtcgaccac      60
gcgtccgcac ttcttcatca ttccatcaga accttataat gaatttgatg cagattgctt      120
ttgagggggtt tatctctcag tcctaaacat ataggggcat gttagaaaat ttgggattct      180
aggtgtgatg cctgaaaagg gactgatata actgagc atg gct atg cag tct gtg      235
                               Met Ala Met Gln Ser Val
                               1             5

ata aga aaa caa ttc aca gct cta gct ggc ttc tgc ttc tgg ttc tgt      283
Ile Arg Lys Gln Phe Thr Ala Leu Ala Gly Phe Cys Phe Trp Phe Cys
                10             15             20

ctc ttt acc tta gca gtc ctg agt ctc acc ttg ctt atc tgc aaa ctg      331
Leu Phe Thr Leu Ala Val Leu Ser Leu Thr Leu Leu Ile Cys Lys Leu
                25             30             35

agg ata atg cca ttt aaa ctt gaa ggt ttg ttt caa gaa tta aat aaa      379
Arg Ile Met Pro Phe Lys Leu Glu Gly Leu Phe Gln Glu Leu Asn Lys
                40             45             50

tca tgg cat atg aag ctc ttg tca caa gat agg gag tta ata aat atg      427
Ser Trp His Met Lys Leu Leu Ser Gln Asp Arg Glu Leu Ile Asn Met
                55             60             65             70

ctg ttg ctc tta atg ggc agg tcc taa gtgat ggcttagaaa cctaagattg      479
Leu Leu Leu Leu Met Gly Arg Ser *
                75

gaaggcatct tggagatgtt ctggctcaac ctcctaacaa tgcaaaagtt tgtcctagaa      539
cactcctgga agatggatct ttaggctctc attagataac ccagggatcc cactgtctca      599
aaaggcagtc tgtgcatatt tttggtcagg tctaattctt aatgataata acacacattt      659
tattttgtggg ttacgaaatg cttttacgtc atttatttaa cttgactgt      708

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&lt;210&gt; 102

&lt;211&gt; 3969

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (52) .. (3618)

&lt;400&gt; 102

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cgcgccccc gccgcgctg cacaccggac ccagccgccc tgccgcgggc c atg gac      57
                               Met Asp
                               1

ctg ccc agg ggc ctg gtg gtg gcc tgg gcg ctc agc ctg tgg cca ggg      105
Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp Pro Gly

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5	10	15	
ttc acg gac acc ttc aac atg gac acc agg aag ccc cgg gtc atc cct			153
Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val Ile Pro			
20	25	30	
ggc tcc agg acc gcc ttc ttt ggc tac aca gtg cag cag cac gac atc			201
Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His Asp Ile			
35	40	45	50
agt ggc aat aag tgg ctg gtc gtg ggc gcc cca ctg gaa acc aat ggc			249
Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr Asn Gly			
55	60	65	
tac cag aag acg gga gac gtg tac aag tgt cca gtg atc cac ggg aac			297
Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His Gly Asn			
70	75	80	
tgc acc aaa ctc aac ctg gga agg gtc acc ctg tcc aac gtg tcc gag			345
Cys Thr Lys Leu Asn Leu Gly Arg Val Thr Leu Ser Asn Val Ser Glu			
85	90	95	
cgg aaa gac aac atg cgc ctc ggc ctt agt ctc gcc acc aac ccc aag			393
Arg Lys Asp Asn Met Arg Leu Gly Leu Ser Leu Ala Thr Asn Pro Lys			
100	105	110	
gac aac agc ttc ctg gcc tgc agc ccc ctc tgg tct cat gag tgt ggg			441
Asp Asn Ser Phe Leu Ala Cys Ser Pro Leu Trp Ser His Glu Cys Gly			
115	120	125	130
agc tcc tac tac acc aca ggg atg tgt tca aga gtc aac tcc aac ttc			489
Ser Ser Tyr Tyr Thr Thr Gly Met Cys Ser Arg Val Asn Ser Asn Phe			
135	140	145	
agg ttc tcc aag acc gtg gcc cca gct ctc caa agg tgc cag acc tac			537
Arg Phe Ser Lys Thr Val Ala Pro Ala Leu Gln Arg Cys Gln Thr Tyr			
150	155	160	
atg gac atc gtc att gtc ctg gat ggc tcc aac agc atc tac ccc tgg			585
Met Asp Ile Val Ile Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp			
165	170	175	
gtg gag gtt cag cac ttc ctc atc aac atc ctg aaa aag ttt tac att			633
Val Glu Val Gln His Phe Leu Ile Asn Ile Leu Lys Lys Phe Tyr Ile			
180	185	190	
ggc cca ggg cag atc cag gtt gga gtt gtg cag tat ggc gaa gat gtg			681
Gly Pro Gly Gln Ile Gln Val Gly Val Val Gln Tyr Gly Glu Asp Val			
195	200	205	210
gtg cat gag ttt cac ctc aac gac tac agg tct gta aaa gat gtg gtg			729
Val His Glu Phe His Leu Asn Asp Tyr Arg Ser Val Lys Asp Val Val			
215	220	225	
gaa gct gcc agc cac att gag cag aga gga gga aca gag acc cgg acg			777
Glu Ala Ala Ser His Ile Glu Gln Arg Gly Gly Thr Glu Thr Arg Thr			
230	235	240	
gca ttt ggc att gaa ttt gca cgc tca gag gct ttc cag aag ggt gga			825
Ala Phe Gly Ile Glu Phe Ala Arg Ser Glu Ala Phe Gln Lys Gly Gly			
245	250	255	
agg aaa gga gcc aag aag gtg atg att gtc atc aca gat ggg gag tcc			873
Arg Lys Gly Ala Lys Lys Val Met Ile Val Ile Thr Asp Gly Glu Ser			

260	265	270	
cac gac agc cca gac ctg gag aag gtg atc cag caa agc gaa aga gac His Asp Ser Pro Asp Leu Glu Lys Val Ile Gln Gln Ser Glu Arg Asp 275 280 285 290			921
aac gta aca aga tat gcg gtg gcc gtc ctg ggc tac tac aac cgc agg Asn Val Thr Arg Tyr Ala Val Ala Val Leu Gly Tyr Tyr Asn Arg Arg 295 300 305			969
ggg atc aat cca gaa act ttt cta aat gaa atc aaa tac atc gcc agt Gly Ile Asn Pro Glu Thr Phe Leu Asn Glu Ile Lys Tyr Ile Ala Ser 310 315 320			1017
gac cct gat gac aag cac ttc ttc aat gtc act gat gag gct gcc ttg Asp Pro Asp Asp Lys His Phe Phe Asn Val Thr Asp Glu Ala Ala Leu 325 330 335			1065
aag gac att gtc gat gcc ctg ggg gac aga atc ttc agc ctg gaa ggc Lys Asp Ile Val Asp Ala Leu Gly Asp Arg Ile Phe Ser Leu Glu Gly 340 345 350			1113
acc aac aag aac gag acc tcc ttt ggg ctg gag atg tca cag acg ggc Thr Asn Lys Asn Glu Thr Ser Phe Gly Leu Glu Met Ser Gln Thr Gly 355 360 365 370			1161
ttt tcc tcg cac gtg gtg gag gat ggg gtt ctg ctg gga gcc gtc ggt Phe Ser Ser His Val Val Glu Asp Gly Val Leu Leu Gly Ala Val Gly 375 380 385			1209
gcc tat gac tgg aat gga gct gtg cta aag gag acg agt gcc ggg aag Ala Tyr Asp Trp Asn Gly Ala Val Leu Lys Glu Thr Ser Ala Gly Lys 390 395 400			1257
gtc att cct ctc cgc gag tcc tac ctg aaa gag ttc ccc gag gag ctc Val Ile Pro Leu Arg Glu Ser Tyr Leu Lys Glu Phe Pro Glu Glu Leu 405 410 415			1305
aag aac cat ggt gca tac ctg ggg tac aca gtc aca tcg gtc gtg tcc Lys Asn His Gly Ala Tyr Leu Gly Tyr Thr Val Thr Ser Val Val Ser 420 425 430			1353
tcc agg cag ggg cga gtg tac gtg gcc gga gcc ccc cgg ttc aac cac Ser Arg Gln Gly Arg Val Tyr Val Ala Gly Ala Pro Arg Phe Asn His 435 440 445 450			1401
acg ggc aag gtc atc ctg ttc acc atg cac aac aac cgg agc ctc acc Thr Gly Lys Val Ile Leu Phe Thr Met His Asn Asn Arg Ser Leu Thr 455 460 465			1449
atc cac cag gct atg cgg ggc cag cag ata ggc tct tac ttt ggg agt Ile His Gln Ala Met Arg Gly Gln Gln Ile Gly Ser Tyr Phe Gly Ser 470 475 480			1497
gaa atc acc tcg gtg gac atc gac ggc gac ggc gtg act gat gtc ctg Glu Ile Thr Ser Val Asp Ile Asp Gly Asp Gly Val Thr Asp Val Leu 485 490 495			1545
ctg gtg ggc gca ccc atg tac ttc aac gag ggc cgt gag cga ggc aag Leu Val Gly Ala Pro Met Tyr Phe Asn Glu Gly Arg Glu Arg Gly Lys 500 505 510			1593
gtg tac gtc tat gag ctg aga cag aac cgg ttt gtt tat aac gga acg Val Tyr Val Tyr Glu Leu Arg Gln Asn Arg Phe Val Tyr Asn Gly Thr 515 520 525 530			1641

515	520	525	530	
cta aag gat tca cac agt tac cag aat gcc cga ttt ggg tcc tcc att				1689
Leu Lys Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Ser Ile				
	535	540	545	
gcc tca gtt cga gac ctc aac cag gat tcc tac aat gac gtg gtg gtg				1737
Ala Ser Val Arg Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val				
	550	555	560	
gga gcc ccc ctg gag gac aac cac gca gga gcc atc tac atc ttc cac				1785
Gly Ala Pro Leu Glu Asp Asn His Ala Gly Ala Ile Tyr Ile Phe His				
	565	570	575	
ggc ttc cga ggc agc atc ctg aag aca cct aag cag aga atc aca gcc				1833
Gly Phe Arg Gly Ser Ile Leu Lys Thr Pro Lys Gln Arg Ile Thr Ala				
	580	585	590	
tca gag ctg gct acc ggc ctc cag tat ttt ggc tgc agc atc cac ggg				1881
Ser Glu Leu Ala Thr Gly Leu Gln Tyr Phe Gly Cys Ser Ile His Gly				
	595	600	605	610
caa ttg gac ctc aat gag gat ggg ctc atc gac ctg gca gtg gga gcc				1929
Gln Leu Asp Leu Asn Glu Asp Gly Leu Ile Asp Leu Ala Val Gly Ala				
	615	620	625	
ctt ggc aac gct gtg att ctg tgg tcc cgc cca gtg gtt cag atc aat				1977
Leu Gly Asn Ala Val Ile Leu Trp Ser Arg Pro Val Val Gln Ile Asn				
	630	635	640	
gcc agc ctc cac ttt gag cca tcc aag atc aac atc ttc cac aga gac				2025
Ala Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Arg Asp				
	645	650	655	
tgc aag cgc agt ggc agg gat gcc acc tgc ctg gcc gcc ttc ctc tgc				2073
Cys Lys Arg Ser Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys				
	660	665	670	
ttc acg ccc atc ttc ctg gca ccc cat ttc caa aca aca act gtt ggc				2121
Phe Thr Pro Ile Phe Leu Ala Pro His Phe Gln Thr Thr Thr Val Gly				
	675	680	685	690
atc aga tac aac gcc acc atg gat gag agg cgg tat aca ccg agg gcc				2169
Ile Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Thr Pro Arg Ala				
	695	700	705	
cac ctg gac gag ggc ggg gac cga ttc acc aac aga gcc gta ctg ctc				2217
His Leu Asp Glu Gly Gly Asp Arg Phe Thr Asn Arg Ala Val Leu Leu				
	710	715	720	
tcc tcc ggc cag gag ctc tgt gag cgg atc aac ttc cat gtc ctg gac				2265
Ser Ser Gly Gln Glu Leu Cys Glu Arg Ile Asn Phe His Val Leu Asp				
	725	730	735	
act gct gac tac gtg aag cca gtg acc ttc tca gtc gag tat tcc ctg				2313
Thr Ala Asp Tyr Val Lys Pro Val Thr Phe Ser Val Glu Tyr Ser Leu				
	740	745	750	
gag gac cct gac cat ggc ccc atg ctg gac gac ggc tgg ccc acc act				2361
Glu Asp Pro Asp His Gly Pro Met Leu Asp Asp Gly Trp Pro Thr Thr				
	755	760	765	770
ctc aga gtc tcg gtg ccc ttc tgg aac ggc tgc aat gag gat gag cac				2409
Leu Arg Val Ser Val Pro Phe Trp Asn Gly Cys Asn Glu Asp Glu His				

775															780					785					
tgt	gtc	cct	gac	ctt	gtg	ttg	gat	gcc	cgg	agt	gac	ctg	ccc	acg	gcc	2457									
Cys	Val	Pro	Asp	Leu	Val	Leu	Asp	Ala	Arg	Ser	Asp	Leu	Pro	Thr	Ala										
			790				795				800														
atg	gag	tac	tgc	cag	agg	gtg	ctg	agg	aag	cct	gcg	cag	gac	tgc	tcc	2505									
Met	Glu	Tyr	Cys	Gln	Arg	Val	Leu	Arg	Lys	Pro	Ala	Gln	Asp	Cys	Ser										
			805				810				815														
gca	tac	acg	ctg	tcc	ttc	gac	acc	aca	gtc	ttc	atc	ata	gag	agc	aca	2553									
Ala	Tyr	Thr	Leu	Ser	Phe	Asp	Thr	Thr	Val	Phe	Ile	Ile	Glu	Ser	Thr										
			820				825				830														
cgc	cag	cga	gtg	gcg	gtg	gag	gcc	aca	ctg	gag	aac	agg	ggc	gag	aac	2601									
Arg	Gln	Arg	Val	Ala	Val	Glu	Ala	Thr	Leu	Glu	Asn	Arg	Gly	Glu	Asn										
835				840				845				850													
gcc	tac	agc	acg	gtc	cta	aat	atc	tcg	cag	tca	gca	aac	ctg	cag	ttt	2649									
Ala	Tyr	Ser	Thr	Val	Leu	Asn	Ile	Ser	Gln	Ser	Ala	Asn	Leu	Gln	Phe										
			855				860				865														
gcc	agc	ttg	atc	cag	aag	gag	gac	tca	gac	ggc	agc	att	gag	tgt	gtg	2697									
Ala	Ser	Leu	Ile	Gln	Lys	Glu	Asp	Ser	Asp	Gly	Ser	Ile	Glu	Cys	Val										
			870				875				880														
aac	gag	gag	agg	agg	ctc	cag	aag	caa	gtc	tgc	aac	gtc	agc	tat	ccc	2745									
Asn	Glu	Glu	Arg	Arg	Leu	Gln	Lys	Gln	Val	Cys	Asn	Val	Ser	Tyr	Pro										
			885				890				895														
ttc	ttc	cgg	gcc	aag	gcc	aag	gtg	gct	ttc	cgt	ctt	gat	ttt	gag	ttc	2793									
Phe	Phe	Arg	Ala	Lys	Ala	Lys	Val	Ala	Phe	Arg	Leu	Asp	Phe	Glu	Phe										
			900				905				910														
agc	aaa	tcc	atc	ttc	cta	cac	cac	ctg	gag	atc	gag	ctc	gct	gca	ggc	2841									
Ser	Lys	Ser	Ile	Phe	Leu	His	His	Leu	Glu	Ile	Glu	Leu	Ala	Ala	Gly										
915				920				925				930													
agt	gac	agt	aat	gag	cgg	gac	agc	acc	aag	gaa	gac	aac	gtg	gcc	ccc	2889									
Ser	Asp	Ser	Asn	Glu	Arg	Asp	Ser	Thr	Lys	Glu	Asp	Asn	Val	Ala	Pro										
			935				940				945														
tta	cgc	ttc	cac	ctc	aaa	tac	gag	gct	gac	gtc	ctc	ttc	acc	agg	agc	2937									
Leu	Arg	Phe	His	Leu	Lys	Tyr	Glu	Ala	Asp	Val	Leu	Phe	Thr	Arg	Ser										
			950				955				960														
agc	agc	ctg	agc	cac	tat	gag	gtc	aag	ccc	aac	agc	tcg	ctg	gag	aga	2985									
Ser	Ser	Leu	Ser	His	Tyr	Glu	Val	Lys	Pro	Asn	Ser	Ser	Leu	Glu	Arg										
			965				970				975														
tac	gat	ggc	atc	ggg	cct	ccc	ttc	agc	tgc	atc	ttc	agg	atc	cag	aac	3033									
Tyr	Asp	Gly	Ile	Gly	Pro	Pro	Phe	Ser	Cys	Ile	Phe	Arg	Ile	Gln	Asn										
			980				985				990														
ttg	ggc	ttg	ttc	ccc	atc	cac	ggg	atg	atg	atg	aag	atc	acc	att	ccc	3081									
Leu	Gly	Leu	Phe	Pro	Ile	His	Gly	Met	Met	Met	Lys	Ile	Thr	Ile	Pro										
995				1000				1005				1010													
atc	gcc	acc	agg	agc	ggc	aac	cgc	cta	ctg	aag	ctg	agg	gac	ttc	ctc	3129									
Ile	Ala	Thr	Arg	Ser	Gly	Asn	Arg	Leu	Leu	Lys	Leu	Arg	Asp	Phe	Leu										
			1015				1020				1025														
acg	gac	gag	gcg	aac	acg	tcc	tgt	aac	atc	tgg	ggc	aat	agc	act	gag	3177									
Thr	Asp	Glu	Ala	Asn	Thr	Ser	Cys	Asn	Ile	Trp	Gly	Asn	Ser	Thr	Glu										

	1030	1035	1040	
tac cgg ccc acc cca gtg gag gaa gac ttg cgt cgt gct cca cag ctg				3225
Tyr Arg Pro Thr Pro Val Glu Glu Asp Leu Arg Arg Ala Pro Gln Leu				
1045	1050	1055		
aat cac agc aac tct gat gtc gtc tcc atc aac tgc aat ata cgg ctg				3273
Asn His Ser Asn Ser Asp Val Val Ser Ile Asn Cys Asn Ile Arg Leu				
1060	1065	1070		
gtc ccc aac cag gaa atc aat ttc cat cta ctg ggg aac ctg tgg ttg				3321
Val Pro Asn Gln Glu Ile Asn Phe His Leu Leu Gly Asn Leu Trp Leu				
1075	1080	1085	1090	
agg tcc cta aaa gca ctc aag tac aaa tcc atg aaa atc atg gtc aac				3369
Arg Ser Leu Lys Ala Leu Lys Tyr Lys Ser Met Lys Ile Met Val Asn				
1095	1100	1105		
gca gcc ttg cag agg cag ttc cac agc ccc ttc atc ttc cgt gag gag				3417
Ala Ala Leu Gln Arg Gln Phe His Ser Pro Phe Ile Phe Arg Glu Glu				
1110	1115	1120		
gat ccc agc cgc cag atc gtg ttt gag atc tcc aag caa gag gac tgg				3465
Asp Pro Ser Arg Gln Ile Val Phe Glu Ile Ser Lys Gln Glu Asp Trp				
1125	1130	1135		
cag gtc ccc atc tgg atc att gta ggc agc acc ctg ggg ggc ctc cta				3513
Gln Val Pro Ile Trp Ile Ile Val Gly Ser Thr Leu Gly Gly Leu Leu				
1140	1145	1150		
ctg ctg gcc ctg ctg gtc ctg gca ctg tgg aag ctc ggc ttc ttt aga				3561
Leu Leu Ala Leu Leu Val Leu Ala Leu Trp Lys Leu Gly Phe Phe Arg				
1155	1160	1165	1170	
agt gcc agg cgc agg agg gag cct ggt ctg gac ccc acc ccc aaa gtg				3609
Ser Ala Arg Arg Arg Arg Glu Pro Gly Leu Asp Pro Thr Pro Lys Val				
1175	1180	1185		
ctg gag tga ggctcca gaggagactt tgagttgatg ggggccagga caccagtcca				3665
Leu Glu *				
ggtagtggtg agaccaggg ctgtggcccc accgagctgg agcggagagg aagccagctg				3725
gctttgcact tgacctcatc toccgagcaa tggcgccctgc tccctocaga atggaactca				3785
agctgggtttt aagtggaact gccctactgg gagactggga cacctttaac acagaccct				3845
agggatttaa agggacaccc ctacacacac ccaggccac gccaaaggcct ccctcaggct				3905
ctgtggaggg catttgctgc ccagctact aagggtctat gaattcgtaa tcatcccat				3965
tctc				3969

<210> 103  
 <211> 735  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

&lt;222&gt; (305)..(463)

<400> 103  
 gtgatgatac ccgctccggaa ttcccggggtc gacccacgcg tccgctaatt tctaattctt 60  
 ctgtagcatt tattaagaaa agttaaaata actgcttaat ttgagatgaa attaacacat 120  
 gagaacttca ctcatagggt ggtatgttct gtgactgttg tttaatgtgt attttatggc 180  
 agttttgact gccattttgt catttgagaa aggtgaaatg aagtactatt ttgggctgcg 240  
 aaacctgaag ttgtagggaa acctgtgttt gaagaccatt aagaagttgt tttgcatact 300  
 aaga atg gca ctg aac atc att atc aat cct gtg tgg ttt tgc cac tgc 349  
 Met Ala Leu Asn Ile Ile Ile Asn Pro Val Trp Phe Cys His Cys  
 1 5 10 15  
 ttg act tgc aca att cac att gat ttt cat att tta ttc att aaa att 397  
 Leu Thr Cys Thr Ile His Ile Asp Phe His Ile Leu Phe Ile Lys Ile  
 20 25 30  
 ttt aaa cac atg ttt ttt agg tgc ctt tgg tca tct tgg ctt agc cat 445  
 Phe Lys His Met Phe Phe Arg Ser Leu Trp Ser Ser Trp Leu Ser His  
 35 40 45  
 caa ctt gat cac ata tga tgatcg cttcaacctg aaaagtattg aggagcagct 499  
 Gln Leu Asp His Ile \*  
 50  
 gggaacagaa attaaacctt ttccgagcaa cattgataag agcctgtatg tggcagaata 559  
 ccacagcgag cctgtagaag atgagaaacc ttaacaagca tgtacgtccc tgacagaaca 619  
 gctaagagga acctttaaat gagggaaatc aaaatcttct ttctgtgttg aaattttagt 679  
 gcacaccata tataatagca atataagggc ggactccccc ctagcataaa tgacag 735

<210> 104  
 <211> 633  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (48)..(281)

<400> 104  
 gaccagcggc caccacgcg tccggctctga atcttattcc tttgtag atg gcc att 56  
 Met Ala Ile  
 1  
 ttt cct ctt tgg aag ctc ttg aat gtt ttg gta tgc ata ttt tcc tca 104  
 Phe Pro Leu Trp Lys Leu Leu Asn Val Leu Val Cys Ile Phe Ser Ser  
 5 10 15  
 ttc atc atg ctg aat att tac tgt acc ctt ttg atc tgg aaa ttt att 152  
 Phe Ile Met Leu Asn Ile Tyr Cys Thr Leu Leu Ile Trp Lys Phe Ile  
 20 25 30 35  
 tat tca gct ttt ttc tgt tat att act tct ttg atg att ttc ccc ttt 200  
 Tyr Ser Ala Phe Phe Cys Tyr Ile Thr Ser Leu Met Ile Phe Pro Phe



	40	45	50	
agt ttt ttc tgt tct ttc ttt cta gac ctt ctt aaa gtc ata gtt tat				248
Ser Phe Phe Cys Ser Phe Phe Leu Asp Leu Leu Lys Val Ile Val Tyr				
	55	60	65	
atc ttc ttc ctt tat ctg tac tcc tca aga taa atgctaga agttgggtaa				299
Ile Phe Phe Leu Tyr Leu Tyr Ser Ser Arg *				
	70	75		
gccaggactt aaaccagct tgtagcttta taagctgggt tttgaacctc agttttctag				359
ttagtaaagt gatcatgaga ataacgacct caaaggatat catgaggatt aaattagatt				419
tttttaaagt ccttagcact atgcccagta catacagcat tcaataatgt taggaattgt				479
tgctgtcatg ttcactatta atttatttaa caaatattta ttgaatgcta atacaaatgt				539
gccatgctct tctaggtgac cccagtaag gtagaggact aagaagacat gagatttatg				599
tgaaaaagca tttttaaga agaccattgg caat				633

<210> 105  
 <211> 810  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (147)..(293)

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tctaattgatg ctatagagtt gttatagaaa gttgaatctt tgtcatctat tgaatgcttg	120
aaatttagct aaaagtgtct caggag atg ggc tac ctt ctg tgg tta gta ctg	173
Met Gly Tyr Leu Leu Trp Leu Val Leu	
1 5	
tct atc ttg gtg tgt aca gaa ttg gga ctt ggc agg ttg acc ttc cct	221
Ser Ile Leu Val Cys Thr Glu Leu Gly Leu Gly Arg Leu Thr Phe Pro	
10 15 20 25	
ctg gat tca gaa agc ccc agg act tct tat aaa gtt agg cca tgg gtc	269
Leu Asp Ser Glu Ser Pro Arg Thr Ser Tyr Lys Val Arg Pro Trp Val	
30 35 40	
gtc ttg gag gct tgg gtc tgg taa ataattgagc ctgagctcac aatcctgccc	323
Val Leu Glu Ala Trp Val Trp *	
45	
ctgggtccag gtggctgggc tgctgcccc aaaagcctga ccttcttggt cctgtggggtc	383
tgtcagtaag gcaggtagcc atagctggag agagacagcc accaggctgg gatcttgagc	443
agtcctaca tttctgtgta atcctggact aggcagggca tggagtagat ggaaaaatggc	503
ggccatcttg gaaatgtgcc ataacaactc acttttcaag accgtcccct agaggagaaa	563
agtaccgccc tgggtagctc aattaacgaa ttttcaagac ccaggccttg gcgctccttg	623

cccggagatc	cAACggagac	tttagtccga	cgccagagtg	gatcacagag	cggacaggga	683
tacactgaaa	aaaaacggtc	aggagggacg	ttgcgcccc	cgcttggtag	aacaggacga	743
ccgctggcct	cgcggagttg	aggccaataa	ccccgcggac	cccatgttga	cccggaagag	803
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<210> 106
<211> 746
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (324)..(734)
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[illegible]

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Cys Leu Ala Pro Leu Leu Val Pro Cys Lys Cys Ala Phe Pro Leu Tyr
      125              130              135

tgattatatt ct      746

<210> 107
<211> 930
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (81)..(779)

<400> 107
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cgatcgaggg tgcctcagcc      atg gca tgg atc cct ctc ttc ctc ggc gtc      110
      Met Ala Trp Ile Pro Leu Phe Leu Gly Val
      1              5              10

ctt gct tac tgc aca gga tcc gtg gcc tcc tat gag ctg act cag cca      158
Leu Ala Tyr Cys Thr Gly Ser Val Ala Ser Tyr Glu Leu Thr Gln Pro
      15              20              25

ccc tca gtg tcc gtg tcc cca gga cag aca gcc agc atc acc tgc tct      206
Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser
      30              35              40

gga gat aaa ttg ggg gat aaa tat gct tgc tgg tat cag cag aag cca      254
Gly Asp Lys Leu Gly Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro
      45              50              55

ggc cag tcc cct gtg ctg gtc atc tat caa gat agc aag cgg ccc tca      302
Gly Gln Ser Pro Val Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser
      60              65              70

ggg atc cct gag cga ttc tct ggc tcc aac tct ggg aac aca gcc act      350
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
      75              80              85              90

ctg acc atc agc ggg acc cag gct atg gat gag gct gac tat tac tgt      398
Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys
      95              100              105

cag gcg tgg gac agc agc act ctt tat gtc ttc gga act ggg acc aag      446
Gln Ala Trp Asp Ser Ser Thr Leu Tyr Val Phe Gly Thr Gly Thr Lys
      110              115              120

gtc acc gtc cta ggt cag ccc aag gcc aac ccc act gtc act ctg ttc      494
Val Thr Val Leu Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe
      125              130              135

ccg ccc tcc tct gag gag ctc caa gcc aac aag gcc aca cta gtg tgt      542
Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
      140              145              150

ctg atc agt gac ttc tac ccg gga gct gtg aca gtg gcc tgg aag gca      590
Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
      155              160              165              170

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gat ggc agc ccc gtc aag gcg gga gtg gag acc acc aaa ccc tcc aaa 638  
 Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys  
 175 180 185

cag agc aac aac aag tac gcg gcc agc agc tac ctg agc ctg acg cct 686  
 Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro  
 190 195 200

gag cag tgg aag tcc cac aga agc tac agc tgc cag gtc acg cat gaa 734  
 Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu  
 205 210 215

ggg agc acc gtg gag aag aca gtg gcc cct aca gaa tgt tca tag gtt 782  
 Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser \*  
 220 225 230

ctaaaccctc acctcccccc acgggagact agagctgcag gatcccaggg gaggggtctc 842

tcctcccacc ccaaggcatc aagcccttct cctgcactc aataaaccct caataaatat 902

tctcattgtc aatcaaaaaa aaaagtcg 930

<210> 108  
 <211> 3133  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (219) .. (1028)

<400> 108

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atgccaaagt ctatgtggct aaagtggact gcacggccca ctccgacgtg tgctccgccc 120

aggggggtgcg aggatacccc accttaaagc ttttcaagcc aggccaaagaa gctgtgaagt 180

accaggggtcc tcgggacttc cagacactgg aaaactgg atg ctg cag aca ctg 233  
 Met Leu Gln Thr Leu  
 1 5

aac gag gag cca gtg aca cca gag ccg gaa gtg gaa ccg ccc agt gcc 281  
 Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu Pro Pro Ser Ala  
 10 15 20

ccc gag ctg aag caa ggg ctg tat gag ctg tca gca agc aac ttt gag 329  
 Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser Ala Ser Asn Phe Glu  
 25 30 35

ctg cac gtt gca caa ggc gac cac ttt atc aag ttc ttc gct ccg tgg 377  
 Leu His Val Ala Gln Gly Asp His Phe Ile Lys Phe Phe Ala Pro Trp  
 40 45 50

tgt ggt cac tgc aaa gcc ctg gct cca acc tgg gag cag ctg gct ctg 425  
 Cys Gly His Cys Lys Ala Leu Ala Pro Thr Trp Glu Gln Leu Ala Leu  
 55 60 65

ggc ctt gaa cat tcc gaa act gtc aag att ggc aag gtt gat tgt aca 473  
 Gly Leu Glu His Ser Glu Thr Val Lys Ile Gly Lys Val Asp Cys Thr

70	75	80	85	
cag cac tat gaa ctc tgc tcc gga aac cag gtt cgt ggc tat ccc act				521
Gln His Tyr Glu Leu Cys Ser Gly Asn Gln Val Arg Gly Tyr Pro Thr				
	90	95	100	
ctt ctc tgg ttc cga gat ggg aaa aag gtg gat cag tac aag gga aag				569
Leu Leu Trp Phe Arg Asp Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys				
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cgg gat ttg gag tca ctg agg gag tac gtg gag tcg cag ctg cag cgc				617
Arg Asp Leu Glu Ser Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg				
	120	125	130	
aca gag act gga gcg acg gag acc gtc acg ccc tca gag gcc ccg gtg				665
Thr Glu Thr Gly Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val				
	135	140	145	
ctg gca gct gag ccc gag gct gac aag ggc act gtg ttg gca ctc act				713
Leu Ala Ala Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr				
	150	155	160	165
gaa aat aac ttc gat gac acc att gca gaa gga ata acc ttc atc aag				761
Glu Asn Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys				
	170	175	180	
ttt tat gct cca tgg tgt ggt cat tgt aag act ctg gct cct act tgg				809
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp				
	185	190	195	
gag gaa ctc tct aaa aag gaa ttc cct ggt ctg gcg ggg gtc aag atc				857
Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys Ile				
	200	205	210	
gcc gaa gta gac tgc act gct gaa cgg aat atc tgc agc aag tat tcg				905
Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys Tyr Ser				
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gta cga ggc tac ccc acg tta ttg ctt ttc cga gga ggg aag aaa gtc				953
Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly Lys Lys Val				
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agt gag cac agt gga ggc aga gac ctt gac tcg tta cac cgc ttt gtc				1001
Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu His Arg Phe Val				
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ctg agc caa gcg aaa gac gaa ctt tag gaaca cagttggagg tcacctctcc				1053
Leu Ser Gln Ala Lys Asp Glu Leu *				
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cggcagcca gaagttaatg tgctgggtcaa agaaccggac gcgtgggtcg acccggaat	3093
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&lt;210&gt; 109

&lt;211&gt; 1471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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1               5	
ctg ggg cca ggc tcc ggg ctt ggt gct gtc gtc tct caa cat ccg agc Leu Gly Pro Gly Ser Gly Leu Gly Ala Val Val Ser Gln His Pro Ser	160
10            15            20	
agg gtt atc tgt aag agt gga acc tct gtg aag atc gag tgc cgt tcc Arg Val Ile Cys Lys Ser Gly Thr Ser Val Lys Ile Glu Cys Arg Ser	208
25            30            35	
ctg gac ttt cag gcc aca act atg ttt tgg tat cgt cag ttc ccg aaa Leu Asp Phe Gln Ala Thr Thr Met Phe Trp Tyr Arg Gln Phe Pro Lys	256
40            45            50            55	
cag agt ctc atg ctg atg gca act tcc aat gag ggc tcc aag gcc aca Gln Ser Leu Met Leu Met Ala Thr Ser Asn Glu Gly Ser Lys Ala Thr	304
60                65                70	
tac gag caa ggc gtc gag aag gac aag ttt ctc atc aac cat gca agc Tyr Glu Gln Gly Val Glu Lys Asp Lys Phe Leu Ile Asn His Ala Ser	352
75            80            85	
ctg acc ttg tcc act ctg aca gtg acc agt gcc cat cct gaa gac agc Leu Thr Leu Ser Thr Leu Thr Val Thr Ser Ala His Pro Glu Asp Ser	400
90            95            100	
agc ttc tac atc tgc agt gct aga gag tcg act agc gat cca aaa aat Ser Phe Tyr Ile Cys Ser Ala Arg Glu Ser Thr Ser Asp Pro Lys Asn	448
105            110            115	
gag cag ttc ttc ggg cca ggg aca cgg ctc acg gtc aca gag gac ctg Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Thr Glu Asp Leu	496
120            125            130            135	
aaa aac gtg ttc cca ccc gag gtc gct gtg ttt gag cca tca gaa gca Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala	544
140                145                150	
gag atc tcc cac acc caa aag gcc aca ctg gtg tgc ctg gcc aca ggc Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly	592
155            160            165	
ttc tac ccc gac cac gtg gag ctg agc tgg tgg gtg aat ggg aag gag Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu	640
170            175            180	
gtg cac agt ggg gtc agc aca gac ccg cag ccc ctc aag gag cag ccc Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro	688
185            190            195	
gcc ctc aat gac tcc aga tac tgc ctg agc agc cgc ctg agg gtc tcg Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser	736
200            205            210            215	
qcc acc ttc tqg cag aac ccc cgc aac cac ttc cgctgt caa gtc cag	784

Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln  
 220 225 230

ttc tac ggg ctc tcg gag aat gac gag tgg acc cag gat agg gcc aaa 832  
 Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys  
 235 240 245

cct gtc acc cag atc gtc agc gcc gag gcc tgg ggt aga gca gac tgt 880  
 Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys  
 250 255 260

ggc ttc acc tcc gag tct tac cag caa ggg gtc ctg tct gcc acc atc 928  
 Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile  
 265 270 275

ctc tat gag atc ttg cta ggg aag gcc acc ttg tat gcc gtg ctg gtc 976  
 Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val  
 280 285 290 295

agt gcc ctc gtg ctg atg gcc atg gtc aag aga aag gat tcc aga ggc 1024  
 Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly  
 300 305 310

tagctccaaa accatcccag gtcattcttc atcctcaccc aggattctcc tgtacctgct 1084

cccaatctgt gttcctaaaa gtgattctca ctctgcttct catctcctac ttacatgaat 1144

acttctctct tttttctgtt tccctgaaga ttgagctccc aacccccaag tacgaaatag 1204

gctaaaccaa taaaaaattg tgtgttgggc ctgggtgcat ttcaggagtg tctgtggagt 1264

tctgctcatc actgacctat cttctgattt agggaaagca gcattccctt ggacatctga 1324

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gccctggcgg atggagac atg ctg ccc ctg ctg ctg ctg ccc ctg ctg tgg 111  
 Met Leu Pro Leu Leu Leu Leu Pro Leu Leu Trp  
 1 5 10

ggg ggg tcc ctg cag gag aag cca gtg tac gag ctg caa gtg cag aag 159  
 Gly Gly Ser Leu Gln Glu Lys Pro Val Tyr Glu Leu Gln Val Gln Lys  
 15 20 25

tcg gtg acg gtg cag gag gcc ctg tgc gtc ctt gtg ccc tgc tcc ttc 207  
 Ser Val Thr Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe



30	35	40	
tct tac ccc tgg aga tcc tgg tat tcc tct ccc cca ctc tac gtc tac			255
Ser Tyr Pro Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr			
45	50	55	
tgg ttc cgg gac ggg gag atc cca tac tac gct gag gtt gtg gcc aca			303
Trp Phe Arg Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr			
60	65	70	75
aac aac cca gac aga aga gtg aag cca gag acc cag ggc cga ttc cgc			351
Asn Asn Pro Asp Arg Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg			
80	85	90	
ctc ctt ggg gat gtc cag aag aag aac tgc tcc ctg agc atc gga gat			399
Leu Leu Gly Asp Val Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp			
95	100	105	
gcc aga atg gag gac acg gga agc tat ttc ttc cgc gtg gag aga gga			447
Ala Arg Met Glu Asp Thr Gly Ser Tyr Phe Phe Arg Val Glu Arg Gly			
110	115	120	
agg gat gta aaa tat agc tac caa cag aat aag ctg aac ttg gag gtg			495
Arg Asp Val Lys Tyr Ser Tyr Gln Gln Asn Lys Leu Asn Leu Glu Val			
125	130	135	
aca gcc ctg ata gag aaa ccc gac atc cac ttt ctg gag cct ctg gag			543
Thr Ala Leu Ile Glu Lys Pro Asp Ile His Phe Leu Glu Pro Leu Glu			
140	145	150	155
tcc ggc cgc ccc aca agg ctg agc tgc agc ctt cca gga tcc tgt gaa			591
Ser Gly Arg Pro Thr Arg Leu Ser Cys Ser Leu Pro Gly Ser Cys Glu			
160	165	170	
gcg gga cca cct ctc aca ttc tcc tgg acg ggg aat gcc ctc agc ccc			639
Ala Gly Pro Pro Leu Thr Phe Ser Trp Thr Gly Asn Ala Leu Ser Pro			
175	180	185	
ctg gac ccc gag acc acc cgc tcc tcg gag ctc acc ctc acc ccc agg			687
Leu Asp Pro Glu Thr Thr Arg Ser Ser Glu Leu Thr Leu Thr Pro Arg			
190	195	200	
ccc gag gac cat ggc acc aac ctc acc tgt cag atg aaa cgc caa gga			735
Pro Glu Asp His Gly Thr Asn Leu Thr Cys Gln Met Lys Arg Gln Gly			
205	210	215	
gct cag gtg acc acg gag aga act gtc cag ctc aat gtc tcc tat gct			783
Ala Gln Val Thr Thr Glu Arg Thr Val Gln Leu Asn Val Ser Tyr Ala			
220	225	230	235
cca cag acc atc acc atc ttc agg aac ggc ata gcc cta gag atc ctg			831
Pro Gln Thr Ile Thr Ile Phe Arg Asn Gly Ile Ala Leu Glu Ile Leu			
240	245	250	
caa aac acc tca tac ctt ccg gtc ctg gag ggc cag gct ctg cgg ctg			879
Gln Asn Thr Ser Tyr Leu Pro Val Leu Glu Gly Gln Ala Leu Arg Leu			
255	260	265	
ctc tgt gat gct ccc agc aac ccc cct gca cac ctg agc tgg ttc cag			927
Leu Cys Asp Ala Pro Ser Asn Pro Pro Ala His Leu Ser Trp Phe Gln			
270	275	280	
ggc tcc cct gcc ctg aac gcc acc ccc atc tcc aat acc ggg atc ttg			975
Gly Ser Pro Ala Leu Asn Ala Thr Pro Ile Ser Asn Thr Gly Ile Leu			

285	290	295	
gag ctt cgt cga gta	agg tct gca gaa gaa gga	ggc ttc acc tgc cgc	1023
Glu Leu Arg Arg Val	Arg Ser Ala Glu Glu Gly	Gly Phe Thr Cys Arg	
300	305	310 315	
gct cag cac ccg ctg	ggc tcc ctg caa att ttt	ctg aat ctc tca gtt	1071
Ala Gln His Pro Leu	Gly Ser Leu Gln Ile Phe	Leu Asn Leu Ser Val	
320	325	330	
tac tcc ctc cca cag ttg	ctg ggc ccc tcc tgc tcc	tgg gag gct gag	1119
Tyr Ser Leu Pro Gln	Leu Leu Gly Pro Ser	Cys Ser Trp Glu Ala Glu	
335	340	345	
ggc ctg cac tgc aga tgc	tcc ttt cga gcc cgg ccg	gcc ccc tcc ctg	1167
Gly Leu His Cys Arg	Cys Ser Phe Arg Ala Arg	Pro Ala Pro Ser Leu	
350	355	360	
tgc tgg cgg ctt gag gag	aag ccg ctg gag ggg aac	agc agc cag ggc	1215
Cys Trp Arg Leu Glu	Glu Lys Pro Leu Glu Gly	Asn Ser Ser Gln Gly	
365	370	375	
tca ttc aag gtc aac tcc	agc tca gct ggg ccc tgg	gcc aac agc tcc	1263
Ser Phe Lys Val Asn	Ser Ser Ser Ala Gly	Pro Trp Ala Asn Ser Ser	
380	385	390 395	
ctg atc ctc cac ggg ggg	ctc agc tcc gac ctc aaa	gtc agc tgc aag	1311
Leu Ile Leu His Gly	Gly Leu Ser Ser Asp	Leu Lys Val Ser Cys Lys	
400	405	410	
gcc tgg aac atc tat ggg	tcc cag agc ggc tct gtc	ctg ctg ctg caa	1359
Ala Trp Asn Ile Tyr	Gly Ser Gln Ser Gly	Ser Val Leu Leu Leu Gln	
415	420	425	
ggg aga tgc aac ctc ggg	aca gga gtg gtt cct gca	gcc ctt ggt ggt	1407
Gly Arg Ser Asn Leu	Gly Thr Gly Val Val	Pro Ala Ala Leu Gly Gly	
430	435	440	
gct ggt gtc atg gcc ctg	ctc tgt atc tgt ctg tgc	ctc atc ttc ttt	1455
Ala Gly Val Met Ala	Leu Leu Cys Ile Cys	Leu Cys Leu Ile Phe Phe	
445	450	455	
tta ata gtg aaa gcc cgc	agg aag caa gca gct ggg	aga cca gag aaa	1503
Leu Ile Val Lys Ala	Arg Arg Lys Gln Ala	Gly Arg Pro Glu Lys	
460	465	470 475	
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Met Asp Asp Glu Asp	Pro Ile Met Gly Thr	Ile Thr Ser Gly Ser Arg	
480	485	490	
aag aag ccc tgg cca gac	agc ccc gga gat caa gca	tct cct cct ggg	1599
Lys Lys Pro Trp Pro	Asp Ser Pro Gly Asp	Gln Ala Ser Pro Pro Gly	
495	500	505	
gat gcc cct ccc ttg gaa	gaa caa aag gag ctc cat	tat gcc tcc ctt	1647
Asp Ala Pro Pro Leu	Glu Glu Lys Glu Leu	His Tyr Ala Ser Leu	
510	515	520	
agt ttt tct gag atg aag	tcg agg gag cct aag	gac cag gag gcc cca	1695
Ser Phe Ser Glu Met	Lys Ser Arg Glu Pro	Lys Asp Gln Glu Ala Pro	
525	530	535	
agc acc acg gag tac tcg	gag atc aag aca agc aag	tga ggatttgccc	1744
Ser Thr Thr Glu Tyr	Ser Glu Ile Lys Thr	Ser Lys *	

540

545

550

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1759

&lt;210&gt; 111

&lt;211&gt; 4205

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (548) .. (3733)

&lt;400&gt; 111

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Met Leu Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro

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5

10

agt acc gct gac ttg cct ggc tcc cct gtc agc aac aac ttc atg ggc 637

Ser Thr Ala Asp Leu Pro Gly Ser Pro Val Ser Asn Asn Phe Met Gly  
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tgc ctt aaa gag gtt gtt tat aag aat aat gac atc cgt ctg gag ctg 685

Cys Leu Lys Glu Val Val Tyr Lys Asn Asn Asp Ile Arg Leu Glu Leu  
35 40 45

tct cgc ctg gcc cgg att gcg gac acc aag atg aaa atc tat ggc gaa 733

Ser Arg Leu Ala Arg Ile Ala Asp Thr Lys Met Lys Ile Tyr Gly Glu  
50 55 60

gtt gtg ttt aag tgt gag aat gtg gcc aca ctg gac ccc atc aac ttt 781

Val Val Phe Lys Cys Glu Asn Val Ala Thr Leu Asp Pro Ile Asn Phe  
65 70 75

gag acc cca gag gct tac atc agc ttg ccc aag tgg aac act aaa cgt 829

Glu Thr Pro Glu Ala Tyr Ile Ser Leu Pro Lys Trp Asn Thr Lys Arg  
80 85 90

atg ggc tcc atc tcc ttt gac ttc cgc acc aca gag ccc aat ggc ctg 877

Met Gly Ser Ile Ser Phe Asp Phe Arg Thr Thr Glu Pro Asn Gly Leu  
95 100 105 110

atc ctc ttc act cat gga aag ccc caa gag agg aag gat gct cgg agc 925

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Gln	Lys	Asn	Thr	Lys	Val	Asp	Phe	Phe	Ala	Val	Glu	Leu	Leu	Asp	Gly		
			130					135					140				
aac	ctg	tac	ttg	ctg	ctt	gac	atg	ggc	tct	ggc	acc	atc	aaa	gtg	aaa	1021	
Asn	Leu	Tyr	Leu	Leu	Leu	Asp	Met	Gly	Ser	Gly	Thr	Ile	Lys	Val	Lys		
		145					150					155					
gcc	act	cag	aag	aaa	gcc	aat	gat	ggg	gaa	tgg	tac	cat	gtg	gac	att	1069	
Ala	Thr	Gln	Lys	Lys	Ala	Asn	Asp	Gly	Glu	Trp	Tyr	His	Val	Asp	Ile		
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Gln	Arg	Asp	Gly	Arg	Ser	Gly	Thr	Ile	Ser	Val	Asn	Ser	Arg	Arg	Thr		
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Pro	Phe	Thr	Ala	Ser	Gly	Glu	Ser	Glu	Ile	Leu	Asp	Leu	Glu	Gly	Asp		
			195					200					205				
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Met	Tyr	Leu	Gly	Gly	Leu	Pro	Glu	Asn	Arg	Ala	Gly	Leu	Ile	Leu	Pro		
		210					215					220					
acc	gag	ctg	tgg	act	gcc	atg	ctc	aac	tat	ggc	tac	gtg	ggc	tgc	atc	1261	
Thr	Glu	Leu	Trp	Thr	Ala	Met	Leu	Asn	Tyr	Gly	Tyr	Val	Gly	Cys	Ile		
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Met	Tyr	Met	Lys	Ile	Ile	Met	Pro	Met	Val	Met	His	Thr	Glu	Ala	Glu		
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Leu Gly Asp Phe Leu Gln Leu His Ile Glu Gln Gly Lys Ile Gly Val	
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Val Phe Asn Ile Gly Thr Val Asp Ile Ser Ile Lys Glu Glu Arg Thr	
785 790 795	
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Pro Val Asn Asp Gly Lys Tyr His Val Val Arg Phe Thr Arg Asn Gly	
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cca ttc acc gcc agt ggg gag agc gag atc ctg gac ctg gaa gga gac Pro Phe Thr Ala Ser Gly Glu Ser Glu Ile Leu Asp Leu Glu Gly Asp			1165
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Leu Lys Leu Thr Val Asp Asp Asp Val Ala Glu Gly Thr Met Val Gly			
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Ile Ile Ala Asp Pro Val Thr Phe Lys Thr Lys Ser Ser Tyr Leu Ser			
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aat gac agg ccc agc acg cgg tct gac cgc ctt gcc gtg ggc ttc agc Asn Asp Arg Pro Ser Thr Arg Ser Asp Arg Leu Ala Val Gly Phe Ser 735 740 745 750			2797
acc act gtg aag gat ggc atc ttg gtc cgc atc gac agt gct cca gga Thr Thr Val Lys Asp Gly Ile Leu Val Arg Ile Asp Ser Ala Pro Gly 755 760 765			2845
ctt ggt gac ttc ctc cag ctt cac ata gaa cag ggg aaa att gga gtt Leu Gly Asp Phe Leu Gln Leu His Ile Glu Gln Gly Lys Ile Gly Val 770 775 780			2893
gtc ttc aac att ggc aca gtt gac atc tcc atc aaa gag gag aga acc Val Phe Asn Ile Gly Thr Val Asp Ile Ser Ile Lys Glu Glu Arg Thr 785 790 795			2941
cct gta aat gac ggc aaa tac cat gtg gta cgc ttc acc agg aac ggc Pro Val Asn Asp Gly Lys Tyr His Val Val Arg Phe Thr Arg Asn Gly 800 805 810			2989
ggc aac gcc acc ctg cag gtg gac aac tgg cca gtg aat gaa cat tat Gly Asn Ala Thr Leu Gln Val Asp Asn Trp Pro Val Asn Glu His Tyr 815 820 825 830			3037
cct aca ggc aac act gat aat gaa cgc ttc caa atg gta aaa cag aaa Pro Thr Gly Asn Thr Asp Asn Glu Arg Phe Gln Met Val Lys Gln Lys 835 840 845			3085
atc ccc ttc aaa tat aat cgg cct gta gag gag tgg ctg cag gaa aaa Ile Pro Phe Lys Tyr Asn Arg Pro Val Glu Glu Trp Leu Gln Glu Lys 850 855 860			3133
ggc cgg cag tta acc atc ttc aac act cag gcg caa ata gcc att ggt Gly Arg Gln Leu Thr Ile Phe Asn Thr Gln Ala Gln Ile Ala Ile Gly 865 870 875			3181
gga aag gac aaa gga cgc ctc ttc caa ggc caa ctc tct ggg ctc tat Gly Lys Asp Lys Gly Arg Leu Phe Gln Gly Gln Leu Ser Gly Leu Tyr 880 885 890			3229
tat gat ggt ttg aaa gta ctg aac atg gcg gct gag aac aac ccc aat Tyr Asp Gly Leu Lys Val Leu Asn Met Ala Ala Glu Asn Asn Pro Asn			3277

895	900	905	910	
att aaa atc aat gga agt gtt cgg ctg gtt gga gaa gtc cca tca att				3325
Ile Lys Ile Asn Gly Ser Val Arg Leu Val Gly Glu Val Pro Ser Ile				
915		920	925	
ttg gga aca aca cag acg acc tcc atg cca cca gaa atg tct act act				3373
Leu Gly Thr Thr Gln Thr Thr Ser Met Pro Pro Glu Met Ser Thr Thr				
930		935	940	
gtc atg gaa acc act act aca atg gcg act acc aca acc cgt aag aat				3421
Val Met Glu Thr Thr Thr Met Ala Thr Thr Thr Thr Arg Lys Asn				
945		950	955	
cgc tct aca gcc agc att cag cca aca tca gat gat ctt gtt tca tct				3469
Arg Ser Thr Ala Ser Ile Gln Pro Thr Ser Asp Asp Leu Val Ser Ser				
960		965	970	
gct gaa tgt tca agt gat gat gaa gac ttt gtt gaa tgt gag ccg agt				3517
Ala Glu Cys Ser Ser Asp Asp Glu Asp Phe Val Glu Cys Glu Pro Ser				
975		980	985	990
aca gca aac ccc acg gag ccg gga atc aga ccg gtt ccg ggg gcc tca				3565
Thr Ala Asn Pro Thr Glu Pro Gly Ile Arg Arg Val Pro Gly Ala Ser				
995		1000	1005	
gag gtg atc ccg gag tcg agc agc aca aca ggg atg gtc gtc ggc att				3613
Glu Val Ile Arg Glu Ser Ser Ser Thr Thr Gly Met Val Val Gly Ile				
1010		1015	1020	
gtg gct gct gcc gcc ctc tgc atc ttg atc ctc ctg tac gcc atg tac				3661
Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu Leu Tyr Ala Met Tyr				
1025		1030	1035	
aag tac agg aac agg gac gag ggg tcc tat caa gtg gac gag acg ccg				3709
Lys Tyr Arg Asn Arg Asp Glu Gly Ser Tyr Gln Val Asp Glu Thr Arg				
1040		1045	1050	
aac tac atc agc aac tcc gcc cag agc aac ggc acg ctc atg aag gag				3757
Asn Tyr Ile Ser Asn Ser Ala Gln Ser Asn Gly Thr Leu Met Lys Glu				
1055		1060	1065	1070
aag cag cag agc tcg aag agc ggc cac aag aaa cag aaa aac aag gac				3805
Lys Gln Gln Ser Ser Lys Ser Gly His Lys Lys Gln Lys Asn Lys Asp				
1075		1080	1085	
agg gag tat tac gtg taa acatgc gaacactgct cacacgcgag ttttcacagt				3859
Arg Glu Tyr Tyr Val *				
1090				
tattttctatc cagcctatg aatcttttga cgggtgagatc tcacagatgt cagaactgct				3919
ggaactatga aatgggggtat ataaccacga ctctgggtggg gaaaaccggt ttttaaagga				3979
cacacacaca cacagcgatg catctctctc taaagctcag ccacggctgc ggcaaggctc				4039
cagcggctgc tgggagacag aagggtttgt gccctgctgt atcataaagc acacacttag				4099
cgctctggag ccggacgggtg gctccaccac ttccgcaggc ctagaaaactt ccttctccgg				4159
aggacctttt actaaaaggt agaagacttc atggcttact tgttccataa ctccaagtga				4219
gtctgtaatg tttgtgaagc ttgactgtaa ccatgttttt tctgtttaat tatgtaaaaa				4279

acaaaactac aacaac

4295

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 <212> DNA  
 <213> Homo sapiens

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 <222> (183)..(323)

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 ggcccacgtt ttaccaccag cttgaggctg aggtgggctc tgtgctcctg gtgctgccaa 120  
 gcccttgccct gctatccaca ggcctgaggt gcaggcctcc ctacagacagt gacgggttac 180  
 ac atg ggg tcc ctg atg cca ctc aga ccc ctg gca ctc cac act gcc 227  
 Met Gly Ser Leu Met Pro Leu Arg Pro Leu Ala Leu His Thr Ala  
 1 5 10 15  
 ctt ggg gct gct ctg aac ttc tcc ttg cct tgt gag tgg tca aca ctg 275  
 Leu Gly Ala Ala Leu Asn Phe Ser Leu Pro Cys Glu Trp Ser Thr Leu  
 20 25 30  
 ccc agt gca agt gag gct gga agg ctt tgg gga cct cca agt ttt cag 323  
 Pro Ser Ala Ser Glu Ala Gly Arg Leu Trp Gly Pro Pro Ser Phe Gln  
 35 40 45  
 taaccctgtg ttacccaag ggaattgttt tgcccacaga ttttagcagg ttggagcttt 383  
 caatctgtcc tgttttgggg gtttgtggct tagatgctgg gatgagagaa gccacctaaa 443  
 tccaaaggaa ggagtttgca gcggtgtgca tcagccagcc agcagacacc cagctgtcat 503  
 ttgcattctc agcaacaaaa gccttgcccc ctcatgacta tgggtgtcac ctgccctgtg 563  
 tggcccaggg ccagggtgaa gccatccatg actgagtaaa atcagagtag catcctgctc 623  
 tgctctcctg ttgcaaggg taggagttgg ctgaaaacca gctgaagagt ggcaagtgtg 683  
 aatgct 689

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (118)..(1494)

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 atg gct tgg gca agt agg ctg ggc ctg ctg ctg gca ctg ctg ctg ccc 165

Met	Ala	Trp	Ala	Ser	Arg	Leu	Gly	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Pro	
1				5				10						15		
gtg	gtc	ggg	gcc	tcc	acg	cca	ggc	acc	gtg	gtc	cga	ctc	aac	aag	gca	213
Val	Val	Gly	Ala	Ser	Thr	Pro	Gly	Thr	Val	Val	Arg	Leu	Asn	Lys	Ala	
			20				25					30				
gca	ttg	agc	tac	gtg	tct	gaa	att	ggg	aaa	gcc	cct	ctc	cag	cgg	gcc	261
Ala	Leu	Ser	Tyr	Val	Ser	Glu	Ile	Gly	Lys	Ala	Pro	Leu	Gln	Arg	Ala	
	35					40				45						
ctg	cag	gtc	act	gtc	cct	cat	ttc	ctg	gac	tgg	agt	gga	gag	gcg	ctt	309
Leu	Gln	Val	Thr	Val	Pro	His	Phe	Leu	Asp	Trp	Ser	Gly	Glu	Ala	Leu	
	50					55				60						
cag	ccc	acc	agg	atc	cgg	att	ctg	aat	gtc	cat	gtg	ccc	cgc	ctc	cac	357
Gln	Pro	Thr	Arg	Ile	Arg	Ile	Leu	Asn	Val	His	Val	Pro	Arg	Leu	His	
65				70					75					80		
ctg	aaa	ttc	att	gct	ggg	ttc	gga	gtg	cgc	ctg	ctg	gca	gca	gct	aat	405
Leu	Lys	Phe	Ile	Ala	Gly	Phe	Gly	Val	Arg	Leu	Leu	Ala	Ala	Ala	Asn	
			85					90						95		
ttt	act	ttc	aag	gtc	ttt	cgc	gcc	cca	gag	ccc	ctg	gag	ctg	acg	ctg	453
Phe	Thr	Phe	Lys	Val	Phe	Arg	Ala	Pro	Glu	Pro	Leu	Glu	Leu	Thr	Leu	
			100					105						110		
cct	gtg	gaa	ctg	ctg	gct	gac	acc	cgc	gtg	acc	cag	agc	tcc	atc	agg	501
Pro	Val	Glu	Leu	Leu	Ala	Asp	Thr	Arg	Val	Thr	Gln	Ser	Ser	Ile	Arg	
	115					120					125					
acc	cct	gtg	gtc	agc	atc	tct	gcc	tgc	tct	tta	ttc	tcg	ggc	cac	gcc	549
Thr	Pro	Val	Val	Ser	Ile	Ser	Ala	Cys	Ser	Leu	Phe	Ser	Gly	His	Ala	
	130					135					140					
aac	gag	ttt	gat	ggc	agt	aac	agc	acc	tcc	cac	gcg	ctg	ctg	gtc	ctg	597
Asn	Glu	Phe	Asp	Gly	Ser	Asn	Ser	Thr	Ser	His	Ala	Leu	Leu	Val	Leu	
145				150					155					160		
gtg	cag	aag	cac	att	aaa	gct	gtc	ttg	agt	aac	aag	ctg	tgc	ctg	agc	645
Val	Gln	Lys	His	Ile	Lys	Ala	Val	Leu	Ser	Asn	Lys	Leu	Cys	Leu	Ser	
			165					170						175		
atc	tcc	aac	ctg	gtg	cag	ggg	gtc	aat	gtc	cac	ctg	ggc	acc	tta	att	693
Ile	Ser	Asn	Leu	Val	Gln	Gly	Val	Asn	Val	His	Leu	Gly	Thr	Leu	Ile	
			180					185						190		
ggc	ctc	aac	ccc	gtg	ggg	cct	gag	tcc	cag	atc	cgc	tat	tcc	atg	gtc	741
Gly	Leu	Asn	Pro	Val	Gly	Pro	Glu	Ser	Gln	Ile	Arg	Tyr	Ser	Met	Val	
	195					200					205					
agt	gtg	ccc	act	gtc	acc	agt	gac	tac	att	tcc	ctg	gaa	gtc	aat	gct	789
Ser	Val	Pro	Thr	Val	Thr	Ser	Asp	Tyr	Ile	Ser	Leu	Glu	Val	Asn	Ala	
	210					215					220					
gtt	ctc	ttc	ctg	ctg	ggc	aag	ccc	atc	atc	ctg	ccc	acg	gat	gcc	acc	837
Val	Leu	Phe	Leu	Leu	Gly	Lys	Pro	Ile	Ile	Leu	Pro	Thr	Asp	Ala	Thr	
225					230					235				240		
cct	ttt	gtg	ttg	cca	agg	cat	gtg	ggg	acc	gag	ggc	tcc	atg	gcc	acc	885
Pro	Phe	Val	Leu	Pro	Arg	His	Val	Gly	Thr	Glu	Gly	Ser	Met	Ala	Thr	
			245					250						255		
gtg	ggc	ctc	tcc	cag	cag	ctg	ttt	gac	tct	gcg	ctc	ctg	ctg	ctg	cag	933

Val Gly Leu Ser Gln Gln Leu Phe Asp Ser Ala Leu Leu Leu Leu Gln	
260 265 270	
aag gcc ggt gcc ctc aac ctg gac atc aca ggg cag ctg agg tcg gat	981
Lys Ala Gly Ala Leu Asn Leu Asp Ile Thr Gly Gln Leu Arg Ser Asp	
275 280 285	
gac aac ctg ctg aac acc tct gct ctg ggc cgg ctc atc ccg gag gtg	1029
Asp Asn Leu Leu Asn Thr Ser Ala Leu Gly Arg Leu Ile Pro Glu Val	
290 295 300	
gcc cgc cag ttt ccc gag ccc atg cct gtg gtg ctc aag gtg cgg ctg	1077
Ala Arg Gln Phe Pro Glu Pro Met Pro Val Val Leu Lys Val Arg Leu	
305 310 315 320	
ggt gcc aca cct gtg gcc atg ctc cac aca aac aac gcc acc ctg cgg	1125
Gly Ala Thr Pro Val Ala Met Leu His Thr Asn Asn Ala Thr Leu Arg	
325 330 335	
ctg cag ccc ttc gtg gag gtc ctg gcc aca gcc tcc aac tcg gct ttc	1173
Leu Gln Pro Phe Val Glu Val Leu Ala Thr Ala Ser Asn Ser Ala Phe	
340 345 350	
cag tcc ctc ttc tcc ctg gat gtg gta gtg aac ttg aga ctc cag ctc	1221
Gln Ser Leu Phe Ser Leu Asp Val Val Val Asn Leu Arg Leu Gln Leu	
355 360 365	
tct gtg tcc aag gtg aag ctt cag ggg acc acg tct gtg ctg ggg gat	1269
Ser Val Ser Lys Val Lys Leu Gln Gly Thr Thr Ser Val Leu Gly Asp	
370 375 380	
gtc cag ctc acg gtg gcc tcc tcc aac gtg ggc ttc att gat aca gat	1317
Val Gln Leu Thr Val Ala Ser Ser Asn Val Gly Phe Ile Asp Thr Asp	
385 390 395 400	
cag gtg cgc aca ctg atg ggc acc gtt ttt gag aag ccc ctg ctg gac	1365
Gln Val Arg Thr Leu Met Gly Thr Val Phe Glu Lys Pro Leu Leu Asp	
405 410 415	
cat ctc aat gct ctc ttg gcc atg gga att gcc ctc cct ggt gtg gtc	1413
His Leu Asn Ala Leu Leu Ala Met Gly Ile Ala Leu Pro Gly Val Val	
420 425 430	
aac ctc cac tat gtt gcc cct gag atc ttt gtc tat gag ggc tac gtg	1461
Asn Leu His Tyr Val Ala Pro Glu Ile Phe Val Tyr Glu Gly Tyr Val	
435 440 445	
gtg ata tcc agt gga ctc ttc tac cag agc tga ggcaagac cactgggagg	1512
Val Ile Ser Ser Gly Leu Phe Tyr Gln Ser *	
450 455	
cctgagagtg ggccagctcg ctgctcaggc gaattttctca tttcaagcca ctggggaaac	1572
tgaggcaaaaa ccatacttag tcatcaccaa caagctggac tgcttagctg ggctgtttta	1632
tcttccctga gtgcttgggt ctccctccct cacttotgcc ctttcccttc ctccctctct	1692
tctcctccct cttccctcat ctccccctc cttcctctgc cccacccag gggggagcag	1752
actgctctc caggctgtat agacctgcc tcttgatta aacaacttct cttgagctgc	1812
aaaaaaaaa	1822

<210> 115  
 <211> 674  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (190) .. (390)

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 gataggtgca gaaatttcag taaaaataat gtgacatcgg cagagctgtc atagatctgg 120  
 gatatggctg gaaggacata gagtaaatga tcggtctggt tcatcgctaa aggagactta 180  
 ggaacctag atg aag ttg gta ctt ctg aga aag aca tct ctt tct gtt 228  
 Met Lys Leu Val Leu Leu Arg Lys Thr Ser Leu Ser Val  
 1 5 10  
 ttc act act cta ttc tca gta tcc agt tct cag tac cca gtt ctc agt 276  
 Phe Thr Thr Leu Phe Ser Val Ser Ser Ser Gln Tyr Pro Val Leu Ser  
 15 20 25  
 acc tct att tgt aat act cct gta ttt agt act ttg ttt tta gtg tcc 324  
 Thr Ser Ile Cys Asn Thr Pro Val Phe Ser Thr Leu Phe Leu Val Ser  
 30 35 40 45  
 tgt tct gtt aac cct ctt cct agt acc gta ttt tta gta ctg cta tac 372  
 Cys Ser Val Asn Pro Leu Pro Ser Thr Val Phe Leu Val Leu Leu Tyr  
 50 55 60  
 tca gtt gcc tgt ctg tag taccct tgtacgtagt actcttttct tacaactctg 426  
 Ser Val Ala Cys Leu \*  
 65  
 ttcccagtac ccctatgttt agtcccttgt tctcatgttc tcaactaccc aataacttaat 486  
 atactttgtt ctgagtatcc ttgttgtag taccctgttc tcaactaccc ttttcttagt 546  
 acccctgagg ggggaaaaaa aggatgataa tggggataaa gtctcaaaaa acttttggat 606  
 tgtttgatgtt gaactgagtc aaaggtaaaa ccagtgttct ggagttcgac ttctgggtgc 666  
 aaatccct 674

<210> 116  
 <211> 1029  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (461) .. (982)

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 tgtgcaaadc tagaaaaagt gcccttccct ctggctcctg cagttccagg gtgcccaggc 120



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ccccagccaa gagcgtgtac aggtggccct gctgacacac agaatccttg ggagaacaaa      180
gcctccccgg ggttcgggga caggtggatg ggaggtagtc ctggccagag gtatctgggg      240
aggctggggg ccttcgggg tgaggcaggg caaggggtgtg agtcactgcc aggctgccaa      300
agctcactct gcagctgtcc agtcccctgg ggtagcccca agcctgtcct ttagggaggt      360
ggcagccgga gtctgaactg tcctggggga ccaagcagga gcttaagatg ggcaagacct      420
ggggccctgg gcagacgcat caaagcaggc agaagcaggc  atg gcc agc agg aag      475
                                         Met Ala Ser Arg Lys
                                         1           5

acc aag aag aag gaa ggg ggt gcc ctc cgg gcc cag aga gcc tca tcc      523
Thr Lys Lys Lys Glu Gly Gly Ala Leu Arg Ala Gln Arg Ala Ser Ser
                        10                        15                        20

aat gtc ttc tcc aac ttt gag cag act cag atc cag gag ttc aag gag      571
Asn Val Phe Ser Asn Phe Glu Gln Thr Gln Ile Gln Glu Phe Lys Glu
                        25                        30                        35

gca ttc aca ctc atg gat cag aac cga gat ggc ttc att gac aag gag      619
Ala Phe Thr Leu Met Asp Gln Asn Arg Asp Gly Phe Ile Asp Lys Glu
                        40                        45                        50

gac ctg aag gac acc tat gcc tcc ctg ggc aag acc aac gtc aag gac      667
Asp Leu Lys Asp Thr Tyr Ala Ser Leu Gly Lys Thr Asn Val Lys Asp
                        55                        60                        65

gac gag ctg gac gcc atg ctc aaa gag gcc tcg ggg ccc atc aac ttc      715
Asp Glu Leu Asp Ala Met Leu Lys Glu Ala Ser Gly Pro Ile Asn Phe
                        70                        75                        80                        85

acc atg ttt ctg aac ctg ttt ggg gag aag ctg agc ggt acc gac gcc      763
Thr Met Phe Leu Asn Leu Phe Gly Glu Lys Leu Ser Gly Thr Asp Ala
                        90                        95                        100

gag gag acc att ctt aac gcc ttc aag atg ctg gac ccg gac ggg aaa      811
Glu Glu Thr Ile Leu Asn Ala Phe Lys Met Leu Asp Pro Asp Gly Lys
                        105                        110                        115

ggg aaa atc aac aag gag tac atc aag cgt ctg ctg atg tcc cag gct      859
Gly Lys Ile Asn Lys Glu Tyr Ile Lys Arg Leu Leu Met Ser Gln Ala
                        120                        125                        130

gac aag atg acg gcg gaa gag gtg gac cag atg ttc cag ttc gcc tcc      907
Asp Lys Met Thr Ala Glu Glu Val Asp Gln Met Phe Gln Phe Ala Ser
                        135                        140                        145

atc gat gtg gcg ggc aac ctg gac tac aag gcg ctc agc tac gtg atc      955
Ile Asp Val Ala Gly Asn Leu Asp Tyr Lys Ala Leu Ser Tyr Val Ile
                        150                        155                        160                        165

acc cac ggg gag gag aag gag gag tga gaccc agccgggtca ataaacctgg      1007
Thr His Gly Glu Lys Glu Glu *
                        170

acgcttgga aaaaaaaaaa aa      1029

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<210> 117  
 <211> 878  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (382)..(573)

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aagagctgtc tggccatctt ctttgaacag atgcgtgtgg ctgccctgcc gggatgatta      120
cagcactatg gaactaatat tctttgaatg atgcgctctt attatttgaa aaatcaggag      180
gcctgggtctt caggattccc ctctcttccc actccccatc ctcccttgaga gcagtatata      240
ctgggaatgc ctgtcaggcg acctttcact tacagcccat ggcagctgat agcatttcta      300
gtcgattttg gtccataatt gaggcaaata taagtggggc aggaccttga agaatgatat      360
aattagttag tcgagtgttt t   atg ttg tta gct aag cgc tat gct aag tat      411
                        Met Leu Leu Ala Lys Arg Tyr Ala Lys Tyr
                        1               5               10

ttc att tat ttt atc ttc ttt aat cct gtt tta atc ccc att cta caa      459
Phe Ile Tyr Phe Ile Phe Phe Asn Pro Val Leu Ile Pro Ile Leu Gln
                        15               20               25

aga agg atc ctg aga ctt ggt gag atc cat att gct ggc cag tgc aga      507
Arg Arg Ile Leu Arg Leu Gly Glu Ile His Ile Ala Gly Gln Cys Arg
                        30               35               40

gct ggg tcc ctg cag tct ctg cct tta cct gcc aac ctg cat agc atc      555
Ala Gly Ser Leu Gln Ser Leu Pro Leu Pro Ala Asn Leu His Ser Ile
                        45               50               55

ctg gat att ctt gca tag ccacat agacatttgt ttgtactttt agtatgtgt      609
Leu Asp Ile Leu Ala *
                        60

gggtacagtg catgttttta gctattttct caagcatctg ggaagttcta actctgtttt      669
attgatgagg aaactgggtc ttgaaatcca ggcctatacc tgtctgaatg taacgccccg      729
caggaaagtg ggacattgag aaagagccac aggtgggaaa ccctaatacc tcggattgga      789
tactggctct accgtgaacc aacccttggg attttggaaca agcggctata accctgttgg      849
gccttaactt tcttgatcaa aaaaagaac      878

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<210> 118  
 <211> 1656  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (89)..(1051)

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tgccctgggca gcgcgctgct cttctaag atg gct gcc gct acc ggt gcg gtg 112  
Met Ala Ala Ala Thr Gly Ala Val  
1 5  
gca gcc tcg gcc gcc tcg ggt cag gcg gaa ggt aaa aag atc acc gat 160  
Ala Ala Ser Ala Ala Ser Gly Gln Ala Glu Gly Lys Lys Ile Thr Asp  
10 15 20  
ctg cgg gtc atc gat ctg aag tcc gag ctg aag cgg cgg aac tta gac 208  
Leu Arg Val Ile Asp Leu Lys Ser Glu Leu Lys Arg Arg Asn Leu Asp  
25 30 35 40  
atc acc gga gtc aag acc gtg ctc atc tcc cga ctc aag cag gct att 256  
Ile Thr Gly Val Lys Thr Val Leu Ile Ser Arg Leu Lys Gln Ala Ile  
45 50 55  
gaa gag gaa gga ggc gat cca gat aat att gaa tta act gtt tca act 304  
Glu Glu Glu Gly Gly Asp Pro Asp Asn Ile Glu Leu Thr Val Ser Thr  
60 65 70  
gat act cca aac aag aaa cca act aaa ggc aaa ggt aaa aaa cat gaa 352  
Asp Thr Pro Asn Lys Lys Pro Thr Lys Gly Lys Gly Lys Lys His Glu  
75 80 85  
gca gat gag ttg agt gga gat gct tct gtg gaa gat gat gct ttt atc 400  
Ala Asp Glu Leu Ser Gly Asp Ala Ser Val Glu Asp Asp Ala Phe Ile  
90 95 100  
aag gac tgt gaa ttg gag aat caa gag gca cat gag caa gat gga aat 448  
Lys Asp Cys Glu Leu Glu Asn Gln Glu Ala His Glu Gln Asp Gly Asn  
105 110 115 120  
gat gaa cta aag gac tct gaa gaa ttt ggt gaa aat gaa gaa gaa aat 496  
Asp Glu Leu Lys Asp Ser Glu Glu Phe Gly Glu Asn Glu Glu Glu Asn  
125 130 135  
gtg cat tcc aag gag tta ctc tct gca gaa gaa aac aag aga gct cat 544  
Val His Ser Lys Glu Leu Leu Ser Ala Glu Glu Asn Lys Arg Ala His  
140 145 150  
gaa tta ata gag gca gaa gga ata gaa gat ata gaa aaa gag gac atc 592  
Glu Leu Ile Glu Ala Glu Gly Ile Glu Asp Ile Glu Lys Glu Asp Ile  
155 160 165  
gaa agt cag gaa att gaa gct caa gaa ggt gaa gat gat acc ttt cta 640  
Glu Ser Gln Glu Ile Glu Ala Gln Glu Gly Glu Asp Asp Thr Phe Leu  
170 175 180  
aca gcc caa gat ggt gag gaa gaa gaa aat gag aaa gaa ggg agc cta 688  
Thr Ala Gln Asp Gly Glu Glu Glu Glu Asn Glu Lys Glu Gly Ser Leu  
185 190 195 200  
gct gag gct gat cac aca gct cat gaa gag atg gaa gct cat acg act 736  
Ala Glu Ala Asp His Thr Ala His Glu Glu Met Glu Ala His Thr Thr  
205 210 215  
gtg aaa gaa gct gag gat gac aac atc tcg gtc aca atc cag gct gaa 784  
Val Lys Glu Ala Glu Asp Asp Asn Ile Ser Val Thr Ile Gln Ala Glu  
220 225 230  
gat gcc atc act ctg gat ttt gat ggt gat gac ctc cta gaa aca ggt 832

Asp	Ala	Ile	Thr	Leu	Asp	Phe	Asp	Gly	Asp	Asp	Leu	Leu	Glu	Thr	Gly	
	235						240					245				
aaa	aat	gtg	aaa	att	aca	gat	tgt	gaa	gca	agt	aag	cca	aaa	gat	ggg	880
Lys	Asn	Val	Lys	Ile	Thr	Asp	Cys	Glu	Ala	Ser	Lys	Pro	Lys	Asp	Gly	
	250					255					260					
cag	ggc	gcc	att	gca	cag	agg	ccg	gat	aag	gaa	agc	aag	gat	tat	gag	928
Gln	Gly	Ala	Ile	Ala	Gln	Arg	Pro	Asp	Lys	Glu	Ser	Lys	Asp	Tyr	Glu	
265					270					275				280		
atg	aat	gcg	agc	cat	aaa	gat	ggt	aag	aag	gaa	gac	tgc	gtg	aag	ggt	976
Met	Asn	Ala	Ser	His	Lys	Asp	Gly	Lys	Lys	Glu	Asp	Cys	Val	Lys	Gly	
				285				290						295		
gac	cct	gtc	gag	aag	gaa	gcc	aga	gaa	agt	tct	aag	aaa	gca	gaa	tct	1024
Asp	Pro	Val	Glu	Lys	Glu	Ala	Arg	Glu	Ser	Ser	Lys	Lys	Ala	Glu	Ser	
			300					305					310			
gga	gac	caa	aga	aaa	gga	tta	ctt	tga	agaaa	gggccctcgt	ctactggggc					1076
Gly	Asp	Gln	Arg	Lys	Gly	Leu	Leu	*								
	315					320										
ctctgggtcaa	gcaaagagct	cttcaaagga	atctaaagac	agcaagacat	catctaaaga											1136
tgacaaagga	agtacaagta	gtactagtgg	tagcagtgga	agctcaacta	aaaatatctg											1196
ggttagtgga	ctttcatcta	ataccaaagc	tgctgatttg	aagaacctct	ttggcaaata											1256
tggaagggtt	ctgagtgcaa	aagtagttac	aaatgctcga	agtcctgggg	caaaatgcta											1316
tggcattgta	actatgtctt	caagcacaga	ggtgtccagg	tgtattgcac	atcttcatcg											1376
cactgagctg	catggacagc	tgatttctgt	tgaaaaagta	aaaggtgatc	cctctaagaa											1436
agaaatgaag	aaagaaaatg	atgaaaagag	tagttcaaga	agttctggag	ataaaaaaaaa											1496
tacgagtgat	agaagtagca	agacacaagc	ctctgtcaaa	aaagaagaga	aaagatcgtc											1556
tgagaaatct	gaaaaaaaaag	aaagcaagga	tactaagaaa	atagaaggta	aagatgagaa											1616
gaatgataat	ggagcaagtg	gccaaacatc	agaatcgatt													1656

<210> 119  
 <211> 906  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (221)..(397)

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aggagcacct	ttaagctggc	atgtggttgt	aacagcctaa	ccggtctttt	ttagagtgat	120
aggccatgct	aatcttactc	tctgtccag	ccttgaaact	ggccattttt	tcaaggagcc	180
agggttcttt	ttctttggga	acagttacca	gcattctgagt	atg ctc atc gtt tgc		235
				Met Leu Ile Val Ser		

	1	5	
ggg tat ctc tgc ttc tgt gcc ctt cag tgg act gag cta gga aat gta			283
Gly Tyr Leu Cys Phe Cys Ala Leu Gln Trp Thr Glu Leu Gly Asn Val			
	10	15	20
tgt gtg tgt gca cac ata tgc cgt tgc aca cac atg cag gtt tca ggg			331
Cys Val Cys Ala His Ile Cys Arg Cys Thr His Met Gln Val Ser Gly			
	25	30	35
atc aca agt ccg gtc cat gtc cac atc cat agg gtt ctt tct tgc ctt			379
Ile Thr Ser Pro Val His Val His Ile His Arg Val Leu Ser Cys Leu			
	40	45	50
atc cat ttc acc tct tag agcaga ggactttcac catttctatt gaacatgagt			433
Ile His Phe Thr Ser *			
	55		
ataatatgta gtccttacct aagaggattc tgtggatctt ctctgggggtt ctcaggggcc			493
atggaacatg tcagagcaaa tgttggaatg gattaccacag aatgtgagta gtgtgagtgg			553
ggcactgttg gactcagtcc caacccccta acgcgagttt gcatgaaaaa ttcatatctt			613
acttagggcc atcctaactt tcttgcttcc caaaggaggagg gtagatcaaa acataaggga			673
aaggaggggt cataaacttg ttttgaaggt acccggggga accctaaaca ttataggggt			733
ctagtctatg gccgactagt cgcgactata aacgaagcct tcatcatagg gaaaaagggtg			793
caggactttc ttacacatgg ctagtagaac ggggtctaggc tagcatgaga ccttccatgc			853
accagccagc atcctgtctt gtactactga agccttttcc tctagaaaac acg			906
<210> 120			
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<213> Homo sapiens			
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aacaacaagg ttaggaactc ctctggcagg agccaagttc ctccgagttt agatcacttc			120
acataatgtg cccttgcta atg cat ttg ctg gtt tct cac gcc ttc ctg cct			172
Met His Leu Leu Val Ser His Ala Phe Leu Pro			
	1	5	10
ttt cct ctc cat ggt tac tct ggg agg cag aga ggt gct aag caa tgg			220
Phe Pro Leu His Gly Tyr Ser Gly Arg Gln Arg Gly Ala Lys Gln Trp			
	15	20	25
agg tgt cat ccg gcc cgc gca tct agg gaa cgt cct tca gag gac aac			268
Arg Cys His Pro Ala Arg Ala Ser Arg Glu Arg Pro Ser Glu Asp Asn			
	30	35	40
ttg tca cca gcc gtc aaa gaa gag agt ggc ttt gtg gtc tct gaa cat			316

Leu Ser Pro Ala Val Lys Glu Ser Gly Phe Val Val Ser Glu His  
 45 50 55  
 ctg gca gcg ctg cac agg aag ctg agg ggg tgt cat taa ttgtgatgaa 365  
 Leu Ala Ala Leu His Arg Lys Leu Arg Gly Cys His \*  
 60 65 70  
 ataattttaa ccatcaggaa taaatgaggc tgtaagcta agttcagatt ccatttgcca 425  
 tgcacatgtg tctagcagcc tgtgtgcagt taaaagaaat tgaattatat tagctcatga 485  
 gtagaagtga aacagatact gtaaatgaaa caagttgctg tatagcgatg acatcgtgtt 545  
 gaaccatttc acagagttac agtttgtatg atcactgtat caaaagtggg atattattta 605  
 atgaattttt atattataaa acattcctac ggtatggagt atagtaagga ccagtgggtt 665  
 atgggtaggt agagaggatg tgagctggat gggcagaaca aaacaatcca caggttacgg 725  
 gccttgaagg gagtgggagg gaaatcacgc gtcattggag cccagttgcc ctgttagagc 785  
 ccgaacggag tccacatcac gccgcctgca cttgggcata cgcgatcacg ggaacgctcc 845  
 agtggatcca gatcgac 862  
  
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 <212> DNA  
 <213> Homo sapiens  
  
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 Met Leu Leu Leu Leu Leu Leu Leu Gly  
 1 5  
 cca gca ggc tcc ggg ctt ggt gct gtc gtc tct caa cat ccg agc agg 98  
 Pro Ala Gly Ser Gly Leu Gly Ala Val Val Ser Gln His Pro Ser Arg  
 10 15 20 25  
 gtt atc tgt aag agt gga acc tct gtg aag atc gag tgc cgt tcc ctg 146  
 Val Ile Cys Lys Ser Gly Thr Ser Val Lys Ile Glu Cys Arg Ser Leu  
 30 35 40  
 gac ttt cag gcc aca act atg ttt tgg tat cgt cag ttc ccg aaa cag 194  
 Asp Phe Gln Ala Thr Thr Met Phe Trp Tyr Arg Gln Phe Pro Lys Gln  
 45 50 55  
 agt ctc atg ctg atg gca act tcc aat gag ggc tcc aag gcc aca tac 242  
 Ser Leu Met Leu Met Ala Thr Ser Asn Glu Gly Ser Lys Ala Thr Tyr  
 60 65 70  
 gag caa ggc gtc gag aag gac aag ttt ctc atc aac cat gca agc ctg 290  
 Glu Gln Gly Val Glu Lys Asp Lys Phe Leu Ile Asn His Ala Ser Leu  
 75 80 85  
 acc ttg tcc act ctg aca gtg acc agt gcc cat cct gaa gac agc agc 338  
 Thr Leu Ser Thr Leu Thr Val Thr Ser Ala His Pro Glu Asp Ser Ser

90	95	100	105	
ttc tac atc tgc agt gct agt ggt atg aga cgc aca gat acg cag tat				386
Phe Tyr Ile Cys Ser Ala Ser Gly Met Arg Arg Thr Asp Thr Gln Tyr				
110		115	120	
ttt ggc cca ggc acc cgg ctg aca gtg ctc gag gac ctg aaa aac gtg				434
Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val				
125		130	135	
ttc cca ccc gag gtc gct gtg ttt gag cca tca gaa gca gag atc tcc				482
Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser				
140		145	150	
cac acc caa aag gcc aca ctg gtg tgc ctg gcc aca ggc ttc tac ccc				530
His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro				
155		160	165	
gac cac gtg gag ctg agc tgg tgg gtg aat ggg aag gag gtg cac agt				578
Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser				
170		175	180	185
ggg gtc agc aca gac ccg cag ccc ctc aag gag cag ccc gcc ctc aat				626
Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn				
190		195	200	
gac tcc aga tac tgc ctg agc agc cgc ctg agg gtc tcg gcc acc ttc				674
Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe				
205		210	215	
tgg cag aac ccc cgc aac cac ttc cgc tgt caa gtc cag ttc tac ggg				722
Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly				
220		225	230	
ctc tcg gag aat gac gag tgg acc cag gat agg gcc aaa cct gtc acc				770
Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr				
235		240	245	
cag atc gtc agc gcc gag gcc tgg ggt aga gca gac tgt ggc ttc acc				818
Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr				
250		255	260	265
tcc gag tct tac cag caa ggg gtc ctg tct gcc acc atc ctc tat gag				866
Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu				
270		275	280	
atc ttg cta ggg aag gcc acc ttg tat gcc gtg ctg gtc agt gcc ctc				914
Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu				
285		290	295	
gtg ctg atg gcc atg gtc aag aga aag gat tcc aga ggc tag ctccaaa				963
Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly *				
300		305	310	
accatcccag gtcattcttc atcctcacc aggattctcc tgtacctgct cccaatctgt				1023
gttcctaaaa gtgattctca ctctgcttct catctcctac ttacatgaat acttctctct				1083
ttttctgtt tccctgaaga ttgagctccc				1113

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<211> 767
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (167)..(325)

<220>
<221> misc_feature
<222> (1)...(767)
<223> n = a,t,c or g

<400> 122
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gccctaagtg gttgagagtt cacaaacacc actccctccc tgaggactaa cagccattga      120
ctactggtct gcttggttaac tgactctcca gagctcccca tgagct   atg agt gtg      175
                                   Met Ser Val
                                   1

gga ctt cac ctg gga ttt ctt gct tgg ttt ctt ccc ttt cta att ccc      223
Gly Leu His Leu Gly Phe Leu Ala Trp Phe Leu Pro Phe Leu Ile Pro
   5                10                15

act tct ccc ctt ccc tta cta ttt caa ctg gga gca ctt cct aat gaa      271
Thr Ser Pro Leu Pro Leu Leu Phe Gln Leu Gly Ala Leu Pro Asn Glu
  20                25                30                35

tca ctt gca ctt tat gct tgg ctc agg gat tgc ttc tgg gag aac ata      319
Ser Leu Ala Leu Tyr Ala Trp Leu Arg Asp Cys Phe Trp Glu Asn Ile
          40                45                50

acc taa aatgtccaac aataaggaac agttaatgac atccatccaa cacaatatcc      375
Thr *

tttggctggt aagaacctat ctctgaagaa aacttaaaga catggtaata cattctggat      435
atatcttaac tggaaaaaag tatggcataa ttaactatgt aaaaattata cacaggcaca      495
aattatccag gtgtggtggc ggggtgcttgt actgccagct acttgggagg ctgaggcagg      555
agaatggcgt gaaccaggga ggcggagctt gcagtgagcc gagatccac cactggactc      615
cattctggcg aaagagcaga gactcgtccc aaaaaaaga aaaaaaagg tgtttttgag      675
gggcgggcgg tttttccttt tggggggtaa aattattggg cctgggcggg gtttaaaacg      735
gggggggggaa aaaacngntt ttccnaaaa aa                                767

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<210> 123
<211> 814
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (124)..(324)

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<400> 123  
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 cggcagcagat ctatctgcag agctacctct acattttaac ttaggttagt tgtttccctt 120  
 gga atg tct tct ccg tgt ttt caa tgt ttt cac cta tgt tgt acc att 168  
 Met Ser Ser Pro Cys Phe Gln Cys Phe His Leu Cys Cys Thr Ile  
 1 5 10 15  
 aag gtc tgg ccc ctg tgc cac cac cta cag aaa gcc ttt cct gat ttc 216  
 Lys Val Trp Pro Leu Cys His His Leu Gln Lys Ala Phe Pro Asp Phe  
 20 25 30  
 tct att cat gtc ttc tct gaa agg gat ctt tct tct ttc tgt gaa gtc 264  
 Ser Ile His Val Phe Ser Glu Arg Asp Leu Ser Ser Phe Cys Glu Val  
 35 40 45  
 caa ctt tta aaa ata tgt tta caa aaa tac ttc tta gga tca tta atg 312  
 Gln Leu Leu Lys Ile Cys Leu Gln Lys Tyr Phe Leu Gly Ser Leu Met  
 50 55 60  
 cat tgt tcc taa gtc agagtctct gtgaatttat tctatacaat cttctagtgc 367  
 His Cys Ser \*  
 65  
 tagtatataa actccttaag aacaagaatt tgcctcatgat agtagtcccc tgcagtgtgt 427  
 agattacata agtggtgagt aaatcttgga gatcaggtat cctcattcaa gagggaaatg 487  
 aataagagat ccagttcaga gacctacagt gagtgtcttc cgctgcaggc agggattgat 547  
 gagctgcttc aactcttacc acccaccact ctcaatccta tactctaact aatgaactct 607  
 gctcacggtt gtccaagtga gttgaccctt tggcctttcc atgccgaggc ctgtgcacct 667  
 ttctgaactt ggaatgcctt tacttttttg aaaaaataa gcctctgggc cgaaaaaggc 727  
 cctggttctt tgtgggtccc tgggggtggg aaaaaaatgg tccttttttt tttccccggg 787  
 ggcgggggaa accccaaca aaaggtt 814

<210> 124  
 <211> 784  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (77)..(292)  
 <220>  
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 <222> (1)...(784)  
 <223> n = a,t,c or g

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 tctattcttt gttgat atg gaa aaa tat ttt cac aca gtt atg atc aag 109  
 Met Glu Lys Tyr Phe His Thr Val Met Ile Lys  
 1 5 10

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ttg tgc cat caa ctt tat aac gta tat gtg tgc ttt ttc cat tta att      157
Leu Cys His Gln Leu Tyr Asn Val Tyr Val Cys Phe Phe His Leu Ile
      15              20              25

ggt ttg gga gat att gct ata gac tac att att gtt ccc aat att tcc      205
Val Leu Gly Asp Ile Ala Ile Asp Tyr Ile Ile Val Pro Asn Ile Ser
      30              35              40

tac ctc tct ata tct ata ccc ttt gta gtt act aac att aga ggt aga      253
Tyr Leu Ser Ile Ser Ile Pro Phe Val Val Thr Asn Ile Arg Gly Arg
      45              50              55

gat att ttc cac ccc tgt aat gtg gcc ttg gtc atg tga cttggaatgt      302
Asp Ile Phe His Pro Cys Asn Val Ala Leu Val Met *
      60              65              70

tagtagttct gatgtgcaca gaggtgttac atggactttc agcattgggt ttactctctc      362

gggtttctgc tgttccata caaagaatgt accctgggtg gccaccagc cactgagata      422

tgtgaatcca acttgaactc aactcatggc ctggagccaa gttccaccag tcctaactag      482

cttagccaaa atccagctga tctgaaagtg catgaatgag aaataaaaagc ttattatattt      542

ttttannann aannannnaa aaaaaaaga ctttttttta gggggggggg gggttttctc      602

cttttcgagg ggggaaatta ataaatgag tggcgcccc ctcttcctt gcgcgagggg      662

gtaaaaggcc cggnnnnnnn cgggcccccc ccccgcccc ccccccggc ggaaagccgg      722

aaaaggnggg gggggngggg gngaagtggg gtgtcccccc cccaccccc cccccacta      782

at                                                                 784

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<210> 125  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (314)..(463)

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<400> 125
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gtctactccc tgaatatattg atatatgttca tgttttttagg tgtgataaca tatggctatg      120

ttttttaaaa gacatatatta aaagacatac ctatccatac tgacataaat atggctgaaa      180

agatatgctt gtgtgatgta atttaaataa tttggaggga ggatcaggag ttaatgttga      240

aactcaattg gctttgagtt ggttataatc aagcatgtga gcatttctta tactggaacc      300

tttacttttg cag      atg ttt gta atg ttt tat gaa aat aaa aga aga gaa      349
      Met Phe Val Met Phe Tyr Glu Asn Lys Arg Arg Glu
      1              5              10

tac ctc caa gac atg ctg ctt tct tat aga tta tta gtt gca atc tta      397
Tyr Leu Gln Asp Met Leu Leu Ser Tyr Arg Leu Leu Val Ala Ile Leu

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15	20	25	
ggt ttt ctg aag aaa tta aca gaa ctt aat aca att act ctt att tgc			445
Val Leu Leu Lys Lys Leu Thr Glu Leu Asn Thr Ile Thr Leu Ile Cys			
30	35	40	
aag tct ata att ttc taa acctaa ctctgatgca gtcctactcc taatatttac			499
Lys Ser Ile Ile Phe *			
45	50		
aaggcctaga acaagagtat ataaatggca gccacattc tacgggtcta aatatataca			559
agttataaac caagtcagca aaataaaatg ccatgtat			597

<210> 126  
 <211> 580  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (163)..(318)

<400> 126	
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ttaaaaagta gaatgtttat gtatttaaac agataaaatt tagaatgatt ttaattccag	120
ggtaaaatct gctccgacca gagagaaaaa actaatccat at atg aat ata gta	174
Met Asn Ile Val	
1	
ttt gta atc ctc ttg ttt aaa gac atg caa gtt cta gaa gta ttt gta	222
Phe Val Ile Leu Leu Phe Lys Asp Met Gln Val Leu Glu Val Phe Val	
5 10 15 20	
ctg ctt aat gtt tta aca act cta aca ata ata gca gcg ggc ata ctt	270
Leu Leu Asn Val Leu Thr Thr Leu Thr Ile Ile Ala Ala Gly Ile Leu	
25 30 35	
tgt acc agt ttt tgc tgt aag cct ttt ata tat att aat cct ctt taa	318
Cys Thr Ser Phe Cys Cys Lys Pro Phe Ile Tyr Ile Asn Pro Leu *	
40 45 50	
aaccacccta tcaagtacaa gataataatt tgatatgggt gatgaagcaa ctgatgggaa	378
aaaagagagg ttaaataatt tgcccaaat cttattaagt gatgtagcca gcatctgaac	438
ccaatcagac tgtagactag agcctcctcc caaccactca gctttgctgc ttccacata	498
ctagttacat aactactgta tgactataga ggtcaggta tcagccttct agaatcagta	558
atgttttctg tcaaaaaaaaa aa	580

<210> 127  
 <211> 821  
 <212> DNA  
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<220>

&lt;221&gt; CDS

<222> (91) .. (273)

<400> 127

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cagaaggctg aacagtcctg ggcttttcac atg atc agg ttc gca ctt cca	111
Met Ile Arg Phe Ala Leu Pro	
1 5	
tgg ttc tcc caa ata tgg ctt tct aaa caa act tgg act agg ctc act	159
Trp Phe Ser Gln Ile Trp Leu Ser Lys Gln Thr Trp Thr Arg Leu Thr	
10 15 20	
cac ttg gca ttt ctc ctg cag gaa tgc aac tca atg ttc tat cca aag	207
His Leu Ala Phe Leu Leu Gln Glu Cys Asn Ser Met Phe Tyr Pro Lys	
25 30 35	
gtt tca aga acg aca gtt ttt gga tgt tta ttt aat cct ctc tca agc	255
Val Ser Arg Thr Thr Val Phe Gly Cys Leu Phe Asn Pro Leu Ser Ser	
40 45 50 55	
cgt gtt tgt ttt gaa taa atggca aatgtgatta gtaaattggaa cattcat	309
Arg Val Cys Phe Glu *	
60	
gttagactgc ctctaaactc cagatataaa tgggctggat tttacagctt attttaacat	369
ttcctttttc ctataccctt tctctgatca gctcttcaac ggtgatataa tttcctttta	429
tgcaaattgta caaaacaatg ttagtcctga cttttggcaa gcagttcaca agtttgggtg	489
aaaagacatt gctcttgaaa aacagggtcat ttttagtttt gctatgtctt tccttctcac	549
taggacatat tgtgctgatg cacaacaatg gagctaagga ggtcttttagc ttgtcttgca	609
tctatcacia ctcagcagca ctttctcttt tgacgggtcca tgctattggc tacaatcttt	669
gcccttcccg ccateccact ctatagtccc ccaattcacc cctcgcttg cgggtcgact	729
cacgacactc gggccaggcc gctacaacc agctaccgac tacatcaccc cccctcgcc	789
ttgagaccac tttgccgact ccgggccccac cc	821

<210> 128

<211> 412

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63) .. (329)

<400> 128

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ag atg acc aac ttc ttt cat ctt tta cta cca ctt cta cca tct ctc 107  
Met Thr Asn Phe Phe His Leu Leu Leu Pro Leu Leu Pro Ser Leu  
1 5 10 15

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ttt tcc ccc tcc tca aaa acg cat agc ttc aat att cat aag atc atc      155
Phe Ser Pro Ser Ser Lys Thr His Ser Phe Asn Ile His Lys Ile Ile
                20                25                30

atc atc atc ctt ttc ttc aac agc att ttc ttg tat cct aga gat tac      203
Ile Ile Ile Leu Phe Phe Asn Ser Ile Phe Leu Tyr Pro Arg Asp Tyr
                35                40                45

ctt aaa ata agg aat tgg cta caa agt aat acc ttg gaa aga gaa ata      251
Leu Lys Ile Arg Asn Trp Leu Gln Ser Asn Thr Leu Glu Arg Glu Ile
                50                55                60

gaa tgg atc acc tct ata agg tgc tta tgt aac tct gga act acg ttt      299
Glu Trp Ile Thr Ser Ile Arg Cys Leu Cys Asn Ser Gly Thr Thr Phe
                65                70                75

ata ttt cca tta acc aca aag tcc aca tga g tcatacttat ttttctgtct      350
Ile Phe Pro Leu Thr Thr Lys Ser Thr *
                80                85

caggctacta aaatagaaca tggtctctag aggagaacat caaggagttc ttttatttgt      410
cg                                                                 412

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<210> 129
<211> 2412
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (979) .. (2277)

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<400> 129
cccgcgatct cagacttcct agactccaga actgtaagaa ataaatctct gtttggtata      60

aattaccaag tctcagatat tctattatag cagtacacta acgttcacgt gcattttccc      120

agcggaggaa agatggttgt tcttcatcag agtctggggc ccaagaacgc aggcctccatc      180

tctctccgca ggagccaggc tgatgatgct cgcagggatc ggatactggg agcccctgaa      240

cgcagccaac ccggcgcgca ccggtggggg cgtctgcgct ggcgagcgcg ctccccggga      300

ggacgctggg aacctgctc tagccagccg ctgcgcaggc gcactggggc ccgactgccc      360

gccgcagcgc tacgtgggag cttggccgcg cagtgccgga acccggtctgc agcgggtggga      420

aggcgggggc gtgccggccc agcggggaga ggcactctgca ggggctgctg agagtaaata      480

cttggcgctt ccagctgctg gccaaaggaga cagatggagc tcaagttggg agatacgccc      540

tgagagccga tgatagacac aagtccagat ctggattttt gatactgtat gttccctggg      600

ttctgagag aggacattga ggagtaggag tcggcgatta aggagatcgg tacaattggg      660

aagcctcctg tcagagcttc cagcaatttc ctcatcagag gtggacaagc cctatgggct      720

aagacagagg gtcctcagaa aggagtgcgg acgccgtcat gctgcagcag ctctgatca      780

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ccctgcccac cgaggccagc acctgggtga agttgcgtca tccaaaggcg gccacggagc	840
gggtggccct gtgggaggat gtgactaaga tgtttaaagc agaaggaact gttaaccttc	900
aaggacgtat ctgtggactt cactcaggag gagtgggggc agctggcccc tgctcaccgg	960
aatctgtacc gggaggtg atg ctg gag aac tat ggg aac ctg gtc tca gtg Met Leu Glu Asn Tyr Gly Asn Leu Val Ser Val	1011
1 5 10	
gga tgt cag ctt tcc aaa cct ggc gtg att tcc cag ttg gag aaa gga Gly Cys Gln Leu Ser Lys Pro Gly Val Ile Ser Gln Leu Glu Lys Gly	1059
15 20 25	
gaa gaa cca tgg ctg atg gag aga gat att tca gga gtt cca agt tca Glu Glu Pro Trp Leu Met Glu Arg Asp Ile Ser Gly Val Pro Ser Ser	1107
30 35 40	
gac ttg aag agc aaa aca aaa acc aaa gag tca gcc tta cag aat gat Asp Leu Lys Ser Lys Thr Lys Thr Lys Glu Ser Ala Leu Gln Asn Asp	1155
45 50 55	
att tcg tgg gaa gaa cta cat tgt ggc cta atg atg gaa aga ttt aca Ile Ser Trp Glu Glu Leu His Cys Gly Leu Met Met Glu Arg Phe Thr	1203
60 65 70 75	
aaa gga agc agc atg tat tcc acc ttg gga aga atc tcc aaa tgt aat Lys Gly Ser Ser Met Tyr Ser Thr Leu Gly Arg Ile Ser Lys Cys Asn	1251
80 85 90	
aag cta gaa agc caa caa gag aac caa aga atg ggt aag ggg caa atc Lys Leu Glu Ser Gln Gln Glu Asn Gln Arg Met Gly Lys Gly Gln Ile	1299
95 100 105	
ccc ctg atg tgc aag aaa aca ttc act cag gag aga ggc caa gag tct Pro Leu Met Cys Lys Lys Thr Phe Thr Gln Glu Arg Gly Gln Glu Ser	1347
110 115 120	
aat aga ttt gag aaa aga att aat gtg aag tca gaa gtt atg cca gga Asn Arg Phe Glu Lys Arg Ile Asn Val Lys Ser Glu Val Met Pro Gly	1395
125 130 135	
cca ata ggt ctt cca aga aaa aga gat cgt aaa tat gac aca cct gga Pro Ile Gly Leu Pro Arg Lys Arg Asp Arg Lys Tyr Asp Thr Pro Gly	1443
140 145 150 155	
aag aga agc aga tac aac ata gat tta gtt aat cat tca agg agt tat Lys Arg Ser Arg Tyr Asn Ile Asp Leu Val Asn His Ser Arg Ser Tyr	1491
160 165 170	
aca aaa atg aaa acc ttt gag tgt aat att tgt gaa aaa atc ttc aaa Thr Lys Met Lys Thr Phe Glu Cys Asn Ile Cys Glu Lys Ile Phe Lys	1539
175 180 185	
cag ctt att cac ctt act gaa cac atg aga att cat acc ggg gag aaa Gln Leu Ile His Leu Thr Glu His Met Arg Ile His Thr Gly Glu Lys	1587
190 195 200	
cct ttc aga tgt aag gaa tgt gga aaa gcc ttt agc caa agt tca tct Pro Phe Arg Cys Lys Glu Cys Gly Lys Ala Phe Ser Gln Ser Ser Ser	1635
205 210 215	
ctt att ccg cat cag aga att cat act ggt gag aaa ccc tat gaa tgt Leu Ile Pro His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys	1683

220	225	230	235	
aag gag tgt ggg aaa acc ttc aga cat cct tca tcg ctt act caa cat				1731
Lys Glu Cys Gly Lys Thr Phe Arg His Pro Ser Ser Leu Thr Gln His				
240		245	250	
gtt aga att cat acc ggg gaa aag ccc tat gaa tgt agg gta tgt gag				1779
Val Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Arg Val Cys Glu				
255		260	265	
aaa gcc ttc agc cag agc att gga ctg atc cag cat ttg aga act cat				1827
Lys Ala Phe Ser Gln Ser Ile Gly Leu Ile Gln His Leu Arg Thr His				
270	275		280	
gtt aga gag aaa cct ttt aca tgc aaa gac tgt gga aaa gcg ttt ttc				1875
Val Arg Glu Lys Pro Phe Thr Cys Lys Asp Cys Gly Lys Ala Phe Phe				
285	290		295	
cag att aga cac ctt agg caa cat gag att att cat act ggt gtg aaa				1923
Gln Ile Arg His Leu Arg Gln His Glu Ile Ile His Thr Gly Val Lys				
300	305		310	315
ccc tat att tgt aat gta tgt agt aaa acc ttc agc cat agt aca tac				1971
Pro Tyr Ile Cys Asn Val Cys Ser Lys Thr Phe Ser His Ser Thr Tyr				
320		325		330
cta act caa cac cag aga act cat act gga gaa aga cca tat aaa tgt				2019
Leu Thr Gln His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys				
335		340		345
aag gaa tgt ggg aaa gcc ttt agc cag aga ata cat ctt tct atc cat				2067
Lys Glu Cys Gly Lys Ala Phe Ser Gln Arg Ile His Leu Ser Ile His				
350	355		360	
cag aga gtc cat act gga gta aaa cct tat gaa tgc agt cat tgt ggg				2115
Gln Arg Val His Thr Gly Val Lys Pro Tyr Glu Cys Ser His Cys Gly				
365	370		375	
aaa gcc ttt agg cat gat tca tcc ttt gct aaa cat cag aga att cat				2163
Lys Ala Phe Arg His Asp Ser Ser Phe Ala Lys His Gln Arg Ile His				
380	385		390	395
act gga gaa aaa cct tat gat tgt aat gag tgt gga aaa gcc ttc agc				2211
Thr Gly Glu Lys Pro Tyr Asp Cys Asn Glu Cys Gly Lys Ala Phe Ser				
400		405		410
tgt agt tca tcc ctt att aga cac tgc aaa aca cat tta aga aat acc				2259
Cys Ser Ser Ser Leu Ile Arg His Cys Lys Thr His Leu Arg Asn Thr				
415	420		425	
ttc agc aat gtt gtg tga aatata ctaaactca aagaatctat gttggagcac				2313
Phe Ser Asn Val Val *				
430				
aagattctaa atcagtggtt ccctgatccc tcaaaaatcc atttgttttt ggatttccaa				2373
aaacgaacat taataaaaaa tggtttgga aaaaaaaa				2412

<210> 130  
 <211> 905  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (537)..(707)

&lt;400&gt; 130

taccggtccg gaattcccg gtcgaccac gcgtccgagt tgttacacca tctaccctaa	60
ttcctgaatt ccaaaacctt ggagttcttct ttgatttctt tctcatgttc tccacgtag	120
taggcctgc tgctttccct cctcagtgtg tgctaaactc atttaacttt ctccattttt	180
actgacaatg cacaccatca tactctgtca tctatgccac tgtaacacat tcttaaattg	240
tccctctgtt caactgttgc cctgcaatt cattctatat gtagtggtga aagtgaatac	300
atataaacac aatcaagtt ttgttacttg atggaaaccc tccaataatc attcactatg	360
aataaatcc agaccttttg ctatgacct caagacccca tgtgacctgg tcttgccta	420
cctctctggc cttggctctc acaattctgt ctgtactgat attcaccagt catattgggt	480
gtctcttttt tctaaatta agcactctaa actcatttct gcttcagaga ctgcag	536
atg cca tgc tct gtg cgg gaa act ctc ttt tcc ctt ctc tgg tta gct	584
Met Pro Cys Ser Val Pro Glu Thr Leu Phe Ser Leu Leu Trp Leu Ala	
1 5 10 15	
cct tcc cat cat tca ggt ttc agt tca aat gag gct tct ctg agg act	632
Pro Ser His His Ser Gly Phe Ser Ser Asn Glu Ala Ser Leu Arg Thr	
20 25 30	
gat cta tta ttt gcc aca gcc att ctt tat tct cta tgg cat cct cca	680
Asp Leu Leu Phe Ala Thr Ala Ile Leu Tyr Ser Leu Trp His Pro Pro	
35 40 45	
tat tat ttt ctt tat aat act tct taa tgtgt gaataattac tgtgtggatg	732
Tyr Tyr Phe Leu Tyr Asn Thr Ser *	
50 55	
acttcttac atagttattt atttgtaat gttcttgctt acatttcatt gtcagcttct	792
agaagaagag ctctttaaga gcagtgaccc tgtctgtctt gatcatggaa caaagactgg	852
tatatccaga tgttcaataa atattttcct gtatgaatac atgactatgt ttt	905

&lt;210&gt; 131

&lt;211&gt; 1069

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (141)..(308)

&lt;400&gt; 131

taccattgtc cgcctgcagg taccggtccg gaattcccg gtcgaccac gcgtccgccc	60
acgcgtccga ccatttgaac ttgtaaagaa catgtgttct gcagttttta ggtgttcttt	120
atatattaag ggggttgata atg ttg ttc aca tca ttt gtg tat ggg ctg	170



	Met	Leu	Phe	Thr	Ser	Phe	Val	Tyr	Gly	Leu	
	1				5					10	
att ttt att ttg ttt gat ttt tat ttt cta tca ttt gtt gaa agg gat											218
Ile Phe Ile Leu Phe Asp Phe Tyr Phe Leu Ser Phe Val Glu Arg Asp											
			15				20			25	
gtt aaa atc ttc aac tgt aat ggt gaa ata gta ttg ttt cca ttt aat											266
Val Lys Ile Phe Asn Cys Asn Gly Glu Ile Val Leu Phe Pro Phe Asn											
			30				35			40	
tct gtt cat ttt tgc ctg ata tgt ctt tat ata cac att taa gattatg											315
Ser Val His Phe Cys Leu Ile Cys Leu Tyr Ile His Ile *											
			45				50			55	
tcttctgat gagttgtgaa ttagaacatt atgaaatggt attctccggg aatattattc											375
tctccttaca gtctatttta ctcaatattg atatagcaac tccatccttt atatacttac											435
tgtttacatg gtgtgccttt tcagaagcat ttaqtttcaa ttatagatag catatagatg											495
agacttggtt ttttttaaatt ctattctgaa aatttctgat tttattatta ggaatattta											555
ggggaaatgt ttaataaatt aatattttgg gtttttcttt ctgccatttt tcatatttat											615
ccctcctcct cccccaggaa aaattcaaaa ctcttttctt caaactagta cgaaggataa											675
aaatacgtt ccccaccact cgtgggctcc tctctcatcg tcaccctttc ttacaactct											735
caaaccccc ttacataata tctctggac cctcaacctc tcatgtgctg caattcgccg											795
acaactttct gtctcccgcc atttcacctt ccattctctg ccaacctgaa gcctccgctc											855
gctatcactt ttgctatata acctcttctc aacctaccta ctatacagtc cagcttctct											915
tcattaggta gattcttcaa tatatactcc tcgctaaacc tacaccctag cgccctgaac											975
tactcccccc gcattccact ccaagctcgc cacctatcct ctccacgact aatacgctat											1035
gaccacctcc ataacctccc gctctcgtaa ttcc											1069

&lt;210&gt; 132

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (99) .. (245)

&lt;400&gt; 132

cacgagagaa attggttgca aattgtgaaa tttattgttg tataatgcta atagatcagt										60
tgctctgatg tctttgctgt aatgatttct ttataaaa										
						atg atc tta aat ctg				113
						Met Ile Leu Asn Leu				
						1			5	
agc tcc cta act tta gtt ttt gcc tgg aat tac cca tta cat ttg atg										161
Ser Ser Leu Thr Leu Val Phe Ala Trp Asn Tyr Pro Leu His Leu Met										
			10				15		20	

ata tct cta aat gtc agt tgt agc tgt tac tct gat gat ata agt gga 209  
 Ile Ser Leu Asn Val Ser Cys Ser Cys Tyr Ser Asp Asp Ile Ser Gly  
 25 30 35  
 ata tac aga agc gta ctt aga caa aag tta ggt taa tatc tgaactactt 259  
 Ile Tyr Arg Ser Val Leu Arg Gln Lys Leu Gly \*  
 40 45  
 cctccttgtg tatttaagag aatattgact taagtttcta gaatcctcaa ctaatcctaa 319  
 gtttatttttc tttgtctaga atactatgct gtttttgttt ttggaaggaa gagatatagg 379  
 catagtttcc tgctctcaag gagcttcaaa ggctgtacca gtggggatgc cattgggtatt 439  
 tttagctgga tagttgttat tcagaaaagc aggacaagta attatgattc ctggtccgta 499  
 cctggtaatg ccagtaatgt taactctagc tggttgttga catctggtca tttagttggc 559  
 aatctttctt tttttttttt ggcgtatggg gaaaagggtt agagcttcaa agacggcccc 619  
 ggtaaagtca acgcagggcc tccacagggg tggcggtact ccgggtttcc cgcgctgagc 679  
 gggttacaga ctgattttgt ggcgcgaccg aggcggggcc ccggcagcgg ggattgcatc 739  
 gcggcgcccc accggggggg agctcgccac ccgctgccgt ccggaaccgg ggcacacccc 799  
 cgcggacgca cggagccggg gctctcgggg cccccccgcc aggagccgcc caacacacgc 859  
 gggcgcgacg tcacgcgggg ggcgcgacgc ggcacgggtg ggcgacgcgt tatteggcgc 919  
 gtcgcggccc cgcgcggggc ctgcctcagt accggggcgac cgcctccgcg gcgactcctc 979  
 ccgctagctc cccctctcgc gtacaccgac gcgcggaaag ggcgggcccgc gggcacctca 1039  
 tagtcgcgca cggcgtgaac tgcgggaaca ccgacaccgc gcggctggat agagcgaact 1099  
 cgcgcgacac tcgcgtgccg ggcggggcgag atatgcggtc agaggggtcta agcgcgcgcg 1159  
 tgcgcgaagg ggggcggggg tgccgcgggc ttcgcgcgcg ccagaccacc tgccgtgggg 1219  
 cgctattgtg cataggcggg ggcgtatacc cacgggcaaa cgtgggcc 1266

<210> 133  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (129)..(344)

<220>  
 <221> misc\_feature  
 <222> (1)...(495)  
 <223> n = a,t,c or g

<400> 133  
 tcctcgagg taccggtccg gaattcccgg gtcgaccac gcgtccgccc acgcgtccga 60  
 agaatgggtt ccttactaaa tgagaaaagt tgagcccttt ccactaaaat gggttaaata 120

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aaaacttc atg tgt tta att ctg gtt atc tgg aaa att cac tat gca gaa 170
      Met Cys Leu Ile Leu Val Ile Trp Lys Ile His Tyr Ala Glu
        1             5             10

ctt ata atg tta aat aaa cga gtt gtt aat aaa tgt aga tca tgt ctt 218
Leu Ile Met Leu Asn Lys Arg Val Val Asn Lys Cys Arg Ser Cys Leu
  15             20             25             30

atc caa aaa tgc cta tct aca tgt cat agt aca gtc att gtt tta tat 266
Ile Gln Lys Cys Leu Ser Thr Cys His Ser Thr Val Ile Val Leu Tyr
          35             40             45

caa tgc aga gag gaa gaa gct gtg atg tta ata aag ttg aat ttt aaa 314
Gln Cys Arg Glu Glu Glu Ala Val Met Leu Ile Lys Leu Asn Phe Lys
          50             55             60

atg aaa atc caa aga act ata tgt ata tag g ccaaataaaa agttacttga 365
Met Lys Ile Gln Arg Thr Ile Cys Ile *
        65             70

ttacttaata atatggatta aaatgagtaa tcaactgtaat tcatatatc aagaagtttt 425

cttttcaagt taacatttta agtcctgcca tgccattccc tgtccataaa aatccnnnnn 485

aaaaaaaaa 495

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<210> 134  
 <211> 792  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (75)..(323)

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<400> 134
tgcacctgcg gtaccggtcc ggaattcccg ggtcgaccca cgcgtccgct tacatcagtt 60

taaaatgagt tacc atg aac aat atg aac tta aag aga ctt tta cta ttt 110
      Met Asn Asn Met Asn Leu Lys Arg Leu Leu Leu Phe
        1             5             10

ttg gct aaa atg ttt agc gca atc ttt tcc tta cct act cat cct tct 158
Leu Ala Lys Met Phe Ser Ala Ile Phe Ser Leu Pro Thr His Pro Ser
  15             20             25

cat ttc ccc att tcc att tat gac aac att ggt cat tgg cct cag tca 206
His Phe Pro Ile Ser Ile Tyr Asp Asn Ile Gly His Trp Pro Gln Ser
  30             35             40

ccg aaa gtc agg agg aag gaa gga aat gaa tat tta ttg aac ccc aat 254
Pro Lys Val Arg Arg Lys Glu Gly Asn Glu Tyr Leu Leu Asn Pro Asn
  45             50             55             60

atg tgc cag acc ctg gat tta aca ctt tta ggg ata gga gat tat tta 302
Met Cys Gln Thr Leu Asp Leu Thr Leu Leu Gly Ile Gly Asp Tyr Leu
          65             70             75

acc tca ata acc tct ccc tga gg gcaggaagtg gatttataga tgcggaaca 355
Thr Ser Ile Thr Ser Pro *
        80

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```

gaggttctgc aaagtcaatt gactttgcct ggtaagaggc aaaaccagca tcctttatctt 415
aggcaatcca agtgatgttc atgtcctctg gaacttaaat ttttaaaaca aaaatttaaa 475
cagaaacata ttacaaaaga acaactttat gcatgtgacc ttttggttgc ttttaggaagc 535
cagctagcca tctttatctt aataactaga aggtgagacc tttcctacac catgtaattt 595
taaggcgtct cataacttaa aaataaatga aacacctttt ttttctctgc ctcccttcta 655
gactctacag cctgcccata acacccttgg caaccaccgc tcccacccgc gccacccac 715
gccattccc gtccccaacc tttcttagct gcccgctggc gccactctc accccccca 775
cgccccacc cccctc 792

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<210> 135
<211> 788
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (211)..(483)

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<400> 135
gcctgcaggt accggtccgg aattcccggg tcgacccacg cgctcccca cgcgtccgat 60
ttgttggaga aaagctgcta ttataaagcc tgatgtggac tttttctatc agtgtcactc 120
aagcaagttg gcctttaaag acagtttttt actgcttaat atataggagt tttcttgttt 180
tatttgttca ttttctaat tgaacaaatt atg gct cct ctt cct agc ctc 231
Met Ala Pro Leu Pro Ser Leu
1 5

act cta aga cct tgg tgt gtc ctc atg tta ctg gac ctg tgg gct gca 279
Thr Leu Arg Pro Trp Cys Val Leu Met Leu Leu Asp Leu Trp Ala Ala
10 15 20

ttt ggc aca att act ccc tcc ttg aag cac ttt cat cac ctg cct tcc 327
Phe Gly Thr Ile Thr Pro Ser Leu Lys His Phe His His Leu Pro Ser
25 30 35

ggg aca cag cac tcc ctg gtt ttt gtc ctg tct ctg act ctt cat tct 375
Gly Thr Gln His Ser Leu Val Phe Val Leu Ser Leu Thr Leu His Ser
40 45 50 55

cag ttg tct ttg ctg atg ggc acc tca gct gtc tgt ctt tct gcc tgt 423
Gln Leu Ser Leu Leu Met Gly Thr Ser Ala Val Cys Leu Ser Ala Cys
60 65 70

ttt tct tct ctc agc act ttc cct ggg tgg ttg ctt atc atc tgc aca 471
Phe Ser Ser Leu Ser Thr Phe Pro Gly Trp Leu Leu Ile Ile Cys Thr
75 80 85

ctg atg att taa aca tagagttttt gcctgtatct ctccccctaa gtctaggctt 526
Leu Met Ile *
90

```

atatatctaa ctgcctgctc agtacctcta tttggatggt taataggcat ttcaaattgg 586  
aatccaacct tttgttccta cctctgcagc cctgggtccaa aacaccatca tctcttggcc 646  
agcttattac acctgtagtt accttccatc tgggtcttccc acctccatac ttgcccctc 706  
cagcttggtta ttatagttgc gatagggtac gcttccacaa tttgctcctg cctacctgtc 766  
atgataatca gactatacct tt 788

<210> 136  
<211> 774  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (400) .. (534)

<400> 136  
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tagtaaaact tgcaatatag ttagcataac tagatattta tcctgttgg gatttcacag 120  
ttgcaccttg cctgttattt atattttcct aaattattag aagattttag aaaaagattc 180  
tgtgttatga atgccagggt gagagttaat tactgtatgc attttgacac ctatgtgtt 240  
aaaaagctgt tgttgatagc tgaaccaaga attggtcttt gaccttctgg gcacagttaa 300  
tgagctacta atctttagg gcatgtttct gttggacctc tgcctgggct cattgtcagt 360  
atattattgac actcatccat gtatgcatgg agggtttaa atg cag tca aga ctg 414  
Met Gln Ser Arg Leu  
1 5  
gtg ttc tcc agc caa gct gtt gct ttc agc att cac aaa aac aag gta 462  
Val Phe Ser Ser Gln Ala Val Ala Phe Ser Ile His Lys Asn Lys Val  
10 15 20  
gaa agg aga cct gga caa caa gca cag gca ctt gga ctt tta aaa att 510  
Glu Arg Arg Pro Gly Gln Gln Ala Gln Ala Leu Gly Leu Leu Lys Ile  
25 30 35  
att tta ttt tct gtt ttc ccc tga tatgataaat agtgggtctaa agacctcaga 564  
Ile Leu Phe Ser Val Phe Pro \*  
40 45  
tttcctttat tcatatatgg gtttcctttt taaaaatatt attttcagtg gatttgctta 624  
tggacacatt tattaccagt ttattcaaa aattaaacat ttgttcagca tttgtgtcct 684  
aagctgacag gtcttaaatc ttatttttca aagttatatt ggaagttata ttagaagaag 744  
aaccggcttc ctaggcccag acatatctgc 774

<210> 137  
<211> 764

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (212) .. (388)

<400> 137  
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cgtccgggggt ttttataaaa atggattcag ggtctgctga aataaatttt ttttaaaaat 120  
ttcagtcctat aaaccaaaca aaaatatctg tcctggaatg tgatcaggaa caaaccagaa 180  
aactgtgaac atctgatctt gatactggct t atg ttg tct ctt gtt aag ctt 232  
Met Leu Ser Leu Val Lys Leu  
1 5  
ttg ctt ctt tgc att att cat gac cat tca att aat ttt tgt ata gcc 280  
Leu Leu Leu Cys Ile Ile His Asp His Ser Ile Asn Phe Cys Ile Ala  
10 15 20  
ata cag gta gga tta tta cca agt gcc tac cgt gta cca gga ata gtt 328  
Ile Gln Val Gly Leu Leu Pro Ser Ala Tyr Arg Val Pro Gly Ile Val  
25 30 35  
cta agc ctt gag aat aca gca cta ata agg cag act ccc tgc tca aat 376  
Leu Ser Leu Glu Asn Thr Ala Leu Ile Arg Gln Thr Pro Cys Ser Asn  
40 45 50 55  
aga gcc aac taa tga aaaatcgata aaatagagac taaagagaga tccttagttg 431  
Arg Ala Asn \*  
cgtttaaaat cttagttttt aacttccagg ctggcacagt ttgttaacaa aaaaaaaaaa 491  
aagggggggc cgttttaaaag aatcaaattt tacaaccggg ggctggaaag gaattacttt 551  
ttttataggg cccccaatt caatttcggg ggccgtgttt taacaagggg ggactgggga 611  
aaaaatctgg ttgtcctccg taacacctgc gataagacga tcgacggtag gtctatatcg 671  
acgaaccacc cctccaacat ctcacatcgt tagaacgagg atatcttga cgccggctcg 731  
ggggacacat tgattagact atcccaactc atc 764

<210> 138  
<211> 1126  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (144) .. (707)

<400> 138  
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accagaccag acctcacggg ctccgctggc tgcggtcgcc tgggagctgc cgccaggggc 120  
aggaggggag cggcacctgg aag atg cgc cca ttg gct ggt gct cca gtc 170

Met Arg Pro Leu Ala Gly Ala Pro Val																	
1									5								
ccc	aaa	agg	caa	aaa	tgt	gac	cac	tgg	act	ccc	tgc	cca	tct	gac	acc		218
Pro	Lys	Arg	Gln	Lys	Cys	Asp	His	Trp	Thr	Pro	Cys	Pro	Ser	Asp	Thr		
10					15					20					25		
tat	gcc	tac	agg	tta	ctc	agc	gga	ggt	ggc	aga	agc	aag	tac	gcc	aaa		266
Tyr	Ala	Tyr	Arg	Leu	Leu	Ser	Gly	Gly	Gly	Arg	Ser	Lys	Tyr	Ala	Lys		
				30					35						40		
atc	tgc	ttt	gag	gat	aac	cta	ctt	atg	gga	gaa	cag	ctg	gga	aat	gtt		314
Ile	Cys	Phe	Glu	Asp	Asn	Leu	Leu	Met	Gly	Glu	Gln	Leu	Gly	Asn	Val		
			45					50						55			
gcc	aga	gga	ata	aac	att	gcc	att	gtc	aac	tat	gta	act	ggg	aat	gtg		362
Ala	Arg	Gly	Ile	Asn	Ile	Ala	Ile	Val	Asn	Tyr	Val	Thr	Gly	Asn	Val		
		60					65					70					
aca	gca	aca	cga	tgt	ttt	gat	atg	tat	gaa	ggc	gat	aac	tct	gga	ccg		410
Thr	Ala	Thr	Arg	Cys	Phe	Asp	Met	Tyr	Glu	Gly	Asp	Asn	Ser	Gly	Pro		
		75				80					85						
atg	aca	aag	ttt	att	cag	agt	gct	gct	cca	aaa	tcc	ctg	ctc	ttc	atg		458
Met	Thr	Lys	Phe	Ile	Gln	Ser	Ala	Ala	Pro	Lys	Ser	Leu	Leu	Phe	Met		
		90			95					100					105		
gtg	acc	tat	gac	gac	gga	agc	aca	aga	ctg	aat	aac	gat	gcc	aag	aat		506
Val	Thr	Tyr	Asp	Asp	Gly	Ser	Thr	Arg	Leu	Asn	Asn	Asp	Ala	Lys	Asn		
				110					115						120		
gcc	ata	gaa	gca	ctt	gga	agt	aaa	gaa	atc	agg	aac	atg	aaa	ttc	agg		554
Ala	Ile	Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg	Asn	Met	Lys	Phe	Arg		
			125					130						135			
tct	agc	tgg	gta	ttt	att	gca	gca	aaa	ggc	ttg	gaa	ctc	cct	tcc	gaa		602
Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly	Leu	Glu	Leu	Pro	Ser	Glu		
		140					145					150					
att	cag	aga	gaa	aag	atc	aac	cac	tct	gat	gct	aag	aac	aac	aga	tat		650
Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser	Asp	Ala	Lys	Asn	Asn	Arg	Tyr		
		155				160					165						
tct	ggc	tgg	cct	gca	gag	atc	cag	ata	gaa	ggc	tgc	ata	ccc	aaa	gaa		698
Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln	Ile	Glu	Gly	Cys	Ile	Pro	Lys	Glu		
		170			175					180					185		
cga	agc	tga	cactgca	gggtcctgag	taaagtgtgtt	ctgtataaac	aaatgcagct										754
Arg	Ser	*															
ggaatcgctc	aagaatctta	tttttctaaa	tccaacagcc	catatttgat	gagtattttg												814
ggtttgttgt	aaaccaatga	acatttgcta	gttgtatcaa	atcttgggtac	gcagtatttt												874
tataccagta	ttttatgtag	tgaagatgtc	aattagcagg	aaactaaaat	gaatggaaat												934
tcttaaaggg	aatgatgtga	ttcaagctgg	aaagagggtt	gggagaaaca	gcttgtccag												994
gtggagctat	gttatgatca	gatecgaagtg	tgaccctgt	gtgggtccaga	cagccctgca												1054
gagagaaaac	ctttatttga	ttatcaccaa	gcacctccta	gtttccgaca	gtcatctcct												1114
tctgctggga	at																1126

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<210> 139
<211> 1897
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (534) .. (1805)

<400> 139
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atttttgcct ctggctagga caggggggaa aggggtggcgt ggctacagcc tgaccgatgg      120
gcaccgtcct accctttgtt ctgtgcttcc gagtgtcata catgtgctgg ggtctgtggg      180
cccatgactc agacgggtgag ctctgacctt cctgagccag ggctttgctg tagttgtgcc      240
tggctcaaga gctctaggac aaggggaccg ctccaggctc gcatctacgg tgtggcaggg      300
cccttcggca ctcttgtgca ctagtgtcat ctttccatt gaaatgactg tgaggaccag      360
aatgtgcaca tgcagatggg cagctacttg tctgccttg ccctttatta cacaacttgc      420
tgggggtgga gatgccaccc cccggcagtc agagcccctt tatgatgtca tggggctggt      480
tacatgactg ccaaggggtg ctgctggcca cactgcacta gcaagtttgc cag      atg      536
                                     Met
                                     1

gag gac aag cga tca ttg agt atg gct cgc tgt gaa gaa aga aat tcg      584
Glu Asp Lys Arg Ser Leu Ser Met Ala Arg Cys Glu Glu Arg Asn Ser
          5              10              15

aga gga cag gat cat ggc ttg gaa agg gtg cct ttc cct ccc cag ttg      632
Arg Gly Gln Asp His Gly Leu Glu Arg Val Pro Phe Pro Pro Gln Leu
          20              25              30

cag tca gag acc tac ctt cac cca gca gat cct tcc cct gcc tgg gac      680
Gln Ser Glu Thr Tyr Leu His Pro Ala Asp Pro Ser Pro Ala Trp Asp
          35              40              45

gac ccg ggg tcc act ggg agc cct aac ttg agg ctg ctg aca gaa gaa      728
Asp Pro Gly Ser Thr Gly Ser Pro Asn Leu Arg Leu Leu Thr Glu Glu
          50              55              60              65

atc gct ttc caa cct ctg gcc gag gaa gct tcg ttc aga agg ccg cac      776
Ile Ala Phe Gln Pro Leu Ala Glu Glu Ala Ser Phe Arg Arg Pro His
          70              75              80

cct gac ggt gac gtc ccg ccc cag gga gaa gat aat ctc ctc tcc ctc      824
Pro Asp Gly Asp Val Pro Pro Gln Gly Glu Asp Asn Leu Leu Ser Leu
          85              90              95

ccc ttt cca cag aaa ctg tgg aga ctg gtc agc agc aac cag ttt tcg      872
Pro Phe Pro Gln Lys Leu Trp Arg Leu Val Ser Ser Asn Gln Phe Ser
          100             105             110

tcc atc tgg tgg gat gac agt ggg gct tgt aga gtg atc aat caa aaa      920
Ser Ile Trp Trp Asp Asp Ser Gly Ala Cys Arg Val Ile Asn Gln Lys

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115	120	125	
ctc ttt gaa aag gag att	ctc aaa agg gac	gtc gca cac aaa gtg ttt	968
Leu Phe Glu Lys Glu Ile	Leu Lys Arg Asp	Val Ala His Lys Val Phe	
130	135	140	145
gcc aca act tcg ata aag agc ttc ttc cgc cag cta aac ttg tat ggc			1016
Ala Thr Thr Ser Ile Lys Ser Phe Phe Arg Gln Leu Asn Leu Tyr Gly			
	150	155	160
ttc cga aaa cgg cgt caa tgc act ttc agg acc ttc acc cgc att ttc			1064
Phe Arg Lys Arg Arg Gln Cys Thr Phe Arg Thr Phe Thr Arg Ile Phe			
	165	170	175
tcc gca aaa agg ctg gtc tcc atc ttg aat aag tta gag ttc tac tgc			1112
Ser Ala Lys Arg Leu Val Ser Ile Leu Asn Lys Leu Glu Phe Tyr Cys			
	180	185	190
cat cct tac ttt caa aga gac tcc cct cac ctc ctc gtg agg atg aag			1160
His Pro Tyr Phe Gln Arg Asp Ser Pro His Leu Leu Val Arg Met Lys			
	195	200	205
aga aga gtg ggt gtc aag tct gca cca aga cat cag gag gag gac aag			1208
Arg Arg Val Gly Val Lys Ser Ala Pro Arg His Gln Glu Glu Asp Lys			
	210	215	220
cca gaa gct gct gga tcc tgt ctg gca cca gca gac act gag caa caa			1256
Pro Glu Ala Ala Gly Ser Cys Leu Ala Pro Ala Asp Thr Glu Gln Gln			
	230	235	240
gat cac acg tct ccg aat gag aat gac cag gtc aca ccg caa cac cgg			1304
Asp His Thr Ser Pro Asn Glu Asn Asp Gln Val Thr Pro Gln His Arg			
	245	250	255
gaa ccg gcc ggt ccc aac acc caa atc agg agt ggc tct gct cca cca			1352
Glu Pro Ala Gly Pro Asn Thr Gln Ile Arg Ser Gly Ser Ala Pro Pro			
	260	265	270
gca act cct gtg atg gtg cct gat tcc gcc gtg gcg agt gac aac agt			1400
Ala Thr Pro Val Met Val Pro Asp Ser Ala Val Ala Ser Asp Asn Ser			
	275	280	285
cca gtg acc cag ccg gcc ggc gag tgg tca gag ggc agc cag gct cac			1448
Pro Val Thr Gln Pro Ala Gly Glu Trp Ser Glu Gly Ser Gln Ala His			
	290	295	300
gtc act ccg gtg gcc gct gtc cct ggg cct gca gcg ctg ccc ttc ctc			1496
Val Thr Pro Val Ala Ala Val Pro Gly Pro Ala Ala Leu Pro Phe Leu			
	310	315	320
tat gtc cct gga tct ccc act cag atg aat tct tac ggg cct gtg gtg			1544
Tyr Val Pro Gly Ser Pro Thr Gln Met Asn Ser Tyr Gly Pro Val Val			
	325	330	335
gcc ctt ccc aca gcg tcc cgt agt acc ctt gcc atg gac acc aca gga			1592
Ala Leu Pro Thr Ala Ser Arg Ser Thr Leu Ala Met Asp Thr Thr Gly			
	340	345	350
ctt cct gca cct ggc atg ctg ccc ttt tgc cat ctc tgg gta ccg gtg			1640
Leu Pro Ala Pro Gly Met Leu Pro Phe Cys His Leu Trp Val Pro Val			
	355	360	365
acc cta gtg gct gct ggg gct gca cag cct gct gcc tcc atg gtc atg			1688
Thr Leu Val Ala Ala Gly Ala Ala Gln Pro Ala Ala Ser Met Val Met			

370	375	380	385	
ttc ccc cat ctc cca gct ctg cac cac cat tgc ccc cac agc cac cgc				1736
Phe Pro His Leu Pro Ala Leu His His His Cys Pro His Ser His Arg				
	390	395	400	
acg tca cag tac atg cca gct agc gat ggg ccc cag gcg tac cca gac				1784
Thr Ser Gln Tyr Met Pro Ala Ser Asp Gly Pro Gln Ala Tyr Pro Asp				
	405	410	415	
tac gca gac cag agc aca tag ag ggcagcattt gggcagaata tgtgctggtc				1837
Tyr Ala Asp Gln Ser Thr *				
	420			
aataaatgtg tcagaaaatg agtaattttc tgactgcaca aaaagtcttc atggtctcca				1897
<210> 140				
<211> 1156				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (150)..(584)				
<400> 140				
atttggccct cgaggccaag aattcggcac gagtgaagc attagaagac aattgagtct				60
gtcagaactg caaaatattg ctgagtgtgg attgctctga aatctgaaaa cattacttgt				120
gaattgcttc tattcaaaat gcagacaca atg cca ggt gtt ggt tta ctt gtt				173
		Met Pro Gly Val Gly Leu Leu Val		
		1 5		
tcc cat ttt tca acc ctc gtt tct agg caa agg tgt cca aat tat gca				221
Ser His Phe Ser Thr Leu Val Ser Arg Gln Arg Cys Pro Asn Tyr Ala				
	10	15	20	
gac cca cag aat cta aca gat gtc tct ata ttc ctc ctc cta gaa gtc				269
Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu Glu Val				
	25	30	35 40	
tca ggg gat cca gaa ctg cag cca gtc ctt gct ggg ctg ttc ctg tcc				317
Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe Leu Ser				
	45	50	55	
atg tgc ctg gtc acg gtg ctg ggg aac ctg ctc atc atc ctg gcc atc				365
Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile				
	60	65	70	
agc cct gac tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc aac				413
Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn				
	75	80	85	
ctg tcc ttg cct gac atc ggt ttc acc tcc acc acg gtc ccc aag atg				461
Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Val Pro Lys Met				
	90	95	100	
att gtg gac atc cag tct cac agc aga gtc atc tcc tat gca ggc tgc				509
Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys				
	105	110	115 120	

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ctg act cag atg tct ctc ttt gcc att ttt gga ggc atg gaa gag aga      557
Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Arg
                125                130                135

cat gct cct gag tgt gat ggc cta tga ctggt ttgtagccat ctgtcacccg      609
His Ala Pro Glu Cys Asp Gly Leu *
                140                145

ctatatcatt caccatcatg aaccctgtgt tctgtgcctt tctagttttg ttgtcttttt      669

ttttctcagt ctttttagact ccagctgca caacttgatt gccttacaag tgacctgctt      729

caaggatgtg gaaattccta atttcttctg tgaccttct caactctccc atcttgcag      789

ttgtgacacc ttcaccaata agataatcat gtatttcctt gctgccatat ttggttttct      849

tcccatctca gggacccttt tctcttactc taaaattggt tctccattc tgagggtttc      909

atcatcaggt gggaagtata aagccttctc cacctgtggg tctcacctgt cagttgtttg      969

ctgagtttat ggaacaggcg ttggagggtta cctcagttca gatgatgtgt catcttcccc      1029

cagaaagggg gcagtggcct cagtgatgta cagggtgggc acccccatgc tgaaccctt      1089

catctacagc ctgagaaaca gggatatgaa aagtgtcctg cggcggcgcg atggcagcac      1149

agtctaa                                           1156

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<210> 141
<211> 2898
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1074) .. (2294)

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<400> 141
agcacacctt ccacagcact ggtctctcct ctcagaactg tgtttccac acaggctcac      60

gggctcccaa ggggatacgg ctgcttgagg tgactgagct ccctcctcac agcagagctg      120

aggtctgggc tccaggtccc cagtggagtc cctcgagac agaaatagcc gagaccatac      180

aaccaaccaa atacaccctt aacaagctta agcgacaaat actcaaaaac ataaaacca      240

gtaaagagga aacaccacca cctacacaga caccaaacga cggccacttc cagttttcct      300

gtgaagtctc tgtgatgctc ccctggagca gctgcagcac ggagagaaca atccgcggga      360

cagctcgcaa accccgacag cgcataaacc gcacctggg ctcgtgggtca aaacatcctg      420

tagcaaggag ggtcaatgct tacatgatga agatgatgca gaaggacagg aaggccaggg      480

ctgtggctcc agtccccccg actgctgcca gtgtcacttg tgatacagac ctgccccccg      540

gggccccaca gtgctcagtt gaaggggggc cgggggaccg cagcctccgc ttccgctgct      600

cgtggcccgg cggggccctt gctgcctccc tgcagttcca gggctctccc gaaggcatcc      660

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gcgcggggcc agtgtcctct gtgctgtggtg cgcccgctccc cgcccccccc cggtcagcg	720
gcgtccccat cacctgcctt gctcgccacc tgggtggccac gcgtacctgc acagtcacgc	780
cggggaggcc cctggctcca ggaggcggga gtcgcctgcg gctcagtcaa gatgggcgga	840
aactccacat cggcaacttc agcctggatt gggacctggg aaattactcc gtgctgtgca	900
gtggggccgat ggggtgctggc ggtgaccaga tcacctgcat tgtgagaagg gtctctagag	960
tgcgattgca gcactattct tgcgcgaaa agagtcttga gacctcagtt tctgagagaa	1020
gaacctgag gaacagacgt tccctggcgg ccttggcgcc ttcaaaccga gac atg Met 1	1076
ctg ctg ctg ctg ctg ctg ctg ccc ctg ctc tgg ggg aca aag ggg atg Leu Leu Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Thr Lys Gly Met	1124
5 10 15	
gag gga gac aga caa tat ggg gat ggt tac ttg ctg caa gtg cag gag Glu Gly Asp Arg Gln Tyr Gly Asp Gly Tyr Leu Leu Gln Val Gln Glu	1172
20 25 30	
ctg gtg acg gtg cag gag ggc ctg tgt gtc cat gtg ccc tgc tcc ttc Leu Val Thr Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe	1220
35 40 45	
tcc tac ccc cag gat ggc tgg act gac tct gac cca gtt cat ggc tac Ser Tyr Pro Gln Asp Gly Trp Thr Asp Ser Asp Pro Val His Gly Tyr	1268
50 55 60 65	
tgg ttc cgg gca gga gac aga cca tac caa gac gct cca gtg gcc aca Trp Phe Arg Ala Gly Asp Arg Pro Tyr Gln Asp Ala Pro Val Ala Thr	1316
70 75 80	
aac aac cca gac aga gaa gtg cag gca gag acc cag ggc cga ttc caa Asn Asn Pro Asp Arg Glu Val Gln Ala Glu Thr Gln Gly Arg Phe Gln	1364
85 90 95	
ctc ctt ggg gac att tgg agc aac gac tgc tcc ctg agc atc aga gac Leu Leu Gly Asp Ile Trp Ser Asn Asp Cys Ser Leu Ser Ile Arg Asp	1412
100 105 110	
gcc agg aag agg gat aag ggg tca tat ttc ttt cgg cta gag aga gga Ala Arg Lys Arg Asp Lys Gly Ser Tyr Phe Phe Arg Leu Glu Arg Gly	1460
115 120 125	
agc atg aaa tgg agt tac aaa tca cag ttg aat tac aaa act aag cag Ser Met Lys Trp Ser Tyr Lys Ser Gln Leu Asn Tyr Lys Thr Lys Gln	1508
130 135 140 145	
ctg tct gtg ttt gtg aca gac cct cct tgg aac ttg acc atg act gtc Leu Ser Val Phe Val Thr Asp Pro Pro Trp Asn Leu Thr Met Thr Val	1556
150 155 160	
ttc caa gga gat gcc aca gca tcc aca gcc ctg gga aat ggc tca tct Phe Gln Gly Asp Ala Thr Ala Ser Thr Ala Leu Gly Asn Gly Ser Ser	1604
165 170 175	
ctt tca gtc ctt gag ggc cag tct ctg cgc ctg gtc tgt gct gtc aac Leu Ser Val Leu Glu Gly Gln Ser Leu Arg Leu Val Cys Ala Val Asn	1652
180 185 190	

agc aat ccc cct gcc agg ctg agc tgg acc cgg ggg agc ctg acc ctg	1700
Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Arg Gly Ser Leu Thr Leu	
195 200 205	
tgc ccc tca cgg tcc tca aac cct ggg ctg ctg gag ctg cct cga gtg	1748
Cys Pro Ser Arg Ser Ser Asn Pro Gly Leu Leu Glu Leu Pro Arg Val	
210 215 220 225	
cac gtg agg gat gaa ggg gaa ttc acc tgc cga gct cag aac gct cag	1796
His Val Arg Asp Glu Gly Glu Phe Thr Cys Arg Ala Gln Asn Ala Gln	
230 235 240	
ggc tcc cag cac att tcc ctg agc ctc tcc ctg cag aat gag ggc aca	1844
Gly Ser Gln His Ile Ser Leu Ser Leu Ser Leu Gln Asn Glu Gly Thr	
245 250 255	
ggc acc tca aga cct gta tca caa gtg aca ctg gca gca gtc ggg gga	1892
Gly Thr Ser Arg Pro Val Ser Gln Val Thr Leu Ala Ala Val Gly Gly	
260 265 270	
gct gga gcc aca gcc ctg gcc ttc ctg tcc ttc tgc atc atc ttc atc	1940
Ala Gly Ala Thr Ala Leu Ala Phe Leu Ser Phe Cys Ile Ile Phe Ile	
275 280 285	
ata gtg agg tcc tgc agg aag aaa tcg gca agg cca gca gcg ggc gtg	1988
Ile Val Arg Ser Cys Arg Lys Lys Ser Ala Arg Pro Ala Ala Gly Val	
290 295 300 305	
ggg gat aca ggc atg gaa gat gca aag gcc atc agg ggc tcg gcc tct	2036
Gly Asp Thr Gly Met Glu Asp Ala Lys Ala Ile Arg Gly Ser Ala Ser	
310 315 320	
cag gga ccc ctg act gaa tcc tgg aaa gat ggc aac ccc ctg aag aag	2084
Gln Gly Pro Leu Thr Glu Ser Trp Lys Asp Gly Asn Pro Leu Lys Lys	
325 330 335	
cct ccc cca gct gtt gcc ccc tcg tca ggg gag gaa gga gag ctc cat	2132
Pro Pro Pro Ala Val Ala Pro Ser Ser Gly Glu Glu Gly Glu Leu His	
340 345 350	
tat gca acc ctc agc ttc cat aaa gtg aag cct cag gac ccg cag gga	2180
Tyr Ala Thr Leu Ser Phe His Lys Val Lys Pro Gln Asp Pro Gln Gly	
355 360 365	
cag gag gcc act gac agt gaa tac tcg gag atc aag atc cac aag cga	2228
Gln Glu Ala Thr Asp Ser Glu Tyr Ser Glu Ile Lys Ile His Lys Arg	
370 375 380 385	
gaa act gca gag act cag gcc tgt ttg agg aat cac aac ccc tcc agc	2276
Glu Thr Ala Glu Thr Gln Ala Cys Leu Arg Asn His Asn Pro Ser Ser	
390 395 400	
aaa gaa gtc aga ggc tga ttctca cagaacaaga accctctaga gccccatgct	2330
Lys Glu Val Arg Gly *	
405	
atgcagtagg tcaccagggc tcctctctcc tgtctaacca aaacttgagc caatgtctcc	2390
cctttccccg gctaccaggg acccatccct gcctctagct tctactaccc accattctcc	2450
tctcgacctc tctgagggtg actatcttag attccacata gagatgaggt catgtggtac	2510
ttgcctctct gtgtgtgggt cattttacac aaaaaatat ccctaggtt catccatgtt	2570

ctctcaaatg acagaatcaa gcaactgaata tttttttttc tttgagagat ggagtttcgc 2630  
 tctgttgccc aggttgaggat gcagtgggtc aatctctgct cactgcaacc tccacctcct 2690  
 gggttcaaac gattctcctg cctcagcttc ccaagtagct ggtactacag gcgtgtgtca 2750  
 ccacgccag ctaatttttg tatttttttag tagagacggg gtttctactat aagtgggcca 2810  
 ggctagtctc aaactcctga cctcaagtga tctgcctgcc ttggcctccc aaagtgtctg 2870  
 gatttcaggc atgagccacc gcacccag 2898

<210> 142  
 <211> 478  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (138) .. (356)

<400> 142  
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 ttaatatattt agtgtaaatt ttttatctat gaagtaaaca attttaaaag ctaaatatag 120  
 agtctcattt agaaaat atg tat tat acc ttg tgt aat ttt gta ttc ttt 170  
 Met Tyr Tyr Thr Leu Cys Asn Phe Val Phe Phe  
 1 5 10  
 aca ctt cac atg ata ttg ttt ccc aag tca tta aat att ctt cta agt 218  
 Thr Leu His Met Ile Leu Phe Pro Lys Ser Leu Asn Ile Leu Leu Ser  
 15 20 25  
 aac cag att aga tca gca ata gtt cac tta aaa cag cga aca agc tgc 266  
 Asn Gln Ile Arg Ser Ala Ile Val His Leu Lys Gln Arg Thr Ser Cys  
 30 35 40  
 att aaa aac cag cca gag cct tac caa aga gct gat gct atg aat acc 314  
 Ile Lys Asn Gln Pro Glu Pro Tyr Gln Arg Ala Asp Ala Met Asn Thr  
 45 50 55  
 aat cat agc tta gtt gct gtt cca tat gtt aat tta att tga cagagta 363  
 Asn His Ser Leu Val Ala Val Pro Tyr Val Asn Leu Ile \*  
 60 65 70  
 agagtctttg aagtccaat tctcttttgc atccaataaa ccagttttta tagtgcgtaga 423  
 acttttagac atcagcctgc agctaaactc atgtcgggaa gttgccatga ggtca 478

<210> 143  
 <211> 1322  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (328) .. (549)

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<220>
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<222> (1)...(1322)
<223> n = a,t,c or g

<400> 143
aacggtcgac gatatcggtc tgtgtgtcag ccttcctgga aggcaactaa atgaggttcac      60
agaaggcaaa gtgaaggaca tacgtaggtg actcgagtgt ccaccatcga cctgtttctgc      120
aaccagctg tcaaaatcct gcccgaagct ctttgacata agggtaacttc tggtagaatt      180
tttttaaaac ttaattactt cctgcaggct tcagaatggt tgagcatgaa aacaaatgga      240
agcaggctta ctttcgatgt cttattaagg tctttaccat gatcaatggt acctttatga      300
caagcttcat atgccttggt aggcaga      atg ttt tgg atg gta aaa atc ctg      351
                               Met Phe Trp Met Val Lys Ile Leu
                               1                               5

act ccc aaa gca tca aca ttc caa gta act act tca gtt tca gtt ccg      399
Thr Pro Lys Ala Ser Thr Phe Gln Val Thr Thr Ser Val Ser Val Pro
      10                               15                               20

ctc acc agt gct aca gga gca gcg tgc agc ggg tcc tgc ttc cat tgc      447
Leu Thr Ser Ala Thr Gly Ala Ala Cys Ser Gly Ser Cys Phe His Ser
      25                               30                               35                               40

act ggc tgt gca gga cgg cca caa aca cac gca ggt gca ccc tgc gct      495
Thr Gly Cys Ala Gly Arg Pro Gln Thr His Ala Gly Ala Pro Cys Ala
                               45                               50                               55

tct gag cag aac tct cgg aat gaa gta atg cag acg tcc aca aat gag      543
Ser Glu Gln Asn Ser Arg Asn Glu Val Met Gln Thr Ser Thr Asn Glu
                               60                               65                               70

atg tga ttccactgag ggaggctgat ttttagcagt tgttcctttt ttaacagata      599
Met *

gtctataagt ggaaactgac ctgaaacatt cagctctaaa gaaataatca caaagcacct      659
cggtgccctga tttttgcaag gcagtccttg ccggaggatc gggcattcgt gcacattcac      719
ccggagaccg tgctgtccac ttccagaagg ggaggaaggg cagcgctcag aagcacgccc      779
agactgtctc cagccctgct gccccctgct gaggccatct cgctgtctca gcccccaagt      839
tccccacag tccatgtccc tgggttatga atgtcacctg gtgtctgtca gatccccacc      899
ccattgttct tgtcaatgag caggagtggg gtggacctgc catcctgcga atcctttaca      959
gcctgcagcg ctgcctgcca actcttcaca accattagca cccactaaca atccatttcc      1019
cctggagctc ttcactctaa agatagaaga ccaaaaaata gaagtgtcct cattttctcac      1079
agtactacag gaggaggtga gaaccgatgc atccgtgcat cttaggagaa tctcatttca      1139
gacctgggct ttgagtgcgc ctctgtctca gtcagccctc tccctcgctg caggttgacg      1199
tggtgcagga cagtgcgcag tcaggcagcc ttgattttcg gttctggggg ttggtccaag      1259
gattgaccgg gtccntttt gtccattgcc ccttcntggt gcaaccctg ggtttgtttt      1319

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ggc

1322

<210> 144  
 <211> 672  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (224)..(502)

<400> 144  
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 cctccacccg aggggtcctg agccctatcc tggtttgttg ccggaccccc aagagcattc 120  
 caagcaaadc aacactgaca cattcatgat ctaatgctca gattcattca gctttctctg 180  
 actctccgct gatgcccttc atgcctaagc atgctcccgg tcc atg cac tgc aga 235  
 Met His Cys Arg  
 1  
 cag tta aag gaa gtg ctg cag ctt cct tta acc tgc agc agc tgc tgt 283  
 Gln Leu Lys Glu Val Leu Gln Leu Pro Leu Thr Cys Ser Ser Cys Cys  
 5 10 15 20  
 gtc tgt acc atg acc gtg gca ttt ccc agc gtc cag cag gtg tgg atg 331  
 Val Cys Thr Met Thr Val Ala Phe Pro Ser Val Gln Gln Val Trp Met  
 25 30 35  
 gag act gtg ctg act ctg ggt ggg ctt gat gct gct cag gat gag atc 379  
 Glu Thr Val Leu Thr Leu Gly Gly Leu Asp Ala Ala Gln Asp Glu Ile  
 40 45 50  
 cag gcg gtg agg ctc att ctc ctc cct gag tcc tct cct cag ggg cca 427  
 Gln Ala Val Arg Leu Ile Leu Leu Pro Glu Ser Ser Pro Gln Gly Pro  
 55 60 65  
 cat ggg aac ctg gct ccc tgt tct gca aag ccc ttc ttc ctt ccc caa 475  
 His Gly Asn Leu Ala Pro Cys Ser Ala Lys Pro Phe Phe Leu Pro Gln  
 70 75 80  
 gtc atg ccc ttg ggc aca gcc cct tag ggcta ggggccttca ccctcaggca 527  
 Val Met Pro Leu Gly Thr Ala Pro \*  
 85 90  
 ggctgaccca cccctgcagg ccaggatggc tgagtccttg ctgggggtgga gcacgcctgg 587  
 gcctgcctct acgaaccgaa gcacaggtta gacctcaggc ccgatgaaga ccggcgttac 647  
 cccggcacia ccaaaaggac gcccc 672

<210> 145  
 <211> 1229  
 <212> DNA  
 <213> Homo sapiens



[illegible]

Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Met  
 215 220 225

ctg agt gga gtc ggg ggc ttt gtg ctg ggc ctg ctc ttc ctt ggg gcc 834  
 Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu Phe Leu Gly Ala  
 230 235 240

ggg ctg ttc atc tac ttc agg aat cag aaa gga cac tct gga ctt cag 882  
 Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His Ser Gly Leu Gln  
 245 250 255 260

cca aga gga ttc ctg agc tga ag tgcagatgac acattcaaag aagaactttc 935  
 Pro Arg Gly Phe Leu Ser \*  
 265

tgccccagct ttgcaggatg aaaagctttc cctcctgggc tgttattctt ccacaagaga 995

gggcttttctc aggacctggt tgctactggt tcagcaactg cagaaaatgt cctcccttgt 1055

ggcttctctca gctcctgttc ttggcctgaa gcccacagc tttgatggca gcgcctcatc 1115

ttcaactttt gtgctcccct ttgcctaaac cctatggcct cctgtgcatc tgtactcacc 1175

ctgtaccaca aacacattac attattaaat gttttctcaa gatggagtta aaaa 1229

<210> 146  
 <211> 1651  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (54)..(1031)

<400> 146  
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 Met  
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atg tct cca tcc caa gcc tca ctc tta ttc tta aat gta tgt att ttt 104  
 Met Ser Pro Ser Gln Ala Ser Leu Leu Phe Leu Asn Val Cys Ile Phe  
 5 10 15

att tgt gga gaa gtt gta caa ggt aac tgt gta cat cat tct acg gac 152  
 Ile Cys Gly Glu Val Val Gln Gly Asn Cys Val His His Ser Thr Asp  
 20 25 30

tct tca gta gtt aac att gta gaa gat gga tct aat gca aaa gat gaa 200  
 Ser Ser Val Val Asn Ile Val Glu Asp Gly Ser Asn Ala Lys Asp Glu  
 35 40 45

agt aaa agt aat gat act gtt tgt aag gaa gac tgt gag gaa tca tgt 248  
 Ser Lys Ser Asn Asp Thr Val Cys Lys Glu Asp Cys Glu Glu Ser Cys  
 50 55 60 65

gat gtt aaa act aaa att aca cga gaa gaa aaa cat ttc atg tgt aga 296  
 Asp Val Lys Thr Lys Ile Thr Arg Glu Glu Lys His Phe Met Cys Arg  
 70 75 80

aat ttg caa aat tct att gtt tcc tac aca aga agt acc aaa aaa cta 344  
 Asn Leu Gln Asn Ser Ile Val Ser Tyr Thr Arg Ser Thr Lys Lys Leu

85	90	95	
cta agg aat atg atg gat gag caa caa gct tcc ttg gat tat tta tct Leu Arg Asn Met Met Asp Glu Gln Gln Ala Ser Leu Asp Tyr Leu Ser 100 105 110			392
aat cag gtt aac gag ctc atg aat aga gtt ctc ctt ttg act aca gaa Asn Gln Val Asn Glu Leu Met Asn Arg Val Leu Leu Leu Thr Thr Glu 115 120 125			440
gtt ttt aga aaa cag ctg gat cct ttt cct cac aga cct gtt cag tca Val Phe Arg Lys Gln Leu Asp Pro Phe Pro His Arg Pro Val Gln Ser 130 135 140 145			488
cat ggt tta gat tgc act gat att aag gat acc att ggc tct gtc acc His Gly Leu Asp Cys Thr Asp Ile Lys Asp Thr Ile Gly Ser Val Thr 150 155 160			536
aaa aca ccg agt ggt tta tac ata att cac cca gaa gga tct agc tac Lys Thr Pro Ser Gly Leu Tyr Ile Ile His Pro Glu Gly Ser Ser Tyr 165 170 175			584
cca ttt gag gta atg tgt gac atg gat tac aga gga ggt gga tgg act Pro Phe Glu Val Met Cys Asp Met Asp Tyr Arg Gly Gly Gly Trp Thr 180 185 190			632
gtg ata cag aaa aga att gat ggg ata att gat ttc cag agg ttg tgg Val Ile Gln Lys Arg Ile Asp Gly Ile Ile Asp Phe Gln Arg Leu Trp 195 200 205			680
tgt gat tat ctg gat gga ttt gga gat ctt cta ggt gat gca ttc cgg Cys Asp Tyr Leu Asp Gly Phe Gly Asp Leu Leu Gly Asp Ala Phe Arg 210 215 220 225			728
ggt ctc aaa aaa gaa gat aat caa aat gca atg cct ttt agc aca tca Gly Leu Lys Lys Glu Asp Asn Gln Asn Ala Met Pro Phe Ser Thr Ser 230 235 240			776
gat gtt gat aat gat ggg tgt cgc cct gca tgc ctg gtc aat ggt cag Asp Val Asp Asn Asp Gly Cys Arg Pro Ala Cys Leu Val Asn Gly Gln 245 250 255			824
tct gtg aag agc tgc agt cac ctc cat aac aag acc ggc tgg tgg ttt Ser Val Lys Ser Cys Ser His Leu His Asn Lys Thr Gly Trp Trp Phe 260 265 270			872
aac gag tgt ggt cta gca aat cta aat ggc att cat cac ttc tct gga Asn Glu Cys Gly Leu Ala Asn Leu Asn Gly Ile His His Phe Ser Gly 275 280 285			920
aaa ttg ctt gca act gga att caa tgg ggc acg tgg acc aaa aac aac Lys Leu Leu Ala Thr Gly Ile Gln Trp Gly Thr Trp Thr Lys Asn Asn 290 295 300 305			968
tca cct gtc aag att aaa tct gtt tca atg aaa att aga aga atg tac Ser Pro Val Lys Ile Lys Ser Val Ser Met Lys Ile Arg Arg Met Tyr 310 315 320			1016
aat cca tat ttt aaa taatctcatt taacattgta atgcaagttc tacaatgata Asn Pro Tyr Phe Lys 325			1071
atatattaataa gatttttaaa agttttatctt ttcacttagt gtttcaaaca tattaggcaa			1131

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aatttaactg tagatggcat ttagatgtta tgagtttaat tagaaaactt caattttgta 1191
gtattctata aaagaaaaca tggcttattg tatgttttta cttctgacta tattaacaat 1251
atacaatgaa atttgtttca agtgaactac aacttgtctt cctaaaattt atagtgattt 1311
taaaggattt tgccttttct ttgaagcatt tttaaaccat aatatgttgt aaggaaaatt 1371
gaagggaata ttttacttat ttttatactt tatatgatta tataatctac agataatttc 1431
tactgaagac agttacaata aataacttta tgcagattaa tatataagct acacatgatg 1491
taaaaacctt actattttcta ggtgatgcc aaccatttta aaagtagtaa gagtttgctg 1551
cccaaatagt ttttcttggt ttcatatcta atcatgggta actattttgt tattgtttgt 1611
aataaatata tgtactttta aaaaaaacag aaaaaaaaaa 1651

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<210> 147  
 <211> 737  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (124)..(336)

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<400> 147
agcgtggtgg aattcctcag ccaagatgaa gcatgccttt tcaaaaagaa cacccccaaa 60
taagtatttt accattatct aaaagactac ttttgctggg ttttattttt taatctattg 120
aac  atg aga aca tgg tca aaa gtc ata cct tcc tta tgg ttg aaa ttt 168
    Met Arg Thr Trp Ser Lys Val Ile Pro Ser Leu Trp Leu Lys Phe
        1             5             10             15
tct aga ggt ttt ata ata ttg aga ttt cat ttt tta atg ata att tgg 216
Ser Arg Gly Phe Ile Ile Leu Arg Phe His Phe Leu Met Ile Ile Trp
        20             25             30
cct gac ata cct tcc agt atg tac att tgt atg agt ttt atc aca gca 264
Pro Asp Ile Pro Ser Ser Met Tyr Ile Cys Met Ser Phe Ile Thr Ala
        35             40             45
ttt aaa aat ctc ttt atg ttt gga att aat agg att aaa aaa atc tca 312
Phe Lys Asn Leu Phe Met Phe Gly Ile Asn Arg Ile Lys Lys Ile Ser
        50             55             60
gta gtt tct aga aat act tta tag tgacagtttt gttttttagt cttccagatt 366
Val Val Ser Arg Asn Thr Leu *
        65             70
gttgatatta atgcaaacaa tattaagctt atatcacaaa aatattttca gtaaagcgta 426
ttttttataa actgtgttag gcactgggaa taatacaaaa atgataaata aagcctgtcc 486
cttgccgatg gtcacagtcg ggctacagct gccagaaaca aggccagcaa aattaggata 546
cagcttgcca atgtagtgtg aagaaaggcc ttcggaatac caaagaaaat tctaggggtca 606
gggaaagctt tgaagagaag gtgatgttca gctatgtttg aagaatgggg agggctcatc 666

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agcgatagaa cattctagat aggtttggaa gcatgagagc atggagcaat tgggaaaacc 726  
 caatatgccc g 737

<210> 148  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (3) ..(1217)

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 Met Ala Ser Ser Gly Pro Ala Met Leu Arg Gly Pro Trp Arg Phe  
 1 5 10 15

ttt tgg ctc ttt ctc ctg ctg ctg ctc ccg ggc gcg ccc gac cca cgc 95  
 Phe Trp Leu Phe Leu Leu Leu Leu Leu Pro Gly Ala Pro Asp Pro Arg  
 20 25 30

gtc cgc tcc agg ccg tgg gag gga acc gac gag ccg ggc tcg gcc tgg 143  
 Val Arg Ser Arg Pro Trp Glu Gly Thr Asp Glu Pro Gly Ser Ala Trp  
 35 40 45

gcc tgg ccg ggc ttc cag cgc ctg cag gag cag ctc agg gcg gcg ggt 191  
 Ala Trp Pro Gly Phe Gln Arg Leu Gln Glu Gln Leu Arg Ala Ala Gly  
 50 55 60

gcc ctc tcc aag cgg tac tgg acg ctc ttc agc tgc cag gtg tgg ccc 239  
 Ala Leu Ser Lys Arg Tyr Trp Thr Leu Phe Ser Cys Gln Val Trp Pro  
 65 70 75

gac gac tgt gac gag gac gag gag gca gcc acg ggg ccc ctg ggc tgg 287  
 Asp Asp Cys Asp Glu Asp Glu Glu Ala Ala Thr Gly Pro Leu Gly Trp  
 80 85 90 95

cgc ctt cct ctg ttg ggc cag cgg tac ctg gac ctc ctg acc acg tgg 335  
 Arg Leu Pro Leu Leu Gly Gln Arg Tyr Leu Asp Leu Leu Thr Thr Trp  
 100 105 110

tac tgc agc ttc aaa gac tgc tgc cct aga ggg gat tgc aga atc tcc 383  
 Tyr Cys Ser Phe Lys Asp Cys Cys Pro Arg Gly Asp Cys Arg Ile Ser  
 115 120 125

aac aac ttt aca ggc tta gag tgg gac ctg aat gtg cgg ctg cat ggc 431  
 Asn Asn Phe Thr Gly Leu Glu Trp Asp Leu Asn Val Arg Leu His Gly  
 130 135 140

cag cat ttg gtc cag cag ctg gtc cta aga aca gtg agg ggc tac tta 479  
 Gln His Leu Val Gln Gln Leu Val Leu Arg Thr Val Arg Gly Tyr Leu  
 145 150 155

gag acg ccc cag cca gaa aag gcc ctt gct ctg tcg ttc cac ggc tgg 527  
 Glu Thr Pro Gln Pro Glu Lys Ala Leu Ala Leu Ser Phe His Gly Trp  
 160 165 170 175

tct ggc aca ggc aag aac ttc gtg gca cgg atg ctg gtg gag aac ctg 575  
 Ser Gly Thr Gly Lys Asn Phe Val Ala Arg Met Leu Val Glu Asn Leu

	180	185	190	
tat cgg gac ggg ctg atg agt gac tgt gtc agg atg ttc atc gcc acg				623
Tyr Arg Asp Gly Leu Met Ser Asp Cys Val Arg Met Phe Ile Ala Thr				
	195	200	205	
ttc cac ttt cct cac ccc aaa tat gtg gac ctg tac aag gag cag ctg				671
Phe His Phe Pro His Pro Lys Tyr Val Asp Leu Tyr Lys Glu Gln Leu				
	210	215	220	
atg agc cag atc cgg gag acg cag cag ctc tgc cac cag acc ctg ttc				719
Met Ser Gln Ile Arg Glu Thr Gln Gln Leu Cys His Gln Thr Leu Phe				
	225	230	235	
atc ttc gat gaa gcg gag aag ctg cac cca ggg ctg ctg gag gtc ctt				767
Ile Phe Asp Glu Ala Glu Lys Leu His Pro Gly Leu Leu Glu Val Leu				
	240	245	250	255
ggg cca cac tta gaa cgc cgg gcc cct gag ggc cac agg gct gag tct				815
Gly Pro His Leu Glu Arg Arg Ala Pro Glu Gly His Arg Ala Glu Ser				
	260	265	270	
cca tgg act atc ttt ctg ttt ctc agt aat ctc agg ggc gat ata atc				863
Pro Trp Thr Ile Phe Leu Phe Leu Ser Asn Leu Arg Gly Asp Ile Ile				
	275	280	285	
aat gag gtg gtc cta aag ttg ctc aag gct gga tgg tcc cgg gaa gaa				911
Asn Glu Val Val Leu Lys Leu Lys Ala Gly Trp Ser Arg Glu Glu				
	290	295	300	
att acg atg gaa cac ctg gag ccc cac ctc cag gcg gag att gtg gag				959
Ile Thr Met Glu His Leu Glu Pro His Leu Gln Ala Glu Ile Val Glu				
	305	310	315	
acc ata gac aat ggc ttt ggc cac agc cgt ctt gtg aag gaa aac ctg				1007
Thr Ile Asp Asn Gly Phe Gly His Ser Arg Leu Val Lys Glu Asn Leu				
	320	325	330	335
att gac tac ttc atc ccc ttc ctg cct ttg gag tac cgt cac gtg agg				1055
Ile Asp Tyr Phe Ile Pro Phe Leu Pro Leu Glu Tyr Arg His Val Arg				
	340	345	350	
ctg tgt gca cgg gat gcc ttc ctg agc cag gag ctc ctg tat aaa gaa				1103
Leu Cys Ala Arg Asp Ala Phe Leu Ser Gln Glu Leu Leu Tyr Lys Glu				
	355	360	365	
gag aca ctg gat gaa ata gcc cag atg atg gtg tat gtc ccc aag gag				1151
Glu Thr Leu Asp Glu Ile Ala Gln Met Met Val Tyr Val Pro Lys Glu				
	370	375	380	
gaa caa ctc ttt tct tcc cag ggc tgc aag tct att tcc cag agg att				1199
Glu Gln Leu Phe Ser Ser Gln Gly Cys Lys Ser Ile Ser Gln Arg Ile				
	385	390	395	
aac tac ttc ctg tca tga aggcta gaggaagact tccctggaact gcctttcttc				1253
Asn Tyr Phe Leu Ser *				
	400	405		
ca				1255

&lt;210&gt; 149

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<210> 150
<211> 836
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73)..(210)
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<400>	150	
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ggatacattt at       atg ctt tgc agt ctc ttc cat ata tta ata gtt aca		108
Met Leu Cys Ser Leu Phe His Ile Leu Ile Val Thr		
1                                    5                                    10		
tta ttg ctg gcc atc tca ttt ggg atg tct tct agg aat act ctg aat		156
Leu Leu Leu Ala Ile Ser Phe Gly Met Ser Ser Arg Asn Thr Leu Asn		
15                                    20                                    25		
atg gtc aat tca aag att aaa gag cat tca ctc cat aga aaa ctt gaa		204
Met Val Asn Ser Lys Ile Lys Glu His Ser Leu His Arg Lys Leu Glu		
30                                    35                                    40		
ata tga aatcttatag ctcagatatg aaggaaactt agcagtttcc ccagatttga		260
Ile *		

45

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caattctaaa aattacatgg tgctactaat acatagttga ggatgtaaaa gaagcctcta 320
taaactgcca aaaagaaaaa taaaagggga ttttccatta aaaatgtatg tgctatgtaa 380
ttttaaatga gatcatgcca ttatatagat tttttttttt tggacggagt tttgctcctg 440
ttgcccaggc tggagtgtaa tggggccatc tcggcttgct gcaacctcca cctcctgggt 500
tcaagcgatt ctccagcctc agcctcccaa gtggctgaga ttgcaggcac cgccaccacc 560
cccgcaaaat tttggaattt taagaagata ggggggtcca cattttggcc cggctgggtc 620
taaacttcct gatccaccaa cttaaccctc caaagggcgt ggataacagg gggagccacc 680
cgccctgcca gaatatgaat ttttaaatgg atgtttggag gcacactaca tatttcctag 740
actacttcg atattttttt acggggaacc tatattttac ccattggaaa taaaaaaaaa 800
atattttatt ttaaaaagga ggattggccc ctgggc 836

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<210> 151  
 <211> 871  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (33)..(242)

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<400> 151
ccatcgatta cgccaagctt ggcacgagga tt  atg ttt tgg acc ctg gtt cag 53
                                   Met Phe Trp Thr Leu Val Gln
                                   1 5

ggg atg tcc tta ctg tgt cta act gat gtg ttt cag gct ctt cct tca 101
Gly Met Ser Leu Leu Cys Leu Thr Asp Val Phe Gln Ala Leu Pro Ser
    10 15 20

ata tgt att gcg aat agt gag att tat tac aca gtc cta aca ttg atg 149
Ile Cys Ile Ala Asn Ser Glu Ile Tyr Tyr Thr Val Leu Thr Leu Met
    25 30 35

cag ttt agt tgc ttg tgg atg gtg ttg tca gga aaa aag gta ata ttt 197
Gln Phe Ser Cys Leu Trp Met Val Leu Ser Gly Lys Lys Val Ile Phe
    40 45 50 55

tct tct gaa ctc atg gtt aga aag ggc agg aga agc tgg aag taa gat 245
Ser Ser Glu Leu Met Val Arg Lys Gly Arg Arg Ser Trp Lys *
    60 65 70

atcctccatc ctctttagac atatttacat cacctcttcc aggtttgcat attgcttaca 305

atcaatacag agaagagaaa acaaaggaaa tatgtgataa gttgataaat tactgctaca 365

aaattttaat tctggcccta aagcaataac aaagtagaac atagtgaac aagtacacaa 425

aagatttaaa actggggata cagaagttcc aaagcaagga gaaaaagga aattattata 485

actggactta aaattcaaaa aaatggtatt tagaactaag aaattaattt gagtgaatt 545

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aatgttagaa taaaaataaa attgaaatca acatgagggga agagtctaaa gcatgcatat 605  
 atgattgaaa gagcaagaca actcacagga aaagctaaaa atcaagtaga agcaagattt 665  
 tgactggaaa gaagcagcac gagtgaatgg atggaaatga aaaaaagatc tacagagata 725  
 tccactgcaa gaggagtttt catcgccagg gcaccagctt ctccagttac cttcccctgt 785  
 aagtgggacc acaggccctt cctgtggaag agccctcagt gactaaacag cataactctgg 845  
 cttttctcat ttcttcctta ggggcg 871

<210> 152  
 <211> 650  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (238) .. (381)

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 aatgtatgtc catcaagaaa aggatatatt tgttgagtaa actttaaaat taggaagggg 120  
 atcatctatg atacattaac atatatctga tgatacatga gctgatgata tatgctatga 180  
 tatattagca tattctaatt agcatatatc atcagcatat atgggaatgt cattggc 237  
 atg tat ttg aag ccc tta ata tac ttt tct att ttg ata ttt ttg agt 285  
 Met Tyr Leu Lys Pro Leu Ile Tyr Phe Ser Ile Leu Ile Phe Leu Ser  
 1 5 10 15  
 caa agg agt aaa tta tcc ctt ccc tac aat gtt cac aat tgt atg aat 333  
 Gln Arg Ser Lys Leu Ser Leu Pro Tyr Asn Val His Asn Cys Met Asn  
 20 25 30  
 ata ggt gaa gat agg cga ccc cag aaa gta cag ctg ctt cag ttg tac 381  
 Ile Gly Glu Asp Arg Arg Pro Gln Lys Val Gln Leu Leu Gln Leu Tyr  
 35 40 45  
 taataagtaa tcatcatcct gcaagaagta tggtgtgact tctcctacaa ttaactatca 441  
 tatagtttaa tatatgttta atattattat aaaaagtaga aaaataaaat ttatttagaa 501  
 gcaaggatta gattgcaata attattatat ttataatttc tagcatgttt ggggggggga 561  
 ccatttgagg ttcctaaacc aatggggcgg gtttttttaa aacccaaacc ttcccacaaa 621  
 aatttttagg ctttaacctt aaaaaaggc 650

<210> 153  
 <211> 518  
 <212> DNA  
 <213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; (347) .. (496)

<400> 153  
aaccattgcgg aaccgccccg gaatttccgg gtcgaccac gcgtccggcc cgcctgggcc 60  
tcctaaagtg cttggattac agttgtgagc caccagcccc ggccgactat tttctcttat 120  
ttcaaaatta catattctta tacactatgg aacttggaataa ataagggaaa gcataaagaa 180  
aatTTaaatc acccataatt tcacaaacca gagatgaaac cactgctaac agttgctgta 240  
atttcttcca gtctcttttc tacagtgaga tctgtatttc tagctggcta cacatagtat 300  
aaatctaggt ttagaatcaa gtagaaatag ctctaaagtg ctgccg atg ctg cca 355  
Met Leu Pro  
1  
ttg gct ctg ata gtg gat ctc att tat ccc tgg gtc cag gtg aga ggt 403  
Leu Ala Leu Ile Val Asp Leu Ile Tyr Pro Trp Val Gln Val Arg Gly  
5 10 15  
cct gag gac cca aat cat ggg aca aca gag aga aaa aga gaa gag gtg 451  
Pro Glu Asp Pro Asn His Gly Thr Thr Glu Arg Lys Arg Glu Glu Val  
20 25 30 35  
acc tgc cta ggg gcg gcc cgg ctg agt ttg gaa gcc gca agg tga act 499  
Thr Cys Leu Gly Ala Arg Leu Ser Leu Glu Ala Ala Arg \*  
40 45 50  
ccctccatgg gagaaagct 518

&lt;210&gt; 154

&lt;211&gt; 1016

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (169) .. (879)

<400> 154  
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atcctgggga cgaaccgggc agccggagag ctgcggccgg cccagtcccg ctccgccttt 120  
gaagggtaaa acccaaggcg gggccttggt tctggcagaa gggacgct atg acc gca 177  
Met Thr Ala  
1  
gaa ttc ctc tcc ctg ctt tgc ctc ggg ctg tgt ctg ggc tac gaa gat 225  
Glu Phe Leu Ser Leu Cys Leu Gly Leu Cys Leu Gly Tyr Glu Asp  
5 10 15  
gag aaa aag aat gag aaa ccg ccc aag ccc tcc ctc cac gcc tgg ccc 273  
Glu Lys Lys Asn Glu Lys Pro Pro Lys Pro Ser Leu His Ala Trp Pro  
20 25 30 35  
agc tcg gtg gtt gaa gct gag agc aat gtg acc ctg aag tgt cag gct 321  
Ser Ser Val Val Glu Ala Glu Ser Asn Val Thr Leu Lys Cys Gln Ala  
40 45 50

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cat tcc cag aat gtg aca ttt gtg ctg cgc aag gtg aac gac tct ggg      369
His Ser Gln Asn Val Thr Phe Val Leu Arg Lys Val Asn Asp Ser Gly
          55                      60                      65

tac aag cag gaa cag agc tcg gca gaa aac gaa gct gaa ttc ccc ttc      417
Tyr Lys Gln Glu Gln Ser Ser Ala Glu Asn Glu Ala Glu Phe Pro Phe
          70                      75                      80

acg gac ctg aag cct aag gat gct ggg agg tac ttt tgt gcc tac aag      465
Thr Asp Leu Lys Pro Lys Asp Ala Gly Arg Tyr Phe Cys Ala Tyr Lys
          85                      90                      95

aca aca gcc tcc cat gag tgg tca gaa agc agt gaa cac ttg cag ctg      513
Thr Thr Ala Ser His Glu Trp Ser Glu Ser Ser Glu His Leu Gln Leu
100                      105                      110                      115

gtg gtc aca gat aaa cac gat gaa ctt gaa gct ccc tca atg aaa aca      561
Val Val Thr Asp Lys His Asp Glu Leu Glu Ala Pro Ser Met Lys Thr
          120                      125                      130

gac acc aga acc ata ttt gtc gcc atc ttc agc tgc atc tcc atc ctt      609
Asp Thr Arg Thr Ile Phe Val Ala Ile Phe Ser Cys Ile Ser Ile Leu
          135                      140                      145

ctc ctc ttc ctc tca gtc ttc atc atc tac aga tgc agc cag cac agt      657
Leu Leu Phe Leu Ser Val Phe Ile Ile Tyr Arg Cys Ser Gln His Ser
          150                      155                      160

tca tca tct gag gaa tcc acc aag aga acc agc cat tcc aaa ctt ccg      705
Ser Ser Ser Glu Glu Ser Thr Lys Arg Thr Ser His Ser Lys Leu Pro
          165                      170                      175

gag cag gag gct gcc gag gca gat tta tcc aat atg gaa agg gta tct      753
Glu Gln Glu Ala Ala Glu Ala Asp Leu Ser Asn Met Glu Arg Val Ser
180                      185                      190                      195

ctc tcg acg gca gac ccc caa gga gtg acc tat gct gag cta agc acc      801
Leu Ser Thr Ala Asp Pro Gln Gly Val Thr Tyr Ala Glu Leu Ser Thr
          200                      205                      210

agc gcc ctg ttt gag gca gct tca gac ccc acc cag gag ccc cca gga      849
Ser Ala Leu Phe Glu Ala Ala Ser Asp Pro Thr Gln Glu Pro Pro Gly
          215                      220                      225

ttt cat gaa tat gcg gca ctg aaa gtg tag c aaaaagacag ccctggccac      900
Phe His Glu Tyr Ala Ala Leu Lys Val *
          230                      235

taaaggaggg gggatcgtgc tggccaaggt tatcggaat ctggagatgc agatactgtg      960

tttccttgct ctctgtccat atcaataaaa ttaagtttct cgtcttaaaa aaaaaa      1016

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<210> 155  
 <211> 1414  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (114)..(1028)

<400> 155  
 tttctgtgagg aagttcaagg gcgagagtga gtaccagcag aaggetggga gtctgtagtt 60.  
 tgttctctgct gccaggetcc actgagggga acggggacct gtctgaagag aag atg 116  
 Met  
 1  
 ccc ctg ctg aca ctc tac ctg ctc ctc ttc tgg ctc tca ggc tac tcc 164  
 Pro Leu Leu Thr Leu Tyr Leu Leu Phe Trp Leu Ser Gly Tyr Ser  
 5 10 15  
 att gtc act caa atc acc ggt cca aca aca gtg aat ggc ttg gag cgg 212  
 Ile Val Thr Gln Ile Thr Gly Pro Thr Thr Val Asn Gly Leu Glu Arg  
 20 25 30  
 ggc tcc ttg acc gtg cag tgt gtt tac aga tca ggc ttg gag acc tac 260  
 Gly Ser Leu Thr Val Gln Cys Val Tyr Arg Ser Gly Trp Glu Thr Tyr  
 35 40 45  
 ttg aag tgg tgg tgt cga gga gct att tgg cgt gac tgc aag atc ctt 308  
 Leu Lys Trp Trp Cys Arg Gly Ala Ile Trp Arg Asp Cys Lys Ile Leu  
 50 55 60 65  
 gtt aaa acc agt ggg tca gag cag gag gtg aag agg gac cgg gtg tcc 356  
 Val Lys Thr Ser Gly Ser Glu Gln Glu Val Lys Arg Asp Arg Val Ser  
 70 75 80  
 atc aag gac aat cag aaa aac cgc acg ttc act gtg acc atg gag gat 404  
 Ile Lys Asp Asn Gln Lys Asn Arg Thr Phe Thr Val Thr Met Glu Asp  
 85 90 95  
 ctc atg aaa act gat gct gac act tac tgg tgt gga att gag aaa act 452  
 Leu Met Lys Thr Asp Ala Asp Thr Tyr Trp Cys Gly Ile Glu Lys Thr  
 100 105 110  
 gga aat gac ctt ggg gtc aca gtt caa gtg acc att gac cca gcg tcg 500  
 Gly Asn Asp Leu Gly Val Thr Val Gln Val Thr Ile Asp Pro Ala Ser  
 115 120 125  
 act cct gcc ccc acc acg cct acc tcc act acg ttt aca gca cca gtc 548  
 Thr Pro Ala Pro Thr Thr Pro Thr Ser Thr Phe Thr Ala Pro Val  
 130 135 140 145  
 acc caa gaa gaa act agc agc tcc cca act ctg acc ggc cac cac ttg 596  
 Thr Gln Glu Glu Thr Ser Ser Ser Pro Thr Leu Thr Gly His His Leu  
 150 155 160  
 gac aac agg cac aag ctc ctg aag ctc agt gtc ctc ctg ccc ctc atc 644  
 Asp Asn Arg His Lys Leu Leu Lys Leu Ser Val Leu Leu Pro Leu Ile  
 165 170 175  
 ttc acc ata ttg ctg ctg ctt ttg gtg gcc gcc tca ctc ttg gct tgg 692  
 Phe Thr Ile Leu Leu Leu Leu Val Ala Ala Ser Leu Leu Ala Trp  
 180 185 190  
 agg atg atg aag tac cag cag aaa gca gcc ggg atg tcc cca gag cag 740  
 Arg Met Met Lys Tyr Gln Gln Lys Ala Ala Gly Met Ser Pro Glu Gln  
 195 200 205  
 gta ctg cag ccc ctg gag ggc gac ctc tgc tat gca gac ctg acc ctg 788  
 Val Leu Gln Pro Leu Glu Gly Asp Leu Cys Tyr Ala Asp Leu Thr Leu  
 210 215 220 225

cag ctg gcc gga acc tcc ccg cga aag gct acc acg aag ctt tcc tct 836  
 Gln Leu Ala Gly Thr Ser Pro Arg Lys Ala Thr Thr Lys Leu Ser Ser  
                   230                  235                  240  
  
 gcc cag gtt gac cag gtg gaa gtg gaa tat gtc acc atg gct tcc ttg 884  
 Ala Gln Val Asp Gln Val Glu Val Glu Tyr Val Thr Met Ala Ser Leu  
                   245                  250                  255  
  
 ccg aag gag gac att tcc tat gca tct ctg acc ttg ggt gct gag gat 932  
 Pro Lys Glu Asp Ile Ser Tyr Ala Ser Leu Thr Leu Gly Ala Glu Asp  
                   260                  265                  270  
  
 cag gaa ccg acc tac tgc aac atg ggc cac ctc agt agc cac ctc ccc 980  
 Gln Glu Pro Thr Tyr Cys Asn Met Gly His Leu Ser Ser His Leu Pro  
                   275                  280                  285  
  
 ggc agg ggc cct gag gag ccc acg gaa tac agc acc atc agc agg cct 1028  
 Gly Arg Gly Pro Glu Glu Pro Thr Glu Tyr Ser Thr Ile Ser Arg Pro  
                   290                  295                  300                  305  
  
 tagcctgcac tccaggtccc ttcttgacc ccaggtgtg agcacactcc tgcctcatcg 1088  
 accgtctgcc ccctgtcccc ctcatcagga ccaacccggg gactgggtgcc tctgctgat 1148  
 cagccagcat tgcccctagc tctgggttgg gcttggggcc aagtctcagg gggcttctag 1208  
 gagttgggggt ttcttaaacg tcccctcctc tcctacatag ttgaggaggg ggctagggat 1268  
 atgctctggg gctttcatgg gaatgatgaa gatgataatg agaaaaatgt taccattatt 1328  
 atcatgaagt accattatca taatacaatg aacctttatt tattgcctac cacatgttat 1388  
 gggctgaata atggccccca aagata 1414

<210> 156  
 <211> 842  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (85)..(456)

<400> 156  
 ctcggtaccg gcccgcaatt cccggttcga cgggaggcac gaggggagtc tcactaaacc 60  
 ttccttggtt ggagtcagcc atac atg agg att agt tgc cct tgg tgc ttg 111  
                                   Met Arg Ile Ser Cys Pro Trp Cys Leu  
                                   1                                  5  
  
 tgg aat ctc tcc ttg gaa gtg gga ggc act gtg gcg acc act gcc cag 159  
 Trp Asn Leu Ser Leu Glu Val Gly Gly Thr Val Ala Thr Thr Ala Gln  
                   10                  15                  20                  25  
  
 cag cac ata gca gag gtg tgc aga agc agc cag gca ggg aga ggt ttt 207  
 Gln His Ile Ala Glu Val Cys Arg Ser Ser Gln Ala Gly Arg Gly Phe  
                   30                  35                  40  
  
 ctc cac tgt ttg cac cca gca ctg ggc act tct gga tgc cac cct gtt 255  
 Leu His Cys Leu His Pro Ala Leu Gly Thr Ser Gly Cys His Pro Val  
                   45                  50                  55

cct tgc agc agc tcc ctg gtg ggc ttt gga tgg agg ggc tac tca gga 303  
 Pro Cys Ser Ser Ser Leu Val Gly Phe Gly Trp Arg Gly Tyr Ser Gly  
 60 65 70

gaa gcc agc tgg ggg agg gcc agc agc cgg cca gca gcc ccc act cct 351  
 Glu Ala Ser Trp Gly Arg Ala Ser Ser Arg Pro Ala Ala Pro Thr Pro  
 75 80 85

ccc atg cca gcc aac gta cag gcc gga tgg gaa cag tct gtg agg ctt 399  
 Pro Met Pro Ala Asn Val Gln Ala Gly Trp Glu Gln Ser Val Arg Leu  
 90 95 100 105

ttg tgc cac tcc tgg ctg cgc ttg gca gct ctg cat gtc aca cat gag 447  
 Leu Cys His Ser Trp Leu Arg Leu Ala Leu His Val Thr His Glu  
 110 115 120

gaa tcc tga gtctcaa aatggcccag gaatccagca tgagctgtgc taggagtcaa 503  
 Glu Ser \*

gaggtttgcc acgactgggc ttggttcctt gttcatgagc gagcacgtcc ctgagtctat 563  
 ccactagact ggtgacgttt cctgaacacc aggggagacc aggctctgtt ctaggcacgg 623  
 gcagcagtga ggaagactgc acggcccctg aagctagtgc tgggggacag ggttgggggtg 683  
 gcatggccct catcaccagc cgccctgcgag tctgtgccag agcagattgg ggtgacaaca 743  
 gactgcactg tgtgggggtga ggggcagcat gtggctggcc cccaaatgag gggagatatg 803  
 gttagggagg caccttgccc tgttggaat gggtagggaa 842

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 <211> 877  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (391)..(528)

<400> 157  
 agtgcccctg atcacccaag ttggccagag accctggtgt ggggctgatt ctgtctggat 60  
 atacggggag gggtaagcat gaggaagga agcaggtcct gacaggtact ttgcactaaa 120  
 cagctcctta taaggttctc aatttgctg ctcaatttct acagacattt gtgggaccac 180  
 accagtacat tgtaaaagca ggaaacaatt gagaaaaacc tgagttttat gttggttagga 240  
 gaaatgccta tggaatatgg caaatcggtt ctctgagact tcctccctag taattacata 300  
 tttgttctca aaaacaaatg ccagaaggaa gaagcagatt taatagtga ttttacaagg 360  
 caccattaat ctctaagaag aacaattaaa atg tct cag caa tca tgg ttc 411  
 Met Ser Gln Gln Ser Trp Phe  
 1 5

act gta tat ctt ttc tat ctt ctt aga agt aat ata tgg ctg gaa atg 459  
 Thr Val Tyr Leu Phe Tyr Leu Leu Arg Ser Asn Ile Trp Leu Glu Met

10	15	20	
ggc ata cca aaa tat gtc aag gaa gtg gaa ttg cgt tca tta gat ttc			507
Gly Ile Pro Lys Tyr Val Lys Glu Val Glu Leu Arg Ser Leu Asp Phe			
25	30	35	
acc agt aat tat ttt agt tag ct tcacagatct ctcttccttg cttgttcttg			560
Thr Ser Asn Tyr Phe Ser *			
40	45		
agagcgaggc tttttagtag gaagagaaat tgtctaaaac gattaataac cacaaattca			620
ccaaactatt ttgggtaagt ccctctatct ctctaggtct aaagctagga ataagagtca			680
ttctcatata atgtactgtc ccagaaaggg cattatatta gtctgttttc acgtgtctga			740
taaagacata tccgggattg ggtgatgtat ttaaaaaaag aggtttaatg gactcacagt			800
tccacatgcc tggggagggt tcacaatcat ggaggaaggt gaaaggcaca tcttacatgg			860
tggcagacaa gacagaa			877
<210> 158			
<211> 793			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (49) .. (759)			
<400> 158			
aattccttgt tcgacgattt cgccacgact gaacagagag gactcaac atg gag ttt			57
		Met Glu Phe	
		1	
ggg ctg agc tgc att ttc ctt gct gct att tta aaa ggt gtc cag tgt			105
Gly Leu Ser Cys Ile Phe Leu Ala Ala Ile Leu Lys Gly Val Gln Cys			
5	10	15	
gag gtg cag ctg gtg gag tct ggc gga ggc ttg gta aag ccg ggg ggg			153
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly			
20	25	30	35
tct ctt agg ctc tcc tgt gca gcc tct gga ttc agt ttc agt aaa gcc			201
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Lys Ala			
40	45	50	
tac atg aac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt			249
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
55	60	65	
ggc cgc att aaa act aag aaa gat gct ggg aca aca gac tac gct gca			297
Gly Arg Ile Lys Thr Lys Lys Asp Ala Gly Thr Thr Asp Tyr Ala Ala			
70	75	80	
ccc gtg aaa ggc aga ttc acc atc tca aga gat gat tca gaa aat acg			345
Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Glu Asn Thr			
85	90	95	
tta cat ctg caa ctg aac agc ctg aaa acc gaa gac aca ggc ata tat			393

Leu His Leu Gln Leu Asn Ser Leu Lys Thr Glu Asp Thr Gly Ile Tyr  
 100 105 110 115  
 tat tgt tgt aca gac ccc acc tgg tac gcg gct gtg ggt ggc tcc tac 441  
 Tyr Cys Cys Thr Asp Pro Thr Trp Tyr Ala Ala Val Gly Gly Ser Tyr  
 120 125 130  
 tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc 489  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 135 140 145  
 cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc 537  
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
 150 155 160  
 aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg 585  
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 165 170 175  
 acg gtg tcg tgg aac tca gcc gcc ctg acc agc ggc gtg cac acc ttc 633  
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190 195  
 ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg 681  
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 200 205 210  
 acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg 729  
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
 215 220 225  
 aat cac aag cct gta ttg cgg gcg ctc tag a ggatcaagct tacgtacgag 780  
 Asn His Lys Pro Val Leu Arg Ala Leu \*  
 230 235  
 tgataggcct atc 793

<210> 159  
 <211> 1644  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (66)..(1499)

<400> 159  
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 tcacc atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta 107  
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu  
 1 5 10  
 aga ggt gtc cag tgt cag gtg cag ctg gtg gag tct ggg gga ggc gtg 155  
 Arg Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val  
 15 20 25 30  
 gtc cag cct ggg agg tcc ctg aga ctc tcc tgt gca gcg tct gga ttc 203  
 Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  
 35 40 45



acc ttc agt aat tat ggc atg cac tgg gtc cgc cag gct cca ggc aag	251
Thr Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys	
50 55 60	
ggg ctg gag tgg gtg gca gct ata tgg tat gat gga agt aat aaa tac	299
Gly Leu Glu Trp Val Ala Ala Ile Trp Tyr Asp Gly Ser Asn Lys Tyr	
65 70 75	
tat gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc	347
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser	
80 85 90	
aag aac acg ttg tat atg caa atg aac agc ctg aga gcc gag gac acg	395
Lys Asn Thr Leu Tyr Met Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
95 100 105 110	
gct gtg tat tat tgt gcg aga gag ggt cgg tgg gta cga tat act acg	443
Ala Val Tyr Tyr Cys Ala Arg Glu Gly Arg Trp Val Arg Tyr Thr Thr	
115 120 125	
gtg act act atc gga tac tac ttt gac tac tgg ggc cag gga acc ctg	491
Val Thr Thr Ile Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu	
130 135 140	
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	539
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
145 150 155	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	587
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
160 165 170	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	635
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
175 180 185 190	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	683
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
195 200 205	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	731
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
210 215 220	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	779
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
225 230 235	
acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa act cac	827
Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His	
240 245 250	
aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc	875
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val	
255 260 265 270	
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc	923
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	
275 280 285	
cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag	971
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu	
290 295 300	

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gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag      1019
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
      305                      310                      315

aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc      1067
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
      320                      325                      330

gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag      1115
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
      335                      340                      345                      350

tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc      1163
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
      355                      360                      365

tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc      1211
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
      370                      375                      380

cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg      1259
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
      385                      390                      395

gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat      1307
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
      400                      405                      410

ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc      1355
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
      415                      420                      425                      430

gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc agg      1403
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
      435                      440                      445

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg      1451
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
      450                      455                      460

cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa tga      1499
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
      465                      470                      475

gtgcgacggc cggcaagccc ccgctccccg ggctctcgcg gtcgcacgag gatgcttggc      1559

acgtaccccg tctacatact tcccaggcac ccagcatgga aataaagcac ccaccactgc      1619

cctgggcccc tgcgaaaaaa aaaaaa      1644

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<210> 160  
 <211> 1093  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(876)

<220>  
 <221> misc\_feature

&lt;222&gt; (1)...(1093)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 160

atg gcc atg ctc ctg ggg gca tca gtg ctg att ctg tgg ctt cag cca	48
Met Ala Met Leu Leu Gly Ala Ser Val Leu Ile Leu Trp Leu Gln Pro	
1 5 10 15	
gac tgg gta aac agt caa cag aag aat gat gac cag caa gtt aag caa	96
Asp Trp Val Asn Ser Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln	
20 25 30	
aat tca cca tcc ctg agc gtc cag gaa gga aga att tct att ctg aac	144
Asn Ser Pro Ser Leu Ser Val Gln Glu Gly Arg Ile Ser Ile Leu Asn	
35 40 45	
tgt gac tat act aac agc atg ttt gat tat ttc cta tgg tac aaa aaa	192
Cys Asp Tyr Thr Asn Ser Met Phe Asp Tyr Phe Leu Trp Tyr Lys Lys	
50 55 60	
tac cct gct gaa ggt cct aca ttc ctg ata tct ata agt tcc att aag	240
Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys	
65 70 75 80	
gat aaa aat gaa gat gga aga ttc act gtt ttc tta aac aaa agt gcc	288
Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala	
85 90 95	
aag cag ttc tct ctg cac att gtg ccc tcc cag cct gga gac tct gca	336
Lys Gln Phe Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala	
100 105 110	
gtg tac ttc tgt gca gca agc agc ccc ttt tcg tat tca gga gga ggt	384
Val Tyr Phe Cys Ala Ala Ser Ser Pro Phe Ser Tyr Ser Gly Gly Gly	
115 120 125	
gct gac gga ctc acc ttt ggc aaa ggg act cat cta atc atc cag ccc	432
Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro	
130 135 140	
tat atc cag aac cct gac cct gcc gtg tac cag ctg aga gac tct aaa	480
Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys	
145 150 155 160	
tcc agt gac aag tct gtc tgc cta ttc acc gat ttt gat tct caa aca	528
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr	
165 170 175	
aat gtg tca caa agt aag gat tct gat gtg tat atc aca gac aaa act	576
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr	
180 185 190	
gtg cta gac atg agg tct atg gac ttc aag agc aac agt gct gtg gcc	624
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala	
195 200 205	
tgg agc aac aaa tct gac ttt gca tgt gca aac gcc ttc aac aac agc	672
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser	
210 215 220	
att att cca gaa gac acc ttc ttc ccc agc cca gaa agt tcc tgt gat	720
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp	
225 230 235 240	

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gtc aag ctg gtc gag aaa agc ttt gaa aca gat acg aac cta aac ttt      768
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
                245                      250                      255

caa aac ctg tca gtg att ggg ttc cga atc ctc ctc ctg aaa gtg gcc      816
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
                260                      265                      270

ggg ttt aat ctg ctc atg acg ctg cgg ctg tgg gtc cag ctg aga tct      864
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Val Gln Leu Arg Ser
                275                      280                      285

gca aga ttg taa gga cagcctgtgc tcctctgctc cttcctctggt cattgccct      919
Ala Arg Leu *
                290

cttctccctc tccaaacaga gggggaactt cttccttacc cccaagggag ggtgaaagct      979

ggttaccca cttttgtggc ccccccggg caattgccac ccaattgggt tccttaccac      1039

gantttatgg nttaagggnt tgttgaaga ggttgnccaa acattggttg gcca          1093

<210> 161
<211> 683
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (179)..(322)

<400> 161
ctactgcct ccggaattcc cgggtcgacg atttcgtata tatttctaata gattgggctt      60

tagctttaaa aacattaggc tagatgcctc cctatttttt gtggcatgat ttagctgtaa      120

ctagcctgga ggcaataaca atactaaatg accttttgta gtcacattaa acattgaa      178
atg gta ctg aga ctg cct tgg tgg gga gtt ttg gcc tat ggg aat gat      226
Met Val Leu Arg Leu Pro Trp Trp Gly Val Leu Ala Tyr Gly Asn Asp
  1             5             10             15

gtg ggt ttt ggt ttc tac tcc ttt ctc tgt tat cag ata aat cct cct      274
Val Gly Phe Gly Phe Tyr Ser Phe Leu Cys Tyr Gln Ile Asn Pro Pro
                20             25             30

aca tgt ccc att ctc tgg ctc tgg gaa gta ctg aca gta ggg aaa agt      322
Thr Cys Pro Ile Leu Trp Leu Trp Glu Val Leu Thr Val Gly Lys Ser
                35             40             45

tagtacactc atctcattgt tcagatcaag tttcctgggt gcggttttgc aaaactttct      382

acaagagctg actcaagagt tctcttctat tgtggagatg atcctgctct tatatgtcat      442

actaatttat atccttgaaa ctgtgagcag catcatttgc atgtgttaag ttgggaatga      502

ataaagtgaa aatattttca cacattcctt gagaaaaggg ttccttttgc tgtgcaaadc      562

aacgctccct agatgctgtg gctaaaaagt gaagaattct aggccaacat ttttttacc      622

ctttcatttt ctttactttg ttttttttag aagaggtgcg aggtcctggg cccagaggt      682

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a

683

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<210> 162
<211> 1833
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (143) .. (1252)

<400> 162
gaattcccg gtcgacgatt tcgtcaggag ggagaaggag gagccagcgg aaggacgggtg      60
tgcgggcccg ccagccctgg acgaaagaag agggcccctc caggccagtc tgggcaccct      120
gggatagcgg ctgcagccag gc atg gcc gac tct gca cag gcc cag aag ctg      172
                Met Ala Asp Ser Ala Gln Ala Gln Lys Leu
                1                      5                      10

gtg tac ctg gtc aca ggg ggc tgt ggc ttc ctg gga gag cac gtg gtg      220
Val Tyr Leu Val Thr Gly Gly Cys Gly Phe Leu Gly Glu His Val Val
                15                      20                      25

cga atg ctg ctg cag cgg gag ccc cgg ctc ggg gag ctg cgg gtc ttt      268
Arg Met Leu Leu Gln Arg Glu Pro Arg Leu Gly Glu Leu Arg Val Phe
                30                      35                      40

gac caa cac ctg ggt ccc tgg ctg gag gag ctg aag aca ggg cct gtg      316
Asp Gln His Leu Gly Pro Trp Leu Glu Glu Leu Lys Thr Gly Pro Val
                45                      50                      55

agg gtg act gcc atc cag ggg gac gtg acc cag gcc cat gag gtg gca      364
Arg Val Thr Ala Ile Gln Gly Asp Val Thr Gln Ala His Glu Val Ala
                60                      65                      70

gca gct gtg gcc gga gcc cat gtg gtc atc cac acg gct ggg ctg gta      412
Ala Ala Val Ala Gly Ala His Val Val Ile His Thr Ala Gly Leu Val
                75                      80                      85                      90

gac gtg ttt ggc agg gcc agt ccc aag acc atc cat gag gtc aac gtg      460
Asp Val Phe Gly Arg Ala Ser Pro Lys Thr Ile His Glu Val Asn Val
                95                      100                      105

cag ggt acc cgg aac gtg atc gag gct tgt gtg cag acc gga aca cgg      508
Gln Gly Thr Arg Asn Val Ile Glu Ala Cys Val Gln Thr Gly Thr Arg
                110                      115                      120

ttc ctg gtc tac acc agc agc atg gaa gtt gtg ggg cct aac acc aaa      556
Phe Leu Val Tyr Thr Ser Ser Met Glu Val Val Gly Pro Asn Thr Lys
                125                      130                      135

ggt cac ccc ttc tac agg ggc aac gaa gac acc cca tac gaa gca gtg      604
Gly His Pro Phe Tyr Arg Gly Asn Glu Asp Thr Pro Tyr Glu Ala Val
                140                      145                      150

cac agg cac ccc tat cct tgc agc aag gcc ctg gcc gag tgg ctg gtc      652
His Arg His Pro Tyr Pro Cys Ser Lys Ala Leu Ala Glu Trp Leu Val
                155                      160                      165                      170

ctg gag gcc aac ggg agg aag gtc cgt ggg ggg ctg ccc ctg gtg acg      700

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Leu Glu Ala Asn Gly Arg Lys Val Arg Gly Gly Leu Pro Leu Val Thr  
 175 180 185  
 tgt gcc ctt cgt ccc acg ggc atc tac ggt gaa ggc cac cag atc atg 748  
 Cys Ala Leu Arg Pro Thr Gly Ile Tyr Gly Glu Gly His Gln Ile Met  
 190 195 200  
 agg gac ttc tac cgc cag ggc ctg cgc ctg gga ggt tgg ctc ttc cgg 796  
 Arg Asp Phe Tyr Arg Gln Gly Leu Arg Leu Gly Gly Trp Leu Phe Arg  
 205 210 215  
 gcc atc ccg gcc tct gtg gag cat ggc cgg gtc tat gtg ggc aat gtt 844  
 Ala Ile Pro Ala Ser Val Glu His Gly Arg Val Tyr Val Gly Asn Val  
 220 225 230  
 gcc tgg atg cac gtg ctg gca gcc cgg gag ctg gag cag cgg gca gcc 892  
 Ala Trp Met His Val Leu Ala Ala Arg Glu Leu Glu Gln Arg Ala Ala  
 235 240 245 250  
 ctg atg ggc ggc cag gta tac ttc tgc tac gat gga tca ccc tac agg 940  
 Leu Met Gly Gly Gln Val Tyr Phe Cys Tyr Asp Gly Ser Pro Tyr Arg  
 255 260 265  
 agc tac gag gat ttc aac atg gag ttc ctg ggc ccc tgc gga ctg cgg 988  
 Ser Tyr Glu Asp Phe Asn Met Glu Phe Leu Gly Pro Cys Gly Leu Arg  
 270 275 280  
 ctg gtg ggc gcc cgc cca ttg ctg ccc tac tgg ctg ctg gtg ttc ctg 1036  
 Leu Val Gly Ala Arg Pro Leu Leu Pro Tyr Trp Leu Leu Val Phe Leu  
 285 290 295  
 gct gcc ctc aat gcc ctg ctg cag tgg ctg ctg cgg cca ctg gtg ctc 1084  
 Ala Ala Leu Asn Ala Leu Leu Gln Trp Leu Leu Arg Pro Leu Val Leu  
 300 305 310  
 tac gca ccc ctg ctg aac ccc tac acg ctg gcc gtg gcc aac acc acc 1132  
 Tyr Ala Pro Leu Leu Asn Pro Tyr Thr Leu Ala Val Ala Asn Thr Thr  
 315 320 325 330  
 ttc acc gtc agc acc gac aag gct cag cgc cat ttc ggc tat gag ccc 1180  
 Phe Thr Val Ser Thr Asp Lys Ala Gln Arg His Phe Gly Tyr Glu Pro  
 335 340 345  
 ctg ttc tgc tgg gag gat agc cgg acc cgc acc att ctc tgg gta cag 1228  
 Leu Phe Ser Trp Glu Asp Ser Arg Thr Arg Thr Ile Leu Trp Val Gln  
 350 355 360  
 gcc gct acg ggt tca gcc cag tga cgggtggggct ggggcctgga ggccagata 1282  
 Ala Ala Thr Gly Ser Ala Gln \*  
 365 370  
 cagcacatcc acccaggtcc cgagccctca caccctggac gggaaggac agctgcattc 1342  
 cagagcagga ggcagggctc tggggccaga atggctgtcc ttgtcgtaga gccctccaca 1402  
 ttttcttttt cttttttgag acagggctctt gctctgtcac ccagactgga gtgcagtggc 1462  
 gtgatcatag ctactgcac cctcaacctc ctgggttcaa gcaatcctcc tgcctcagcc 1522  
 tctgaacag ctgggaccac aggtgcacgc caccacacct ggcttttttt tgttgttttt 1582  
 agagacaggg tctcactata ttgctcaggc tggctcttgaa ctctggggct caagtgatct 1642  
 tcccacgtgg gcctcccaaa acgctggaac tacaagtgtg agccaccgcg ccctggccca 1702

agccctccac attttcaatc caggaagcct tgagtctgtg ttgtgtcctg acacctccaa 1762  
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 tctcatccca g 1833

<210> 163  
 <211> 1777  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (299) .. (1042)

<220>  
 <221> misc\_feature  
 <222> (1) ... (1777)  
 <223> n = a,t,c or g

<400> 163  
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 tgaagcattt aaatttaatt tcttcagttt tctacagtta gacaggtgca ggagagcagc 180  
 atctgatata tgcgagctcc gtagatctag agtttggact tcaggatgta aaatctcact 240  
 tatatttgaa tctgttatct gtccctgcat actcattatt ttaatcagtc tgtctttt 298  
 atg ttg gga ggc aaa ggc tta atg tct gtg aga tat ctg gaa ata ttc 346  
 Met Leu Gly Gly Lys Gly Leu Met Ser Val Arg Tyr Leu Glu Ile Phe  
 1 5 10 15  
 ttc atg aag cct ttg cct ccc aac ata aaa gac aga ctg att aaa ata 394  
 Phe Met Lys Pro Leu Pro Pro Asn Ile Lys Asp Arg Leu Ile Lys Ile  
 20 25 30  
 atg agt atg cag gga cag ata aca gat tca aat ata agt gag att tta 442  
 Met Ser Met Gln Gly Gln Ile Thr Asp Ser Asn Ile Ser Glu Ile Leu  
 35 40 45  
 cat cct gaa gtc caa act cta gat cta cgg agc tgc gat ata tca gat 490  
 His Pro Glu Val Gln Thr Leu Asp Leu Arg Ser Cys Asp Ile Ser Asp  
 50 55 60  
 gct gct ctc ctg cac ctg tct aac tgt aga aaa ctg aag aaa tta aat 538  
 Ala Ala Leu Leu His Leu Ser Asn Cys Arg Lys Leu Lys Lys Leu Asn  
 65 70 75 80  
 tta aat gct tca aaa ggg aac cga gtt tct gta act tca gaa gga ata 586  
 Leu Asn Ala Ser Lys Gly Asn Arg Val Ser Val Thr Ser Glu Gly Ile  
 85 90 95  
 aaa gct gtg gct tca tct tgt tca tac cta cac gaa gct tct ttg aaa 634  
 Lys Ala Val Ala Ser Ser Cys Ser Tyr Leu His Glu Ala Ser Leu Lys  
 100 105 110  
 aga tgc tgc aat ctc act gac gaa gga gtc gtt gct ctt gca ctc aat 682  
 Arg Cys Cys Asn Leu Thr Asp Glu Gly Val Val Ala Leu Ala Leu Asn

115	120	125	
tgc cag ctg cta aag atc atc gat tta ggt ggc tgc tta agt att act			730
Cys Gln Leu Leu Lys Ile Ile Asp Leu Gly Gly Cys Leu Ser Ile Thr			
130	135	140	
gat gtg tcc tta cat gca tta gga aaa aac tgc cca ttt ttg cag tgt			778
Asp Val Ser Leu His Ala Leu Gly Lys Asn Cys Pro Phe Leu Gln Cys			
145	150	155	160
gtc gac ttt tca gct act cag gta tct gac agt ggt gtg att gca ctt			826
Val Asp Phe Ser Ala Thr Gln Val Ser Asp Ser Gly Val Ile Ala Leu			
	165	170	175
gtt agt gga cct tgt gcg aag aaa tta gag gag att cat atg gga cat			874
Val Ser Gly Pro Cys Ala Lys Lys Leu Glu Glu Ile His Met Gly His			
	180	185	190
tgt gta aat ctg act gat ggg gct gtc gaa gct gtc ctt act tac tgt			922
Cys Val Asn Leu Thr Asp Gly Ala Val Glu Ala Val Leu Thr Tyr Cys			
	195	200	205
cct caa ata cgt ata tta ctc ttc cat gga tgc ccc ttg ata aca gat			970
Pro Gln Ile Arg Ile Leu Leu Phe His Gly Cys Pro Leu Ile Thr Asp			
	210	215	220
cat tcc cga gaa gtg ttg gag caa tta gta ggc cca aac aaa cta aag			1018
His Ser Arg Glu Val Leu Glu Gln Leu Val Gly Pro Asn Lys Leu Lys			
	225	230	235
caa gtg aca tgg act gtt tat tga tgcttttttg aagatgatca atgctaggaa			1072
Gln Val Thr Trp Thr Val Tyr *			
	245		
agcttatcaa aactactttc ccaggaaacc atctatagag atttgcattc tacttaatgt			1132
taacactatt ttttaattatt ttattgtctt aagttataac tctcagagaa ttagctaagt			1192
cttggtatat acatgggtttg tgctttactc ttaaaccatct ttaaagtgtc attattctat			1252
atctgtttgga tgagtcatta tttttgaaat gataatccta gcatgaactc tgatctatgg			1312
tggttgattc tgtttcttaa ataactttaa aattaactgt tttcccttga gatttccttc			1372
tcctatgtag gtatttgagc tattgttcta agtttacctg taagtataaaa ccttgggaga			1432
atctaagtaa acatatttct aaaagcatag ttaccttctc attttctggc tcttaccttc			1492
ttggagtatt taaatgcca tttgccaaaa gcagacctga acatcaagcc tggttaattc			1552
ntcaaagaat ttaggggatt gggtttccccc gaaatggagt gacttattag ccattcagcg			1612
gtattaggaa tacagaggct cttgccccagc cacatccant ccattgnntt taaggggact			1672
cctcccaggt acattttaag gcaccggtag cnttcctcc ctaggcaa at tgcacccnaa			1732
aggnnggtaaa aaggggnaat acnggatatc cctcnggggc tgggt			1777

<210> 164  
 <211> 1939  
 <212> DNA



<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (1704)

<400> 164

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Met Asp Ser Ile Leu Ile Pro Pro Leu Thr Lys Arg Leu Lys Met Gly	
1 5 10 15	
aag tca ctt tac ctc tct gtg ccg cag ttt cct gct tgt aac acc tac	96
Lys Ser Leu Tyr Leu Ser Val Pro Gln Phe Pro Ala Cys Asn Thr Tyr	
20 25 30	
agc tgc tcc ctg aac ctc aga gat gcc aat gag gcg gat aca ggg acg	144
Ser Cys Ser Leu Asn Leu Arg Asp Ala Asn Glu Ala Asp Thr Gly Thr	
35 40 45	
tac ttc ttt cag gtg gag aga ggt tat tac atg aaa tac agt tac gga	192
Tyr Phe Phe Gln Val Glu Arg Gly Tyr Tyr Met Lys Tyr Ser Tyr Gly	
50 55 60	
aat gag aag ttg ttc ttg cat gtg aca agg cct cct cta agt ctt gag	240
Asn Glu Lys Leu Phe Leu His Val Thr Arg Pro Pro Leu Ser Leu Glu	
65 70 75 80	
ccc gca gtt cct gag aga aga acc ctg agg aac aga cgt tcc ctc gcg	288
Pro Ala Val Pro Glu Arg Arg Thr Leu Arg Asn Arg Arg Ser Leu Ala	
85 90 95	
gcc ctg gca cct cta acc cca gac atg ctg ctg ctg ctg ctg ccc ctg	336
Ala Leu Ala Pro Leu Thr Pro Asp Met Leu Leu Leu Leu Pro Leu	
100 105 110	
ctc tgg ggg agg gag agg gcg gaa gga cag aca agt aaa ctg ctg acg	384
Leu Trp Gly Arg Glu Arg Ala Glu Gly Gln Thr Ser Lys Leu Leu Thr	
115 120 125	
atg cag agt tcc gtg acg gtg cag gaa ggc ctg tgt gtc cat gtg ccc	432
Met Gln Ser Ser Val Thr Val Gln Glu Gly Leu Cys Val His Val Pro	
130 135 140	
tgc tcc ttc tcc tac ccc tcg cat ggc tgg att tac cct ggc cca gta	480
Cys Ser Phe Ser Tyr Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val	
145 150 155 160	
gtt cat ggc tac tgg ttc cgg gaa ggg gcc aat aca gac cag gat gct	528
Val His Gly Tyr Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala	
165 170 175	
cca gtg gcc aca aac aac cca gct cgg gca gtg tgg gag gag act cgg	576
Pro Val Ala Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg	
180 185 190	
gac cga ttc cac ctc ctt ggg gac cca cat acc gag aat tgc acc ctg	624
Asp Arg Phe His Leu Leu Gly Asp Pro His Thr Glu Asn Cys Thr Leu	
195 200 205	
agc atc aga gat gcc aga aga agt gat gcg ggg aga tac ttc ttt cgt	672
Ser Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg	
210 215 220	
atg gag aaa gga agt ata aaa tgg aat tat aaa cat cac cgg ctc tct	720

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu Ser	
225 230 235 240	
gtg aat gtg aca gcc ttg acc cac agg ccc aac atc ctc atc cca ggc	768
Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile Pro Gly	
245 250 255	
acc ctg gag tcc ggc tgc ccc cag aat ctg acc tgc tct gtg ccc tgg	816
Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser Val Pro Trp	
260 265 270	
gcc tgt gag cag ggg aca ccc cct atg atc tcc tgg ata ggg acc tcc	864
Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp Ile Gly Thr Ser	
275 280 285	
gtg tcc ccc ctg gac ccc tcc acc acc cgc tcc tgc gtg ctc acc ctc	912
Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser Ser Val Leu Thr Leu	
290 295 300	
atc cca cag ccc cag gac cat ggc acc agc ctc acc tgt cag gtg acc	960
Ile Pro Gln Pro Gln Asp His Gly Thr Ser Leu Thr Cys Gln Val Thr	
305 310 315 320	
ttc cct ggg gcc agc gtg acc acg aac aag acc gtc cat ctc aac gtg	1008
Phe Pro Gly Ala Ser Val Thr Thr Asn Lys Thr Val His Leu Asn Val	
325 330 335	
tcc tac ccg cct cag aac ttg acc atg act gtc ttc caa gga gac ggc	1056
Ser Tyr Pro Pro Gln Asn Leu Thr Met Thr Val Phe Gln Gly Asp Gly	
340 345 350	
aca gta tcc aca gtc ttg gga aat ggc tca tct ctg tca ctc cca gag	1104
Thr Val Ser Thr Val Leu Gly Asn Gly Ser Ser Leu Ser Leu Pro Glu	
355 360 365	
ggc cag tct ctg cgc ctg gtc tgt gca gtt gat gca gtt gac agc aat	1152
Gly Gln Ser Leu Arg Leu Val Cys Ala Val Asp Ala Val Asp Ser Asn	
370 375 380	
ccc cct gcc agg ctg agc ctg agc tgg aga ggc ctg acc ctg tgc ccc	1200
Pro Pro Ala Arg Leu Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro	
385 390 395 400	
tca cag ccc tca aac ccg ggg gtg ctg gag ctg cct tgg gtg cac ctg	1248
Ser Gln Pro Ser Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu	
405 410 415	
agg gat gaa gct gaa ttc acc tgc aga gct cag aac cct ctc ggc tct	1296
Arg Asp Glu Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser	
420 425 430	
cag cag gtc tac ctg aac gtc tcc ctg cag agc aaa gcc aca tca gga	1344
Gln Gln Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly	
435 440 445	
gtg act cag ggg gtg gtc ggg gga gct gga gcc aca gcc ctg gtc ttc	1392
Val Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	
450 455 460	
ctg tcc ttc tgc gtc atc ttc gtt gta gtg agg tcc tgc agg aag aaa	1440
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys Lys	
465 470 475 480	
tgc gca agg cca gca gcg ggc gtg gga gat acg ggc ata gag gat gca	1488

Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu Asp Ala  
485 490 495

aac gct gtc agg ggt tca gcc tct cag ggg ccc ctg act gaa cct tgg 1536  
Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr Glu Pro Trp  
500 505 510

gca gaa gac agt ccc cca gac cag cct ccc cca gct tct gcc cgc tcc 1584  
Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala Ser Ala Arg Ser  
515 520 525

tca gtg ggg gaa gga gag ctc cag tat gca tcc ctc agc ttc cag atg 1632  
Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser Leu Ser Phe Gln Met  
530 535 540

gtg aag cct tgg gac tcg cgg gga cag gag gcc act gac acc gag tac 1680  
Val Lys Pro Trp Asp Ser Arg Gly Gln Glu Ala Thr Asp Thr Glu Tyr  
545 550 555 560

tcg gag atc aag atc cac aga tga gaaactgcag agactcaccc tgattgaggg 1734  
Ser Glu Ile Lys Ile His Arg \*  
565

atcacagccc ctccaggcaa gggagaagtc agaggctgat tcttgtagaa ttaacagccc 1794

tcaacgtgat gagctatgat aacactatga attatgtgca gagtgaaaag cacacaggct 1854

ttagagtcaa agtatctcaa acctgaatcc acactgtgcc ctccctttta tttttttaac 1914

taaaagacag acaaattcct acctc 1939

<210> 165  
<211> 792  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (590) .. (766)

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cctgatgaca aaagcaaaaa aaaaattttt cctgaattga tacattttca gattaatatt 120

atgaatctca cttataattt atgaaaaatt ctaagggtatt aatatatacg gaaagaacag 180

tagtttgatt tgaccaattt tctaaccatct gaaataaaca cttcaaataa aatattagaa 240

taaaatatat gtactgccaa atggaaagtt aattcatttt cttaattctat aatatatata 300

gacagagatg aagaaaatgt gataattaca aaaaagatga tgaggaaacg cagtgactgt 360

ctgtaaaacc aactttttat tcacacctta gcatcatgct gaagcccact gaatgtaaaag 420

gaaatacttt tcccatgtgt atccatattt ctcaagtaaa ctgaggagtc cgtatattat 480

cgacttcagt ctgtgtacat ctaaaggggg ctactcttgg cttacaagtc aattttttaag 540

atacctgggg ctttgccctt ttttaacagcc cttttgctca gaatgttct atg ctg 595  
Met Leu

1

ttt ggg ctt gcc ttg caa ttg atc ctc gat ttg aaa ctg aca act gtg 643  
 Phe Gly Leu Ala Leu Gln Leu Ile Leu Asp Leu Lys Leu Thr Thr Val  
           5                          10                          15  
 aac cag cga gaa agt gat gtg gca aga gtt gcc acg gct gaa gaa tat 691  
 Asn Gln Arg Glu Ser Asp Val Ala Arg Val Ala Thr Ala Glu Glu Tyr  
           20                          25                          30  
 tca aag aaa ggt ctg ctt gga cag gaa aca ctt cat gct gga tca cag 739  
 Ser Lys Lys Gly Leu Leu Gly Gln Glu Thr Leu His Ala Gly Ser Gln  
           35                          40                          45                          50  
 aca aga atg cag att ctt atc tcc tga gaccc cttgaattcc accgcaagtg 791  
 Thr Arg Met Gln Ile Leu Ile Ser \*  
                                   55  
 g 792

<210> 166  
 <211> 797  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (206) .. (418)

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 ggaagcattg tcaaatatga aatggtgttg ggtttttgag ggctgcattt ttaaaatattg 120  
 ttattagtat gtgttccaaa attatgggaa attcctataa ttctatataa ctcaagtgtac 180  
 attatcagta ataatcataa ttgtt atg tta aaa tta ttg tgt gcc gca gag 232  
                                   1                                  5  
                                   Met Leu Lys Leu Leu Cys Ala Ala Glu  
 gta aca aat gtc ctt ttc aac tgt gtt ttt gac tat ggc tgt cct aaa 280  
 Val Thr Asn Val Leu Phe Asn Cys Val Phe Asp Tyr Gly Cys Pro Lys  
           10                          15                          20                          25  
 act ttt tgt cat cca tgg aca att ttt gtc ttg ttt tgg tcc tct tta 328  
 Thr Phe Cys His Pro Trp Thr Ile Phe Val Leu Phe Trp Ser Ser Leu  
                           30                          35                          40  
 gaa ggt ggc ttt ata atc agc tac aaa act cta aca ggt gct ctt gaa 376  
 Glu Gly Gly Phe Ile Ile Ser Tyr Lys Thr Leu Thr Gly Ala Leu Glu  
                           45                          50                          55  
 tgc agg ttt ctg ata act ttg gag att gtg aca tca gaa tag aggaaaa 425  
 Cys Arg Phe Leu Ile Thr Leu Glu Ile Val Thr Ser Glu \*  
           60                          65                          70  
 acttttcagga ctcatggaga gctataaaat attcatgagt atcaagcaga acaggaatta 485  
 actgcatgga ctgaactgat ctttttgact ttttgcttaa aaagttgctg atctttttgt 545  
 ttgcttttca gagccttaaa actttttcttt tgagctattg gcagctttta acaattttacg 605

atacttccat aaacaaaget, tgcagcctat ttgttgctct ttaactgact tctgccgaat 665  
 tcgcacacta ttcgctcgca ctccctactc atcggccctc cggcaatacc ccacccggcc 725  
 ccaccaatcc tgtgctcctc gatacctaga cccctactgg gcgcacctgc gttcgcctac 785  
 caccgagtgg cg 797

<210> 167  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (241)..(1050)

<400> 167  
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 gggttgactc cgcccccttc tcccaaaggt aaagcaaggt tttcaggcat cactgcaaag 120  
 ggcagctagt attcccatcc ttgtctaaca agctgtaagg agaagttggt tctgagatct 180  
 gagcctgaag agaggggaaca agtcagtcag ccttcgtggt cagaagagaa acctgtgacc 240  
 atg agg agc agc ctg acc atg gtg gga acc ctc tgg gcc ttc ctg tcc 288  
 Met Arg Ser Ser Leu Thr Met Val Gly Thr Leu Trp Ala Phe Leu Ser  
 1 5 10 15  
 ctt gtt act gct gtg acc agt tct acc agt tac ttc cta cct tac tgg 336  
 Leu Val Thr Ala Val Thr Ser Ser Thr Ser Tyr Phe Leu Pro Tyr Trp  
 20 25 30  
 ctc ttt gga tcc cag atg ggg aag cca gtg tca ttc agc aca ttc cgg 384  
 Leu Phe Gly Ser Gln Met Gly Lys Pro Val Ser Phe Ser Thr Phe Arg  
 35 40 45  
 agg tgc aac tac cct gtg cgg gga gag gga cac agt ctg atc atg gtg 432  
 Arg Cys Asn Tyr Pro Val Arg Gly Glu Gly His Ser Leu Ile Met Val  
 50 55 60  
 gaa gaa tgt ggg cgc tat gcc agc ttc aat gcc atc cca agc ctg gcc 480  
 Glu Glu Cys Gly Arg Tyr Ala Ser Phe Asn Ala Ile Pro Ser Leu Ala  
 65 70 75 80  
 tgg cag atg tgc aca gtg gtg aca ggt gcc ggc tgt gct ctg ctg ctc 528  
 Trp Gln Met Cys Thr Val Val Thr Gly Ala Gly Cys Ala Leu Leu Leu  
 85 90 95  
 ctg gtg gca cta gct gct gtc ctg ggt tgc tgc atg gag gag ctc atc 576  
 Leu Val Ala Leu Ala Ala Val Leu Gly Cys Cys Met Glu Glu Leu Ile  
 100 105 110  
 tcc aga atg atg gga cgt tgc atg gga gca gcg cag ttt gtt gga ggg 624  
 Ser Arg Met Met Gly Arg Cys Met Gly Ala Ala Gln Phe Val Gly Gly  
 115 120 125  
 ctg ctg ata agc tca ggc tgt gcc tta tac cct tta gga tgg aat agc 672  
 Leu Leu Ile Ser Ser Gly Cys Ala Leu Tyr Pro Leu Gly Trp Asn Ser

130	135	140	
ccg gag ata atg caa aca tgt ggg aat gtc tcc aat caa ttt cag tta			720
Pro Glu Ile Met Gln Thr Cys Gly Asn Val Ser Asn Gln Phe Gln Leu			
145	150	155	160
ggc acc tgt cgg ctt ggc tgg gcc tat tac tgt gct gga ggt gga aca			768
Gly Thr Cys Arg Leu Gly Trp Ala Tyr Tyr Cys Ala Gly Gly Gly Thr			
165	170	175	
cct gca gcc atg ttg atc tgc ccc tgg ctc tct tgc ttt gct gga aga			816
Pro Ala Ala Met Leu Ile Cys Pro Trp Leu Ser Cys Phe Ala Gly Arg			
180	185	190	
aac ccc cag cct gtc ata ttg ggg ggg aag cac cat gag gaa aac cac			864
Asn Pro Gln Pro Val Ile Leu Gly Gly Lys His His Glu Glu Asn His			
195	200	205	
ttc tta tgc tat gga gct tgg cca ttg ccc tca acc ctt gag ctt cga			912
Phe Leu Cys Tyr Gly Ala Trp Pro Leu Pro Ser Thr Leu Glu Leu Arg			
210	215	220	
aaa gaa gac cgg ggg ggg cgg gca aca ggg aag caa gtg acc ccc caa			960
Lys Glu Asp Arg Gly Gly Arg Ala Thr Gly Lys Gln Val Thr Pro Gln			
225	230	235	240
cca ctt aga ttc cat gtc tct act tgg atg tct agt aga ctt gac aga			1008
Pro Leu Arg Phe His Val Ser Thr Trp Met Ser Ser Arg Leu Asp Arg			
245	250	255	
gtg tac ata tcc ata acc aag atc caa atc ttc caa tcc taa acccat			1056
Val Tyr Ile Ser Ile Thr Lys Ile Gln Ile Phe Gln Ser *			
260	265	270	

<210> 168  
 <211> 958  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (73)..(858)

<220>  
 <221> misc\_feature  
 <222> (1)..(958)  
 <223> n = a,t,c or g

taacgcgatc tgagcctgaa gagagggaaac aagtcagtca gccttcgagg acattttatt	60
tatcctgtga cc atg aag agc agc ctg acc gtg gtg gga acc ctc tgg	108
Met Lys Ser Ser Leu Thr Val Val Gly Thr Leu Trp	
1 5 10	
gcc ttc ctg tcc ctt gtt act gct gtg acc agt tct acc agt tac ttc	156
Ala Phe Leu Ser Leu Val Thr Ala Val Thr Ser Ser Thr Ser Tyr Phe	
15 20 25	
cta cct tac tgg ctc ttt gga tcc cag atg ggg aag cca gtg tca ttc	204

Leu Pro Tyr Trp Leu Phe Gly Ser Gln Met Gly Lys Pro Val Ser Phe	
30 35 40	
agc aca ttc cgg agg tgc aac tac cct gtg cgg gga gag gga cac agt	252
Ser Thr Phe Arg Arg Cys Asn Tyr Pro Val Arg Gly Glu Gly His Ser	
45 50 55 60	
ctg atc atg gtg gaa gaa tgt ggg cgc tat gcc agc ttc aat gcc atc	300
Leu Ile Met Val Glu Glu Cys Gly Arg Tyr Ala Ser Phe Asn Ala Ile	
65 70 75	
cca agc ctg gcc tgg cag atg tgc aca gtg gtg aca ggt gcc ggc tgt	348
Pro Ser Leu Ala Trp Gln Met Cys Thr Val Val Thr Gly Ala Gly Cys	
80 85 90	
gct ctg ctg ctc ctg gag tca cta gct gct gtc ctg ggt tgc tgc atg	396
Ala Leu Leu Leu Leu Glu Ser Leu Ala Ala Val Leu Gly Cys Cys Met	
95 100 105	
gag gag ctc atc tcc aga atg atg gga cgt tgc atg gga gca gcg cag	444
Glu Glu Leu Ile Ser Arg Met Met Gly Arg Cys Met Gly Ala Ala Gln	
110 115 120	
ttt gtt gga ggt cca atg cag ccc ttc tgt gaa gcc ttc cct gat cta	492
Phe Val Gly Gly Pro Met Gln Pro Phe Cys Glu Ala Phe Pro Asp Leu	
125 130 135 140	
ctt ttg aca tct tta gca gat atg aac gat cct gta act cca aga gga	540
Leu Leu Thr Ser Leu Ala Asp Met Asn Asp Pro Val Thr Pro Arg Gly	
145 150 155	
ata tgg ggt aga atg aat ggc ggg ggc tgg ggg ggt ggg ctg ctg ata	588
Ile Trp Gly Arg Met Asn Gly Gly Gly Trp Gly Gly Gly Leu Leu Ile	
160 165 170	
agc tca ggc tgt gcc tta tac cct tta gga tgg aat agc ccg gag ata	636
Ser Ser Gly Cys Ala Leu Tyr Pro Leu Gly Trp Asn Ser Pro Glu Ile	
175 180 185	
atg caa aca tgt ggg aat gtc tcc aat caa ttt cag tta ggt acc tgt	684
Met Gln Thr Cys Gly Asn Val Ser Asn Gln Phe Gln Leu Gly Thr Cys	
190 195 200	
cgg ctt ggc tgg gcc tat tac tgt gct gga ggt gga gca gct gca gcc	732
Arg Leu Gly Trp Ala Tyr Tyr Cys Ala Gly Gly Gly Ala Ala Ala	
205 210 215 220	
atg ttg atc tgc acc tgg ctc tct tgc ttt gct gga aga aac ccc aag	780
Met Leu Ile Cys Thr Trp Leu Ser Cys Phe Ala Gly Arg Asn Pro Lys	
225 230 235	
cct gtc ata ttg gtg gag agc atc atg agg aat acc aat tct tat gct	828
Pro Val Ile Leu Val Glu Ser Ile Met Arg Asn Thr Asn Ser Tyr Ala	
240 245 250	
atg gag ctt gac cat tgc ctc aaa cct tga g ctttgaaaga agattggaga	879
Met Glu Leu Asp His Cys Leu Lys Pro *	
255 260	
gggttgggaa nggggaagga gggagccctg aaaaagaagg tacntaggggt ttaaggccat	939
tttntcaacc tgacttttt	958

<210> 169  
 <211> 1906  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (108)..(1748)

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tggcctggga tgaagagggg actgcctaag gctgggggtgg ctccaag  atg ccg gca      116
                                     Met Pro Ala
                                     1

tgg gaa act ggg ggt ttc ctg gta act gga ctc cta gca aac tcc caa      164
Trp Glu Thr Gly Gly Phe Leu Val Thr Gly Leu Leu Ala Asn Ser Gln
      5              10              15

gga ttc agg atg tcg ctg ctg agc ctg ccc tgg ctg ggc ctc aga ccg      212
Gly Phe Arg Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro
      20              25              30              35

gtg gca acg tcc cca tgg cta ctc ctg ctg ctg gtt gtg ggc tcc tgg      260
Val Ala Thr Ser Pro Trp Leu Leu Leu Leu Leu Val Val Gly Ser Trp
              40              45              50

cta ctc gcc cgc atc ctg gct tgg acc tat gcc ttc tat aac aac tgc      308
Leu Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys
              55              60              65

cgc cgg ctc cag tgt ttc cca cag ccc cca aaa cgg aac tgg ttt tgg      356
Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe Trp
              70              75              80

ggt cac ctg ggc ctg atc act cct aca gag gag ggc ttg aag aac tcg      404
Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys Asn Ser
              85              90              95

acc cag atg tcg gcc acc tat tcc cag ggc ttt acg ata tgg ctg ggt      452
Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Ile Trp Leu Gly
      100              105              110              115

ccc atc atc ccc ttc atc gtt tta tgc cac cct gac acc atc cgg tct      500
Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp Thr Ile Arg Ser
              120              125              130

atc acc aat gcc tca gct gcc att gca ccc aag gat aat ctc ttc atc      548
Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys Asp Asn Leu Phe Ile
              135              140              145

agg ttc ctg aag ccc tgg ctg gga gaa ggg ata ctg ctg agt ggc ggt      596
Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly Ile Leu Leu Ser Gly Gly
              150              155              160

gac aag tgg agc cgc cac cgt cgg atg ctg acg ccc gcc ttc cat ttc      644
Asp Lys Trp Ser Arg His Arg Arg Met Leu Thr Pro Ala Phe His Phe
              165              170              175

aac atc ctg aag tcc tat ata acg atc ttc aac aag agt gca aac atc      692
Asn Ile Leu Lys Ser Tyr Ile Thr Ile Phe Asn Lys Ser Ala Asn Ile

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180	185	190	195	
atg ctt gac aag tgg cag cac ctg gcc tca gag ggc agc agt tgt ctg Met Leu Asp Lys Trp Gln His Leu Ala Ser Glu Gly Ser Ser Cys Leu	200	205	210	740
gac atg ttt gag cac atc agc ctc atg acc ttg gac agt cta cag aaa Asp Met Phe Glu His Ile Ser Leu Met Thr Leu Asp Ser Leu Gln Lys	215	220	225	788
tgc atc ttc agc ttt gac agc cat tgt cag gag agg ccc agt gaa tat Cys Ile Phe Ser Phe Asp Ser His Cys Gln Glu Arg Pro Ser Glu Tyr	230	235	240	836
att gcc acc atc ttg gag ctc agt gcc ctt gta gag aaa aga agc cag Ile Ala Thr Ile Leu Glu Leu Ser Ala Leu Val Glu Lys Arg Ser Gln	245	250	255	884
cat atc ctc cag cac atg gac ttt ctg tat tac ctc tcc cat gac ggg His Ile Leu Gln His Met Asp Phe Leu Tyr Tyr Leu Ser His Asp Gly	260	265	270	932
cgg cgc ttc cac agg gcc tgc cgc ctg gtg cat gac ttc acg gac gct Arg Arg Phe His Arg Ala Cys Arg Leu Val His Asp Phe Thr Asp Ala	280	285	290	980
gtc atc cgg gag cgg cgt cgc acc ctc ccc act cag ggt att gat gat Val Ile Arg Glu Arg Arg Arg Thr Leu Pro Thr Gln Gly Ile Asp Asp	295	300	305	1028
ttt ttc aaa gac aaa gcc aag tcc aag act ttg gat ttc att gat gtg Phe Phe Lys Asp Lys Ala Lys Ser Lys Thr Leu Asp Phe Ile Asp Val	310	315	320	1076
ctt ctg ctg agc aag gat gaa gat ggg aag gca ttg tca gat gag gat Leu Leu Leu Ser Lys Asp Glu Asp Gly Lys Ala Leu Ser Asp Glu Asp	325	330	335	1124
ata aga gca gag gct gac acc ttc atg ttt gga ggc cat gac acc acg Ile Arg Ala Glu Ala Asp Thr Phe Met Phe Gly Gly His Asp Thr Thr	340	345	350	1172
gcc agt ggc ctc tcc tgg gtc ctg tac aac ctt gcg agg cac cca gaa Ala Ser Gly Leu Ser Trp Val Leu Tyr Asn Leu Ala Arg His Pro Glu	360	365	370	1220
tac cag gag cgc tgc cga cag gag gtg caa gag ctt ctg aag gac cgc Tyr Gln Glu Arg Cys Arg Gln Glu Val Gln Glu Leu Leu Lys Asp Arg	375	380	385	1268
gat cct aaa gag att gaa tgg gac gac ctg gcc cag ctg ccc ttc ctg Asp Pro Lys Glu Ile Glu Trp Asp Asp Leu Ala Gln Leu Pro Phe Leu	390	395	400	1316
acc atg tgc gtg aag gag agc ctg agg tta cat ccc cca gct ccc ttc Thr Met Cys Val Lys Glu Ser Leu Arg Leu His Pro Pro Ala Pro Phe	405	410	415	1364
atc tcc cga tgc tgc acc cag gac att gtt ctc cca gat ggc cga gtc Ile Ser Arg Cys Cys Thr Gln Asp Ile Val Leu Pro Asp Gly Arg Val	420	425	430	1412
atc ccc aaa ggc att acc tgc ctc atc gat att ata ggg gtc cat cac Ile Pro Lys Gly Ile Thr Cys Leu Ile Asp Ile Ile Gly Val His His				1460

440	445	450	
aac cca act gtg tgg ccg gat cct gag gtc tac gac ccc ttc cgc ttt			1508
Asn Pro Thr Val Trp Pro Asp Pro Glu Val Tyr Asp Pro Phe Arg Phe			
455	460	465	
gac cca gag aac agc aag ggg agg tca cct ctg gct ttt att cct ttc			1556
Asp Pro Glu Asn Ser Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe			
470	475	480	
tcc gca ggg ccc agg aac tgc atc ggg cag gcg ttc gcc atg gcg gag			1604
Ser Ala Gly Pro Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu			
485	490	495	
atg aaa gtg gtc ctg gcg ttg atg ctg ctg cac ttc cgg ttc ctg cca			1652
Met Lys Val Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro			
500	505	510	515
gac cac act gag ccc cgc agg aag ctg gaa ttg atc atg cgc gcc gag			1700
Asp His Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu			
520	525	530	
ggc ggg ctt tgg ctg cgg gtg gag ccc ctg aat gta agc ttg cag tga			1748
Gly Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Ser Leu Gln *			
535	540	545	
ctttctgacc catccacctg tttttttgca gattgtcatg aataaaacgg tgctgtcaaa			1808
aaaaaaaaag ggggggcccct ttaaagggat caaagtttaa taccgggggc ggggaagggt			1868
aaatcttttt atagggggcc caaaaattaa atctcggg			1906

<210> 170  
 <211> 1882  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (108) .. (1814)

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tggcctggga tgaagagggg actgcctaag gctggggtgg ctccaag atg ccg gca	116
Met Pro Ala	
1	
tgg gaa act ggg ggt ttc ctg gta act gga ctc cta gca aac tcc caa	164
Trp Glu Thr Gly Gly Phe Leu Val Thr Gly Leu Leu Ala Asn Ser Gln	
5 10 15	
gga ttc agg atg tcg ctg ctg agc ctg ccc tgg ctg ggc ctc aga ccg	212
Gly Phe Arg Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro	
20 25 30 35	
gtg gca acg tcc cca tgg cta ctc ctg ctg ctg gtt gtg ggc tcc tgg	260
Val Ala Thr Ser Pro Trp Leu Leu Leu Leu Leu Val Val Gly Ser Trp	
40 45 50	
cta ctc gcc cgc atc ctg gct tgg acc tat gcc ttc tat aac aac tgc	308

Leu Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys	
55 60 65	
cgc cgg ctc cag tgt ttc cca cag ccc cca aaa cgg aac tgg ttt tgg	356
Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe Trp	
70 75 80	
ggt cac ctg ggc ctg atc act cct aca gag gag ggc ttg aag aac tcg	404
Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys Asn Ser	
85 90 95	
acc cag atg tgc gcc acc tat tcc cag ggc ttt acg ata tgg ctg ggt	452
Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Ile Trp Leu Gly	
100 105 110 115	
ccc atc atc ccc ttc atc gtt tta tgc cac cct gac acc atc cgg tct	500
Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp Thr Ile Arg Ser	
120 125 130	
atc acc aat gcc tca gct gcc att gca ccc aag gat aat ctc ttc atc	548
Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys Asp Asn Leu Phe Ile	
135 140 145	
agg ttc ctg aag ccc tgg ctg gga gaa ggg ata ctg ctg agt ggc ggt	596
Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly Ile Leu Leu Ser Gly Gly	
150 155 160	
gac aag tgg agc cgc cac cgt cgg atg ctg acg ccc gcc ttc cat ttc	644
Asp Lys Trp Ser Arg His Arg Arg Met Leu Thr Pro Ala Phe His Phe	
165 170 175	
aac atc ctg aag tcc tat ata acg atc ttc aac aag agt gca aac atc	692
Asn Ile Leu Lys Ser Tyr Ile Thr Ile Phe Asn Lys Ser Ala Asn Ile	
180 185 190 195	
atg ctt gac aag tgg cag cac ctg gcc tca gag ggc agc agt tgt ctg	740
Met Leu Asp Lys Trp Gln His Leu Ala Ser Glu Gly Ser Ser Cys Leu	
200 205 210	
gac atg ttt gag cac atc agc ctc atg acc ttg gac agt cta cag aaa	788
Asp Met Phe Glu His Ile Ser Leu Met Thr Leu Asp Ser Leu Gln Lys	
215 220 225	
tgc atc ttc agc ttt gac agc cat tgt cag gag agg ccc agt gaa tat	836
Cys Ile Phe Ser Phe Asp Ser His Cys Gln Glu Arg Pro Ser Glu Tyr	
230 235 240	
att gcc acc atc ttg gag ctc agt gcc ctt gta gag aaa aga agc cag	884
Ile Ala Thr Ile Leu Glu Leu Ser Ala Leu Val Glu Lys Arg Ser Gln	
245 250 255	
cat atc ctc cag cac atg gac ttt ctg tat tac ctc tcc cat gac ggg	932
His Ile Leu Gln His Met Asp Phe Leu Tyr Tyr Leu Ser His Asp Gly	
260 265 270 275	
cgg cgc ttc cac agg gcc tgc cgc ctg gtg cat gac ttc aca gac gct	980
Arg Arg Phe His Arg Ala Cys Arg Leu Val His Asp Phe Thr Asp Ala	
280 285 290	
gtc atc cgg gag cgg cgt cgc acc ctc ccc act cag ggt att gat gat	1028
Val Ile Arg Glu Arg Arg Arg Thr Leu Pro Thr Gln Gly Ile Asp Asp	
295 300 305	
ttt ttc aaa gac aaa gcc aag tcc aag act ttg gat ttc att gat gtg	1076

Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp	Val	
		310					315					320				
ctt	ctg	ctg	agc	aag	gat	gaa	gat	ggg	aag	gca	ttg	tca	gat	gag	gat	1124
Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp	Glu	Asp	
		325				330					335					
ata	aga	gca	gag	gct	gac	acc	ttc	atg	ttt	gga	ggg	cct	caa	tat	ctg	1172
Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	Pro	Gln	Tyr	Leu	
340					345					350					355	
ggc	gct	gtc	cac	cct	ccg	gtg	ctg	aag	cca	agc	tta	cct	ggc	tgc	tcc	1220
Gly	Ala	Val	His	Pro	Pro	Val	Leu	Lys	Pro	Ser	Leu	Pro	Gly	Cys	Ser	
				360					365					370		
tca	ggc	cat	gac	acc	acg	gcc	agt	ggc	ctc	tcc	tgg	gtc	ctg	tac	aac	1268
Ser	Gly	His	Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	
			375					380					385			
ctt	gcg	agg	cac	cca	gaa	tac	cag	gag	cgc	tgc	cga	cag	gag	gtg	caa	1316
Leu	Ala	Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	
		390					395					400				
gag	ctt	ctg	aag	gac	cgc	gat	cct	aaa	gag	att	gaa	tgg	gac	gac	ctg	1364
Glu	Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu	
	405					410					415					
gcc	cag	ctg	ccc	ttc	ctg	acc	atg	tgc	gtg	aag	gag	agc	ctg	agg	tta	1412
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg	Leu	
420					425					430					435	
cat	ccc	cca	gct	ccc	ttc	atc	tcc	cga	tgc	tgc	acc	cag	gac	att	gtt	1460
His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp	Ile	Val	
				440					445					450		
ctc	cca	gat	ggc	cga	gtc	atc	ccc	aaa	ggc	att	acc	tgc	ctc	atc	gat	1508
Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys	Leu	Ile	Asp	
			455				460						465			
att	ata	ggg	gtc	cat	cac	aac	cca	act	gtg	tgg	ccg	gat	cct	gga	gtc	1556
Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro	Asp	Pro	Gly	Val	
		470					475					480				
tac	gac	ccc	ttc	cgc	ttt	gac	cca	gag	aac	agc	aag	ggg	agg	tca	cct	1604
Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser	Lys	Gly	Arg	Ser	Pro	
	485					490					495					
ctg	gct	ttt	att	ccc	ttc	tcc	gca	ggg	ccc	agg	aac	tgc	atc	ggg	cag	1652
Leu	Ala	Phe	Ile	Pro	Phe	Ser	Ala	Gly	Pro	Arg	Asn	Cys	Ile	Gly	Gln	
500					505					510					515	
gcg	ttc	gcc	atg	gcg	gag	atg	aaa	gtg	gtc	ctg	gcg	ttg	atg	ctg	ctg	1700
Ala	Phe	Ala	Met	Ala	Glu	Met	Lys	Val	Val	Leu	Ala	Leu	Met	Leu	Leu	
				520					525					530		
cac	ttc	cgg	ttc	ctg	cca	gac	cac	act	gag	ccc	cgc	agg	aag	ctg	gaa	1748
His	Phe	Arg	Phe	Leu	Pro	Asp	His	Thr	Glu	Pro	Arg	Arg	Lys	Leu	Glu	
			535					540					545			
ctg	atc	atg	cgc	gcc	gag	ggc	ggg	ctt	tgg	ctg	cgg	gtg	gag	ccc	ctg	1796
Leu	Ile	Met	Arg	Ala	Glu	Gly	Gly	Leu	Trp	Leu	Arg	Val	Glu	Pro	Leu	
		550					555					560				
aat	gta	ggc	ttg	cag	tga	ctttct	gaaccatcca	cctgtttttt	tgcagattgt							1850

Asn Val Gly Leu Gln \*  
565

catgaataaaa acggtgctgt caaaaaaaaa aa

1882

<210> 171  
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<212> DNA  
<213> Homo sapiens

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<221> CDS  
<222> (100)..(1389)

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gcctcaggat ctcaccctcc atcctgtctg ccctgcagg atg ccg cag ctg agc 114  
Met Pro Gln Leu Ser  
1 5  
ctg tcc tgg ctg ggc ctc ggg cag gtg gca gca ttc ccg tgg ctg ctc 162  
Leu Ser Trp Leu Gly Leu Gln Val Ala Ala Phe Pro Trp Leu Leu  
10 15 20  
ctg ctg ctg gct ggg gcc tcc cgg ctc ctg gcc ggc ttc ctg gcc tgg 210  
Leu Leu Leu Ala Gly Ala Ser Arg Leu Leu Ala Gly Phe Leu Ala Trp  
25 30 35  
acc tat gcc ttc tat gac aac tgc cgc cgc ctt cag tac ttt cca caa 258  
Thr Tyr Ala Phe Tyr Asp Asn Cys Arg Arg Leu Gln Tyr Phe Pro Gln  
40 45 50  
ccc cca aaa cag aaa tgg ttt tgg ggt caa cca gga cct cct gct att 306  
Pro Pro Lys Gln Lys Trp Phe Trp Gly Gln Pro Gly Pro Pro Ala Ile  
55 60 65  
gcg ccc aag gat gat ctc tcc atc agg ttc ctg aag ccc tgg ctg gga 354  
Ala Pro Lys Asp Asp Leu Ser Ile Arg Phe Leu Lys Pro Trp Leu Gly  
70 75 80 85  
gaa ggg ata ctg ctg agt ggc ggt gac aag tgg agc cgc cac cgt cgg 402  
Glu Gly Ile Leu Leu Ser Gly Gly Asp Lys Trp Ser Arg His Arg Arg  
90 95 100  
atg ctg acg ccc gcc ttc cat ttc aac atc ctg aaa ccc tat ata aag 450  
Met Leu Thr Pro Ala Phe His Phe Asn Ile Leu Lys Pro Tyr Ile Lys  
105 110 115  
atc ttc aac agg agt gtg aac atc atg cac gac aag tgg cag cac ctg 498  
Ile Phe Asn Arg Ser Val Asn Ile Met His Asp Lys Trp Gln His Leu  
120 125 130  
gcc tca gag ggc agc agt cgt ctg gac atg ttt gag cac atc agc ctc 546  
Ala Ser Glu Gly Ser Ser Arg Leu Asp Met Phe Glu His Ile Ser Leu  
135 140 145  
atg acc ttg gac agt ctg cag aaa tgc atc ttc agc ttt gac agc cat 594  
Met Thr Leu Asp Ser Leu Gln Lys Cys Ile Phe Ser Phe Asp Ser His  
150 155 160 165

tgt cag gag agg ccc agt gaa tat att gct acc atc ttg gag ctc agt	642
Cys Gln Glu Arg Pro Ser Glu Tyr Ile Ala Thr Ile Leu Glu Leu Ser	
170 175 180	
gcc ctt gta gaa aaa aga aac cag cat atc ctc cag cac atg gac ttt	690
Ala Leu Val Glu Lys Arg Asn Gln His Ile Leu Gln His Met Asp Phe	
185 190 195	
ctg tat tac ctc tcc cat gac ggg tgg cgc ttc cgc agg gcc tgc cgc	738
Leu Tyr Tyr Leu Ser His Asp Gly Trp Arg Phe Arg Arg Ala Cys Arg	
200 205 210	
ctg gtg cac gac ttc aca gat gcc gtc atc cag gag cgg cgc cat acc	786
Leu Val His Asp Phe Thr Asp Ala Val Ile Gln Glu Arg Arg His Thr	
215 220 225	
ctt ccc act cag ggc cat gac acc aca gcc agt ggt ctc tcc tgg gtc	834
Leu Pro Thr Gln Gly His Asp Thr Thr Ala Ser Gly Leu Ser Trp Val	
230 235 240 245	
ctg tac aac ctc gcg agg cac cca gaa tac cag gag cac tgc cgg cag	882
Leu Tyr Asn Leu Ala Arg His Pro Glu Tyr Gln Glu His Cys Arg Gln	
250 255 260	
gag gtg caa gag ctt ctg aag gac cgc gat cct aaa gag att gaa tgg	930
Glu Val Gln Glu Leu Leu Lys Asp Arg Asp Pro Lys Glu Ile Glu Trp	
265 270 275	
gac gac ctg gcc cag ctg ccc ttc ctg acc atg tgc gtg aag gag agc	978
Asp Asp Leu Ala Gln Leu Pro Phe Leu Thr Met Cys Val Lys Glu Ser	
280 285 290	
ctg agg tta cat ccc cca gct ccc ttc atc tcc cga tgc tgc acc cag	1026
Leu Arg Leu His Pro Pro Ala Pro Phe Ile Ser Arg Cys Cys Thr Gln	
295 300 305	
gac att gtt ctc cca gat ggc cga gtc atc ccc aaa ggc att acc tgc	1074
Asp Ile Val Leu Pro Asp Gly Arg Val Ile Pro Lys Gly Ile Thr Cys	
310 315 320 325	
ctc atc gat att ata ggg gtc cat cac aac cca act gtg tgg ccg gat	1122
Leu Ile Asp Ile Ile Gly Val His His Asn Pro Thr Val Trp Pro Asp	
330 335 340	
cct gag gtc tac gac ccc ttc cgc ttt gac cca gag aac agc aag ggg	1170
Pro Glu Val Tyr Asp Pro Phe Arg Phe Asp Pro Glu Asn Ser Lys Gly	
345 350 355	
agg tca cct ctg gct ttt att cct ttc tcc gca ggg ccc agg aac tgc	1218
Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro Arg Asn Cys	
360 365 370	
atc ggg cag gcg ttc gcc atg gcg gag atg aaa gtg gtc ctg gcg ttg	1266
Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val Val Leu Ala Leu	
375 380 385	
atg ctg ctg cac ttc cgg ttc ctg cca gac cac act gag ccc cgc agg	1314
Met Leu Leu His Phe Arg Phe Leu Pro Asp His Thr Glu Pro Arg Arg	
390 395 400 405	
aag ctg gaa ttg atc atg cgc gcc gag ggc ggg ctt tgg ctg cgg gtg	1362
Lys Leu Glu Leu Ile Met Arg Ala Glu Gly Leu Trp Leu Arg Val	
410 415 420	

gag ccc ctg aat gta agc ttg cag tga ctttc tgacccatcc acctgttttt 1414  
 Glu Pro Leu Asn Val Ser Leu Gln \*  
 425 430

ttgcagattg tcatgaataa aacggtgctg tcaaaaaaaaa aaaagggggg gcccttttaa 1474

gggatcaaaag ttttaataccc ggggcgggga agggtaaatac tttttatagg gggcccaaaa 1534

attaaatctc ggg 1547

<210> 172  
 <211> 1005  
 <212> DNA  
 <213> Homo sapiens

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 <221> CDS  
 <222> (257)..(400)

<220>  
 <221> misc\_feature  
 <222> (1)...(1005)  
 <223> n = a,t,c or g

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 gggctctgccc tcgaccgcn nnncttcgac gggctgatgt atataactat ctattcgatg 60

atgaagatac cccaccaaac ccaaaaaaag agatctctcg aggatccgaa ttcgcggccg 120

cgtcgaccac ttgctgaact ggctcctggg gccatgaggc tgactgccc actgctgctg 180

ctgctgctgg gagcctgggc catcccaggg ggcctcgggg acagggcgcc actcacagcc 240

acagcccccac aactgg atg atg agg aga tgt act cag ccc aca tgc ccg 289  
 Met Met Arg Arg Cys Thr Gln Pro Thr Cys Pro  
 1 5 10

ctc acc tgc gct gtg atg cct gca gag ctg tgg ctt acc aga tgt ggc 337  
 Leu Thr Cys Ala Val Met Pro Ala Glu Leu Trp Leu Thr Arg Cys Gly  
 15 20 25

aaa atc tgg caa agg cag aga cca aac ttc ata cct caa act ctg ggg 385  
 Lys Ile Trp Gln Arg Gln Arg Pro Asn Phe Ile Pro Gln Thr Leu Gly  
 30 35 40

ggc ggc ggg agc tga gcgagttggt ctacacggat gtcttgacc ggagctgctc 440  
 Gly Gly Gly Ser \*  
 45

ccggaactgg caggactacg gagttcgaga agtggaccaa gtgaaacgtc tcacaggccc 500

aggacttagc gaggggccag agccaagcat cagcgtgatg gtcacagggg gcccttgccc 560

taccaggctc tccaggacat gtttgacta cttgggggag tttggagaag accagatcta 620

tgaagcccac caacaaggcc gaggggctct ggaggcattg ctatgtgggg gacccaggg 680

ggcctgctca gagaagggtg cagccacaag agaagagctc tagtctgga ctctaccctc 740

ctctgaaaga agctgggggt tgctctgacg gtctccactc ccgtctgcag gcagccagga 800

gggcaggaag cccttgctct gtgctgccat cctgcctccc tcctccagcc tcagggcact 860  
 cgggcctggg tgggagtcaa cgccttcccc tctggactca aataaaacgt cgacgcggcc 920  
 gcgaattcgg atcctcgaga gatctctttt ttggggttg gtggggatc ttcacatcg 980  
 aatagatagt tatatacatc agccc 1005

<210> 173  
 <211> 1406  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (782)..(1327)

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 agcaccagag gaaaagagca gggatttacc ctgttcttac aggataacag ctccctgctc 120  
 ttttcagcta gcttttcaaa ggacagggat aggacagccc cctgccttat ttcggatact 180  
 tggatctata acctccagaa attcaagctg aagtagctgg aggtcggaga ggaatgagaa 240  
 ctgcctgggt ggggtctgcc agccagacac tgccaggata gccacaagga gacaacttgg 300  
 aagaacagac agcaaccacg ttggactcag gcagtcctgg gtttgaatcc tgtctctgtc 360  
 accacctagc ctgatgacct tgggcacatc ctgagcacc tgtgccttat ctgtaaaatg 420  
 gaaacaatca tgccgacctt tcagggtggt tttgaggatt agagactagc tcctgacaca 480  
 cagtaggtaa tcgtaaattg gtgctattat ttggcccgac ccacgttata ggacagaacg 540  
 tctaacggat gcgtcagaac ctgcgccctc cggatcttgg agggtagaga gggcgcccct 600  
 cggcctcctc cctttcggag gtggggacaa ggtggaggaa gggctgcagg aggaggagct 660  
 ctgacatcgc gacccgcccc gtcccgcca gtctggcctg ggcgcgcgg gaacgtgtc 720  
 ctagctgcg ccaccgaac agcctgtcct ggtgccccgg ctccctgccc cgcgccagt 780  
 c atg acc ctg cgc ccc tca ctc ctc ccg ctc cat ctg ctg ctg ctg 826  
 Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu  
 1 5 10 15  
 ctg ctg ctc agt gcg gcg gtg tgc cgg gct gag gct ggg ctc gaa acc 874  
 Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr  
 20 25 30  
 gaa agt ccc gtc cgg acc ctc caa gtg gag acc ctg ggg gag ccc cca 922  
 Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Gly Glu Pro Pro  
 35 40 45  
 aaa cca tgt gcc gag ccc gct gct ttt gga gac acg ctt cac ata cac 970  
 Lys Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His  
 50 55 60  
 tac acg gga agc ttg gta gat gga cgt att att gac acc tcc ctg acc 1018



Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr  
 65 70 75  
 aga gac cct ctg gtt ata gaa ctt ggc caa aag cag gtg att cca ggt 1066  
 Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly  
 80 85 90 95  
 ctg gag cag agt ctt ctc gac atg tgt gtg gga gag aag cga agg gca 1114  
 Leu Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala  
 100 105 110  
 atc att cct tct cac ttg gcc tat gga aaa cgg gga ttt cca cca tct 1162  
 Ile Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser  
 115 120 125  
 gtc cca gcg gat gca gtg gtg cag tat gac gtg gag ctg att gca cta 1210  
 Val Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu  
 130 135 140  
 atc cga gcc aac tac tgg cta aag ctg gtg aag ggc att ttg cct ctg 1258  
 Ile Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu  
 145 150 155  
 gta ggg atg gcc atg gtg ccc acg cct cct ggg cct cat tgg gta tca 1306  
 Val Gly Met Ala Met Val Pro Thr Pro Pro Gly Pro His Trp Val Ser  
 160 165 170 175  
 cct ata cag aaa ggc caa tag ac ccaaagtctc caaaaagaag ctcaaggaag 1359  
 Pro Ile Gln Lys Gly Gln \*  
 180  
 agaaacgaaa caagagcaaa aagaaataat aaataataaa ttttaaa 1406

<210> 174  
 <211> 2383  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (937) .. (2037)

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 agggcccctg cggtcggcaa gctgggtccc cgggtggcca ccgggacccc cgagcccaat 180  
 ggcggggggc gcggcaaat cgacaacact gtagagatca cccccacctc caacggacag 240  
 gtcgggaccc tcggagatgc ggtgcccacg gagcagctgc aggggtgagc ggagcgcgag 300  
 cgggaggggg agggagacgc gggcggcgac ggaactgggca gcagcctgtc gctggccgtg 360  
 cccccaggcc ccctcagctt tgaggcgctg ctcgcccagg tgggggcgct gggcggcggc 420  
 cagcagctgc agctcggcct ctgctgcctg ccggtgctct tcgtggctct ggcatggcc 480  
 tcggacccca tcttcacgct ggcgcccccg ctgcattgcc actacggggc cttccccct 540

aatgcctctg gctgggagca gcctcccaat gccagcggcg tcagcgtcgc cagcgtgcc	600
ctagcagcca ggcgcgccag ccgtgtcgcc accagtaccg acccctcgtg cagcggcttc	660
gccccgccgg acttcaacca ttgcctcaag gattgggact ataatggcct tcctgtgctc	720
acccccaacg ccacgcgcca gtgggatctg gtgtgtgacc tgggctggca ggtgatcctg	780
gagcagatcc tcttcattctt gggttttgcc tccggctacc tgttcctggg ttaccccgca	840
gacagatttg gccatcgcg gattgtgctg ctgaccttgg ggctgggtggg ccctgtgga	900
gtaggagggg ctgctgcagg ctctccaca ggcgtc atg gcc ctc cga ttc ctc	954
Met Ala Leu Arg Phe Leu	
1 5	
ttg ggc ttt ctg ctt gcc ggt gtt gac ctg ggt gtc tac ctg atg cgc	1002
Leu Gly Phe Leu Leu Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg	
10 15 20	
ctg gag ctg tgc gac cca acc cag agg ctt cgg gtg gcc ctg gca ggg	1050
Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly	
25 30 35	
gag ttg gtg ggg gtg gga ggg cac ttc ctg ttc ctg ggc ctg gcc ctt	1098
Glu Leu Val Gly Val Gly His Phe Leu Phe Leu Gly Leu Ala Leu	
40 45 50	
gtc tct aag gat tgg cga ttc cta cag cga atg atc acc gct ccc tgc	1146
Val Ser Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys	
55 60 65 70	
atc ctc ttc ctg ttt tat ggc tgg cct ggt ttg ttc ctg gag tcc gca	1194
Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala	
75 80 85	
cgg tgg ctg ata gtg aag cgg cag att gag gag gct cag tct gtg ctg	1242
Arg Trp Leu Ile Val Lys Arg Gln Ile Glu Glu Ala Gln Ser Val Leu	
90 95 100	
agg atc ctg gct gag cga aac cgg ccc cat ggg cag atg ctg ggg gag	1290
Arg Ile Leu Ala Glu Arg Asn Arg Pro His Gly Gln Met Leu Gly Glu	
105 110 115	
gag gcc cag gag gcc ctg cag gac ctg gag aat acc tgc cct ctc cct	1338
Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu Asn Thr Cys Pro Leu Pro	
120 125 130	
gca aca tcc tcc ttt tcc ttt gct tcc ctc ctc aac tac cgc aac atc	1386
Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu Leu Asn Tyr Arg Asn Ile	
135 140 145 150	
tgg aaa aat ctg ctt atc ctg ggc ttc acc aac ttc att gcc cat gcc	1434
Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr Asn Phe Ile Ala His Ala	
155 160 165	
att cgc cac tgc tac cag cct gtg gga gga gga ggg agc cca tgc gac	1482
Ile Arg His Cys Tyr Gln Pro Val Gly Gly Gly Gly Ser Pro Ser Asp	
170 175 180	
ttc tac ctg tgc tct ctg ctg gcc agc ggc acc gca gcc ctg gcc tgt	1530
Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly Thr Ala Ala Leu Ala Cys	
185 190 195	

gtc ttc ctg ggg gtc acc gtg gac cga ttt ggc cgc cgg ggc atc ctt 1578  
 Val Phe Leu Gly Val Thr Val Asp Arg Phe Gly Arg Arg Gly Ile Leu  
 200 205 210

ctt ctc tcc atg acc ctt acc ggc att gct tcc ctg gtc ctg ctg ggc 1626  
 Leu Leu Ser Met Thr Leu Thr Gly Ile Ala Ser Leu Val Leu Leu Gly  
 215 220 225 230

ctg tgg gat tat ctg aac gag gct gcc atc acc act ttc tct gtc ctt 1674  
 Leu Trp Asp Tyr Leu Asn Glu Ala Ala Ile Thr Thr Phe Ser Val Leu  
 235 240 245

ggg ctc ttc tcc tcc caa gct gcc gcc atc ctc agc acc ctc ctt gct 1722  
 Gly Leu Phe Ser Ser Gln Ala Ala Ile Leu Ser Thr Leu Leu Ala  
 250 255 260

gct gag gtc atc ccc acc act gtc cgg ggc cgt ggc ctg ggc ctg atc 1770  
 Ala Glu Val Ile Pro Thr Thr Val Arg Gly Arg Gly Leu Gly Leu Ile  
 265 270 275

atg gct cta ggg gcg ctt gga gga ctg agc ggc ccg gcc cag cgc ctc 1818  
 Met Ala Leu Gly Ala Leu Gly Gly Leu Ser Gly Pro Ala Gln Arg Leu  
 280 285 290

cac atg ggc cat gga gcc ttc ctg cag cac gtg gtg ctg gcg gcc tgc 1866  
 His Met Gly His Gly Ala Phe Leu Gln His Val Val Leu Ala Ala Cys  
 295 300 305 310

gcc ctc ctc tgc att ctc agc att atg ctg ctg ccg gag acc aag cgc 1914  
 Ala Leu Leu Cys Ile Leu Ser Ile Met Leu Leu Pro Glu Thr Lys Arg  
 315 320 325

aag ctc ctg ccc gag gtg ctc cgg gac ggg gag ctg tgt cgc cgg cct 1962  
 Lys Leu Leu Pro Glu Val Leu Arg Asp Gly Glu Leu Cys Arg Arg Pro  
 330 335 340

tcc ctg ctg cgg cag cca ccc cct acc cgc tgt gac cac gtc ccg ctg 2010  
 Ser Leu Leu Arg Gln Pro Pro Thr Arg Cys Asp His Val Pro Leu  
 345 350 355

ctt gcc acc ccc aac cct gcc ctc tga gcggc ctctgagtac cctggcggga 2062  
 Leu Ala Thr Pro Asn Pro Ala Leu \*  
 360 365

ggctggccca cacagaaagg tggcaagaag atcggaaga ctgagtaggg aaggcagggc 2122

tgcccagaag tctcagaggc acctcagcc agccatcgcg gagagctcag agggccgtcc 2182

ccaccctgcc tctccctgc tgctttgcat tcaacttcctt ggccagagtc aggggacagg 2242

gagagagctc cacactgtaa ccaactgggtc tgggtccat cctgcgcccc aagacatcca 2302

cccagacctc attattttctt gctctatcat tctgtttcaa taaagacatt tggaataaac 2362

gagcatatca taaaaaaaaa a 2383

&lt;210&gt; 175

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (32) .. (286)

&lt;400&gt; 175

```

aacaataaaa gaaaaaacgt tagaccaaac a   atg cgg ccg acc aac agt ggt   52
                                   Met Arg Pro Thr Asn Ser Gly
                                   1                               5

ccg acc tct agc ccg agg gtt caa aac gcc ctc aaa gta acc gtc ttt   100
Pro Thr Ser Ser Pro Arg Val Gln Asn Ala Leu Lys Val Thr Val Phe
      10                15                20

aaa ctg aac tca aag aat gca aaa gcg gca agt tca gaa aat aaa agg   148
Lys Leu Asn Ser Lys Asn Ala Lys Ala Ala Ser Ser Glu Asn Lys Arg
      25                30                35

cga gaa cag gac ttt aag tgc att tca aac cca cgg gcc aga aat cgt   196
Arg Glu Gln Asp Phe Lys Cys Ile Ser Asn Pro Arg Ala Arg Asn Arg
      40                45                50                55

acc acc gtc aac cag ccg cac cat ttg gtc caa gat ttc ctc ttc acc   244
Thr Thr Val Asn Gln Pro His His Leu Val Gln Asp Phe Leu Phe Thr
                60                65                70

att ctg aaa ctg ggt tta tcc aac aca ctg ata cat tca taa aatttgg   293
Ile Leu Lys Leu Gly Leu Ser Asn Thr Leu Ile His Ser *
                75                80                85

aagagtcagt ggaagtcaca aggaccgaat atttgcactc tttcagtgaa tgccagcaaa   353

tctgttatcc cataaataaaa aaagt   378

```

&lt;210&gt; 176

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (222) .. (383)

&lt;400&gt; 176

```

ctgcaggtac cggtcgga tccccgggtc gacccacgcg tccgcactgt gtgcacaaga   60

gagcgataag cactctggat catttaaagg aaaaggagat gcgactccta ccttcagaag   120

gttataatgg acttattata atggacttat tatacggaca aacaaatgaa cagttacaca   180

catgcaaagc tacagcagta caagatagta tgtcatgagt g   atg tgc tta atg   233
                                   Met Cys Leu Met
                                   1

aaa cag atc ata tat ctg ctg tat gta ggg ctc tgt tca att ctc aca   281
Lys Gln Ile Ile Tyr Leu Leu Tyr Val Gly Leu Cys Ser Ile Leu Thr
      5                10                15                20

gca ttc tta ttt act cct cac cat gtc ctt gag agg tat agg tat tat   329
Ala Phe Leu Phe Thr Pro His His Val Leu Glu Arg Tyr Arg Tyr Tyr
      25                30                35

```

tgt cct gat ttt aga gag att aag aaa ctt ggt caa ggc tat aca act 377  
 Cys Pro Asp Phe Arg Glu Ile Lys Lys Leu Gly Gln Gly Tyr Thr Thr  
 40 45 50

aat tag tagaagaatt aaaattcaat cctaagtctg tctgacccca aagcccatga 433  
 Asn \*

atactcttaa ctccatgct gtaaatataa aaagactgaa cgggggccag acgtgggtggc 493  
 tcatgcctgt aatcccagca ctttgggagg atggtttgag cccaggagtt caagaccagc 553  
 ctgggcacta tagtgagacc ctgtctccat tcaaaaaaaaa aaaaaagggg gggcctctta 613  
 aaaggetcaa ttttacttac cgcgtgctgg aaagttatat gtttttatc 662

<210> 177  
 <211> 659  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (274) .. (591)

<400> 177  
 ctgaggcacc gcgccggaat tccccgggtcg acccacgcgt ccggtagaat aatatttgtt 60  
 tgttttttgc aatgtacaaa ttaagggcat gaatcctgga gccaaactaa ctgagttcca 120  
 aatcctgatg ctgccccata ttaattctgt gaattcgggc aaatgactta gtttgtctaa 180  
 acctcaatta tctcatctat aaaaggcagc tagatcttaa ctactgggt tctcgtgagg 240  
 attaaatgag atagtgcgcc taaggtttct ggt atg aag gag gca ctc ctt aaa 294  
 Met Lys Glu Ala Leu Leu Lys  
 1 5

tgt tcg aga ctt gcc aga ggg ctt ctt ctc tgt ctg gac tgt gct aat 342  
 Cys Ser Arg Leu Ala Arg Gly Leu Leu Leu Cys Leu Asp Cys Ala Asn  
 10 15 20

gac cac aga tcc ccg gtt gag agg aat gcc cag acc aca ctc atc cta 390  
 Asp His Arg Ser Pro Val Glu Arg Asn Ala Gln Thr Thr Leu Ile Leu  
 25 30 35

cac tca tcc cta tac tca ttg tcc ctt ggg aac caa ctg cag gga gga 438  
 His Ser Ser Leu Tyr Ser Leu Ser Leu Gly Asn Gln Leu Gln Gly Gly  
 40 45 50 55

ggg gaa atg gcc acc act gga ggg agt act cag cag gcc aag act tat 486  
 Gly Glu Met Ala Thr Thr Gly Gly Ser Thr Gln Gln Ala Lys Thr Tyr  
 60 65 70

ggg gga ctc ttc caa att ggg gcc atg gaa ccg gca cta ttt cta ctc 534  
 Gly Gly Leu Phe Gln Ile Gly Ala Met Glu Pro Ala Leu Phe Leu Leu  
 75 80 85

ttt att ttc ctt ttg gca tcc ttt tgg gtt cac ccg agc tat aga ata 582  
 Phe Ile Phe Leu Leu Ala Ser Phe Trp Val His Pro Ser Tyr Arg Ile  
 90 95 100

acc tac tga gacgaat ttagcaaata cattactgaa gcttctccct cggaagttgg 638  
 Thr Tyr \*  
 105

gcccaagcca tgtgaatggg c 659

<210> 178  
 <211> 664  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (91)..(234)

<400> 178  
 cctgcaggca cgggtccgga attcccgggt cgacccacgc gtccgttttt cccaataatt 60

acttcaactc acagttagtt aaagcataac atg ttg gaa act ttc ttg ttt 111  
 Met Leu Glu Thr Phe Leu Phe  
 1 5

aaa ctc ttc cta ttc ttc acc tta ttg gtt aat tta ttt att acc aat 159  
 Lys Leu Phe Leu Phe Phe Thr Leu Leu Val Asn Leu Phe Ile Thr Asn  
 10 15 20

gac caa ctc agt gtg ggt agt att ttt ctc agc ttc cag ctc cca gct 207  
 Asp Gln Leu Ser Val Gly Ser Ile Phe Leu Ser Phe Gln Leu Pro Ala  
 25 30 35

ttc ttt ctt gat atg gct gaa ttt tga gatac tcaaagcaag cagaccataa 259  
 Phe Phe Leu Asp Met Ala Glu Phe \*  
 40 45

agagagacag ataaaactgg acctgggtgt tcatatgtgt atgtgtgatt gtgtgttga 319

gggttattat cccttttttaa agaactactt ataggatggg ggcaggacct ttgaaattgc 379

aggctgaatt gattattagc atatgtaaat ttgggtaagt tattaagcaa ctttcaaagt 439

gttttttggtt tctcttctgt aaaagtagga ggataataat atctaattgat cttgtttag 499

attaaatgat gaaaagcacc ttacacagtg agtgttacgt agtaagtaga caataaatgg 559

taacatgact attatcatca tgctgctgct atcgtggata tttgcatttt atagctttgg 619

caaactgaaa acttcctttt gttgtgaaat atcttgatga acgca 664

<210> 179  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (105)..(245)

```
<210> 180
<211> 669
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (299) .. (421)
```

257

agcacattcc cctggaggag tacgctgcga acctaaagag cat 669

```
<210> 181
<211> 616
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (83) .. (247)
```

<400> 181	
atttggccct cgaggccaag aattcggcac gagaatttga agtatattta aagtcaataa	60
gcaaacattc aaaaacactt gt atg act ctc cta aat ctt tat tat tta aat	112
Met Thr Leu Leu Asn Leu Tyr Tyr Leu Asn	
1 5 10	
agt ttt cta ttg tac tcg aaa aga ttt gaa ggt ata tcc ttc tgt gtc	160
Ser Phe Leu Leu Tyr Ser Lys Arg Phe Glu Gly Ile Ser Phe Cys Val	
15 20 25	
caa aag gtc agt ata ata tta tgt ata cat tat ctt cgt agc aca act	208
Gln Lys Val Ser Ile Ile Leu Cys Ile His Tyr Leu Arg Ser Thr Thr	
30 35 40	
att tgg aat aag ctt ttc ttc aga gat gta tcg gca taa aggagctctg	257
Ile Trp Asn Lys Leu Phe Phe Arg Asp Val Ser Ala *	
45 50 55	
atttgtttaa atatttttaa aggtatttaa atatattttc atttgagaac ctccccata	317
tactcaggaa agctcacctt ttcaaaacct gagtgttaac tctttccaaa cgttctgtaa	377
tgtttatcaa aaacaaaaaa taatgaaaag aggtgaacat tattttggag agcctcattg	437
gcttcaccta ctcatcat ccacaatcac tggagaggag gcagaatttt gtacttgga	497
cagcagtcac ttgaccaga atcctctacc gattccctcc agggagccct tccattggc	557
tctttcctag aaatttcattg tttttgggtt aacctcagat aaaacttttq ccttaaacac	616

```
<210> 182
<211> 993
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (158)..(703)
```

<400> 182  
gattggactt atttcccaca ttttttcaag ctctggatat taccacactt ttcactattt 60  
acctatctgg aaaagcaaat atctttatat ttaaattttt ataacctcaa tcatcagtga 120  
aaacatttct aatgtttata tcacttgctt gtaaatc atg cat ttt cct gtg aac 175



															Met	His	Phe	Pro	Val	Asn			
															1						5		
tgt	ttc	ttc	aag	tca	tta	cat	att	ttt	ctt	tta	cta	cag	gtt	ttt	ctt	223							
Cys	Phe	Phe	Lys	Ser	Leu	His	Ile	Phe	Leu	Leu	Leu	Gln	Val	Phe	Leu								
			10				15						20										
gcc	act	ttt	ttg	aga	aaa	aaa	tta	agt	aag	gta	gcc	ttc	agt	tgt	ctt	271							
Ala	Thr	Phe	Leu	Arg	Lys	Lys	Leu	Ser	Lys	Val	Ala	Phe	Ser	Cys	Leu								
			25				30						35										
gtt	gaa	ttt	ttc	tac	tat	tgt	tat	tat	ttt	tta	gac	ttt	gct	agt	agt	319							
Val	Glu	Phe	Phe	Tyr	Tyr	Cys	Tyr	Tyr	Phe	Leu	Asp	Phe	Ala	Ser	Ser								
			40				45						50										
gtt	tct	ttt	ttg	ttt	tgt	ttt	gtt	ttg	ctt	ttg	aga	cgg	agt	ctt	act	367							
Val	Ser	Phe	Leu	Phe	Cys	Phe	Val	Leu	Leu	Leu	Arg	Arg	Ser	Leu	Thr								
			55				60						65			70							
ctg	tca	ccc	agg	ctg	gag	tgc	agt	gac	acg	atc	ttg	gct	cac	tgc	aac	415							
Leu	Ser	Pro	Arg	Leu	Glu	Cys	Ser	Asp	Thr	Ile	Leu	Ala	His	Cys	Asn								
			75						80						85								
ctt	cgc	ctc	cgc	ggg	tca	cgc	tat	tct	tct	gcc	tca	acc	tcc	cga	gta	463							
Leu	Arg	Leu	Pro	Gly	Ser	Arg	Tyr	Ser	Ser	Ala	Ser	Thr	Ser	Arg	Val								
			90						95						100								
gct	ggg	att	aca	ggg	gtg	cac	cac	cac	acc	tat	gta	aat	ttt	gta	tgg	511							
Ala	Gly	Ile	Thr	Gly	Val	His	His	His	Thr	Tyr	Val	Asn	Phe	Val	Trp								
			105						110						115								
aca	gta	cag	aag	gcg	gtt	cac	tgt	gtt	ggc	cag	gct	agc	tgg	gaa	ctc	559							
Thr	Val	Gln	Lys	Ala	Val	His	Cys	Val	Gly	Gln	Ala	Ser	Trp	Glu	Leu								
			120						125						130								
ctg	acc	tca	agg	gat	cca	ccc	acc	ttg	gcc	tcc	cac	agg	gct	ggg	att	607							
Leu	Thr	Ser	Arg	Asp	Pro	Pro	Thr	Leu	Ala	Ser	His	Arg	Ala	Gly	Ile								
			135						140						145		150						
aca	ggc	atg	agc	cac	cgc	acc	tgg	gca	aaa	gtg	ttc	ctt	aaa	aga	gtg	655							
Thr	Gly	Met	Ser	His	Arg	Thr	Trp	Ala	Lys	Val	Phe	Leu	Lys	Arg	Val								
			155						160						165								
att	ttt	cta	aat	aga	gaa	tac	gat	ttg	act	atg	ttt	tgc	ttt	tta	aaa	703							
Ile	Phe	Leu	Asn	Arg	Glu	Tyr	Asp	Leu	Thr	Met	Phe	Cys	Phe	Leu	Lys								
			170						175						180								
tagacatact catctctgac tggtattcta aggattaagt gctatataaa gcacagcaaa																	763						
taattttgcc agatgcaata gaaattagtt tcttgaggaa tgtgtcaata tctagcaatt																	823						
ttacataggc atttaccctt tgaaccagaa acttcactta tagaaatcta tcctaaagac																	883						
acacagtcaa aaattcaaga cgggcatggg ggctcatggc tgcaatccca gcactttagg																	943						
agacagagga ggagggttgca gaattccacc aactgacta tggactcgaa																	993						

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (133) .. (333)

&lt;400&gt; 183

```

ttcgagcttc tcttcaatac ccataatgtat ctcaaagtaa tgtaatcagc aaattagcag      60
tgtaaaaatg ctagataact tattctgaaa tccacttccg aaatcatttg agcagctaag      120
tttgaaaaac tc      atg ttg gta cca aca ttt ctc tct tta gtg tgt gat      168
                    Met Leu Val Pro Thr Phe Leu Ser Leu Val Cys Asp
                    1              5              10

ttt tcc ctt ttt gtg ctt ctc ctc ctt ggc tgt ctc tcc ttt ctc ctt      216
Phe Ser Leu Phe Val Leu Leu Leu Leu Gly Cys Leu Ser Phe Leu Leu
                    15              20              25

ccc cct cac tta cct tgc act tcc ttc cct ctc cat ctc tgg agg ctt      264
Pro Pro His Leu Pro Cys Thr Ser Phe Pro Leu His Leu Trp Arg Leu
                    30              35              40

ctc tct cct ttt ata tct ttt ctg tac tta ctg ctg ctt ctt agt tat      312
Leu Ser Pro Phe Ile Ser Phe Leu Tyr Leu Leu Leu Leu Leu Ser Tyr
                    45              50              55              60

aaa atg aat tgt ata att taa ac tgtttaataa atggactttg gtatttggaa      365
Lys Met Asn Cys Ile Ile *
                    65

ttttcaagtc gggactaaaa acctttataa ccttagcccc ccttccttga accctctaga      425
attaacacaa tcatgttaag gtttatatag caagtccttg tgatatactt tttgttgata      485
ttgctaggca aatatgctct taacaagtaa ttgcctgagg caggaggaat gcttgagccc      545
aagaatccga gtttgcaggg agctgggac accactggac tctattcttg acaacagagc      605
cggacactgt gtcaaaaaaa aaa      628

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&lt;210&gt; 184

&lt;211&gt; 717

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (71) .. (295)

&lt;400&gt; 184

```

ctcaggctgc ctgctttttg ttgcatag ctggtcctgt tacctctcat tttcctcct      60
ggaggcagtt      atg ttg cct cta ttt aag cac tca cca gtc aga atc ttc      109
                    Met Leu Pro Leu Phe Lys His Ser Pro Val Arg Ile Phe
                    1              5              10

cta ttc tgc tta aat acc caa cat ttg tca gta aga aat aat ttt gta      157
Leu Phe Cys Leu Asn Thr Gln His Leu Ser Val Arg Asn Asn Phe Val
                    15              20              25

ttt aat tgt gta tcc cca gga att ttg ccc att tct ctt tgc ctt gct      205

```

Gln Leu Lys Gln Glu Leu Arg Leu Asn Tyr Leu Thr Leu Thr Gln Phe  
 20 25 30  
 Trp Gln Arg Cys Tyr Ser Glu Met Ile Phe Phe Cys Leu Ser Lys Val  
 35 40 45  
 Phe Leu His Val Phe Gln Asp Gly Leu Glu His His Leu Glu \*  
 50 55 60 62

&lt;210&gt; 322

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 322

Met Leu Gln Val Lys Tyr Leu Leu Asn Gln Gly Ile Val Leu Pro Gln  
 1 5 10 15  
 Ile Val Thr Gly Val Ala Ala Asn Leu Val Asn Ala Leu Ala Asn Tyr  
 20 25 30  
 Leu Phe Leu His Gln Leu His Leu Gly Val Ile Gly Ser Ala Leu Ala  
 35 40 45  
 Asn Leu Ile Ser Gln Tyr Thr Leu Ala Leu Leu Leu Phe Leu Tyr Ile  
 50 55 60  
 Leu Gly Lys Lys Leu His Gln Ala Thr Trp Gly Gly Trp Ser Leu Glu  
 65 70 75 80  
 Cys Leu Gln Asp Cys Ala Ser Phe Leu Arg Leu Ala Ile Pro Ser Met  
 85 90 95  
 Leu Met Leu Cys Met Glu Trp Trp Ala Tyr Glu Val Gly Ser Phe Leu  
 100 105 110  
 Ser Gly Ile Leu Gly Met Val Glu Leu Gly Ala Gln Ser Ile Val Tyr  
 115 120 125  
 Glu Leu Ala Ile Ile Val Tyr Met Val Pro Ala Gly Phe Ser Val Ala  
 130 135 140  
 Ala Ser Val Arg Val Gly Asn Ala Leu Gly Ala Gly Asp Met Glu Gln  
 145 150 155 160  
 Ala Arg Lys Ser Ser Thr Val Ser Leu Leu Ile Thr Val Leu Phe Ala  
 165 170 175  
 Val Ala Phe Ser Val Leu Leu Leu Ser Cys Lys Asp His Val Gly Tyr  
 180 185 190  
 Ile Phe Thr Thr Asp Arg Asp Ile Ile Asn Leu Val Ala Gln Val Val  
 195 200 205  
 Pro Ile Tyr Ala Val Ser His Leu Phe Glu Ala Leu Ala Cys Thr Ser  
 210 215 220  
 Gly Gly Val Leu Arg Gly Ser Gly Asn Gln Lys Val Gly Ala Ile Val  
 225 230 235 240  
 Asn Thr Ile Gly Tyr Tyr Val Ala Gly Leu Pro Ile Gly Ile Ala Leu  
 245 250 255  
 Met Phe Ala Thr Thr Leu Gly Val Met Gly Leu Trp Ser Gly Ile Ile  
 260 265 270  
 Ile Cys Thr Val Phe Gln Ala Val Cys Phe Leu Gly Phe Ile Ile Gln  
 275 280 285  
 Leu Asn Trp Lys Lys Ala Cys Gln Gln Gly Ala Leu Lys Thr Leu Lys  
 290 295 300  
 Glu Phe \*  
 305 306

&lt;210&gt; 323

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

WO 01/55437

PCT/US01/02623

<211> 77  
<212> PRT  
<213> Homo sapiens

<400> 318  
Met Phe Lys Val Val Phe Cys Phe Gly Leu Val Trp Phe Cys Phe Gln  
1 5 10 15  
Arg Ala His Lys Pro Ile Arg Phe Glu Lys His Asn Phe Thr Ile Asn  
20 25 30  
Glu Gly Asn Leu Phe Ser Met Asn Ile Pro Ile Val Thr Ile Arg Ser  
35 40 45  
His His Arg Thr Ser Cys Tyr His Lys Leu Ile Thr Cys Glu Gln Gln  
50 55 60  
Thr Val Phe Thr Asn Ile Lys Arg His Ser Lys Leu \*  
65 70 75 76

<210> 319  
<211> 54  
<212> PRT  
<213> Homo sapiens

<400> 319  
Met Asn Leu Tyr Leu Phe Ala Val Leu Phe Phe Tyr Val Phe Leu His  
1 5 10 15  
Ile Lys Ile Ile Phe Ile Cys Phe Ala Thr Lys Trp His Asn Leu Phe  
20 25 30  
Ser Lys Phe Ser Tyr Phe Cys Ile Leu His Val Lys Ala Leu Ser Leu  
35 40 45  
Asn Leu Gly Ser Gly \*  
50 53

<210> 320  
<211> 64  
<212> PRT  
<213> Homo sapiens

<400> 320  
Met Lys Ile Ala Ser Phe Leu Leu Gln Asn Asn Gly Met Tyr Ser Leu  
1 5 10 15  
Ser Leu Gln Leu Pro Val Leu Cys Val Leu Lys Ser Phe Lys Ala Tyr  
20 25 30  
Ser Leu Leu Trp Gly Val Ser Thr Gly Val Lys Glu Gly Phe Ala Gly  
35 40 45  
Arg Thr Ile Val Asn His Glu Ser Tyr Tyr Leu Arg Ile Val Trp \*  
50 55 60 63

<210> 321  
<211> 63  
<212> PRT  
<213> Homo sapiens

<400> 321  
Met Cys Thr Leu Phe Met His Leu Leu Phe Cys His Leu Gln Ser Ile  
1 5 10 15

Leu Ser Gly Leu Pro Pro Pro Pro Ala Glu Pro Glu Pro Glu Pro Glu  
 65 70 75 80  
 Pro Glu Pro Glu Pro Ala Leu Asp Leu Ala Ala Leu Arg Ala Val Ala  
 85 90 95  
 Cys Asp Cys Leu Leu Gln Glu His Phe Tyr Leu Arg Arg Arg Arg Arg  
 100 105 110  
 Val His Arg Tyr Glu Glu Ser Glu Val Ile Ser Leu Pro Phe Leu Asp  
 115 120 125  
 Gln Leu Val Ser Thr Leu Val Gly Leu Leu Ser Pro His Asn Pro Ala  
 130 135 140  
 Leu Ala Ala Ala Ala Leu Asp Tyr Arg Cys Pro Val His Phe Tyr Trp  
 145 150 155 160  
 Val Arg Gly Glu Glu Ile Ile Pro Arg Gly His Arg Arg Gly Arg Ile  
 165 170 175  
 Asp Asp Leu Arg Tyr Gln Ile Asp Asp Lys Pro Asn Asn Gln Ile Arg  
 180 185 190  
 Ile Ser Lys Gln Leu Ala Glu Phe Val Pro Leu Asp Tyr Ser Val Pro  
 195 200 205  
 Ile Glu Ile Pro Thr Ile Lys Cys Lys Pro Asp Lys Leu Pro Leu Phe  
 210 215 220  
 Lys Arg Gln Tyr Glu Asn His Ile Phe Val Gly Ser Lys Thr Ala Asp  
 225 230 235 240  
 Pro Cys Cys Tyr Gly His Thr Gln Phe His Leu Leu Pro Asp Lys Leu  
 245 250 255  
 Arg Arg Glu Arg Leu Leu Arg Gln Asn Cys Ala Asp Gln Ile Glu Val  
 260 265 270  
 Val Phe Arg Ala Asn Ala Ile Ala Ser Leu Phe Ala Trp Thr Gly Ala  
 275 280 285  
 Gln Ala Met Tyr Gln Gly Phe Trp Ser Glu Ala Asp Val Thr Arg Pro  
 290 295 300  
 Phe Val Ser Gln Ala Val Ile Thr Asp Gly Lys Tyr Phe Ser Phe Phe  
 305 310 315 320  
 Cys Tyr Gln Leu Asn Thr Leu Ala Leu Thr Thr Gln Ala Asp Gln Asn  
 325 330 335  
 Asn Pro Arg Lys Asn Ile Cys Trp Gly Thr Gln Ser Lys Pro Leu Tyr  
 340 345 350  
 Glu Thr Ile Glu Asp Asn Asp Val Lys Gly Phe Asn Asp Asp Val Leu  
 355 360 365  
 Leu Gln Ile Val His Phe Leu Leu Asn Arg Pro Lys Glu Glu Lys Ser  
 370 375 380  
 Gln Leu Leu Glu Asn  
 385 389

&lt;210&gt; 317

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 317

Met Ser Leu Lys Arg Ile Ile Leu Arg Lys Asp Leu Arg Phe Lys Lys  
 1 5 10 15  
 Ser Ile Thr Leu His Glu Gln Phe His Val Phe Lys Phe Tyr Lys Lys  
 20 25 30  
 Thr Gln Thr Ser Ser Val Ile Val Glu Gly Arg Arg Arg Gly Arg Tyr  
 35 40 45  
 Tyr Lys Gly Thr Cys Glu Asn Phe Leu Glu  
 50 55 58

&lt;210&gt; 318

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 315

```

Met Cys Gly Arg Phe Leu Arg Arg Leu Leu Ala Glu Glu Ser Arg Arg
 1          5          10          15
Ser Thr Pro Val Gly Arg Leu Leu Leu Pro Val Leu Leu Gly Phe Arg
          20          25          30
Leu Val Leu Leu Ala Ala Ser Gly Pro Gly Val Tyr Gly Asp Glu Gln
          35          40          45
Ser Glu Phe Val Cys His Thr Gln Gln Pro Gly Cys Lys Ala Ala Cys
          50          55          60
Phe Asp Ala Phe His Pro Leu Ser Pro Leu Arg Phe Trp Val Phe Gln
 65          70          75          80
Val Ile Leu Val Ala Val Pro Ser Ala Leu Tyr Met Gly Phe Thr Leu
          85          90          95
Tyr His Val Ile Trp His Trp Glu Leu Ser Gly Lys Gly Lys Glu Glu
          100          105          110
Glu Thr Leu Ile Gln Gly Arg Glu Gly Asn Thr Asp Val Pro Gly Ala
          115          120          125
Gly Ser Leu Arg Leu Leu Trp Ala Tyr Val Ala Gln Leu Gly Ala Arg
          130          135          140
Leu Val Leu Glu Gly Ala Ala Leu Gly Leu Gln Tyr His Leu Tyr Gly
145          150          155          160
Phe Gln Met Pro Ser Ser Phe Ala Cys Arg Arg Glu Pro Cys Leu Gly
          165          170          175
Ser Ile Thr Cys Asn Leu Ser Arg Pro Ser Glu Lys Thr Ile Phe Leu
          180          185          190
Lys Thr Met Phe Gly Val Ser Gly Phe Cys Leu Leu Phe Thr Phe Leu
          195          200          205
Glu Leu Val Leu Leu Gly Leu Gly Arg Trp Trp Arg Thr Trp Lys His
          210          215          220
Lys Ser Ser Ser Ser Lys Tyr Phe Leu Thr Ser Glu Ser Thr Arg Arg
225          230          235          240
His Lys Lys Ala Thr Asp Ser Leu Pro Val Val Glu Thr Lys Glu Gln
          245          250          255
Phe Gln Glu Ala Asp Gly Lys Leu Pro Val Pro Asn Lys Ser Gly Cys
          260          265          270
Leu Gln Met Ser Leu Pro Leu Gln Leu Arg Asn Phe Phe Leu Ala Ser
          275          280          285
Asp Trp Leu Leu Ser Ala Lys His Glu Leu Ala Lys Gly Lys Leu Leu
          290          295          300          304

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&lt;210&gt; 316

&lt;211&gt; 389

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 316

```

Met Thr Ala Asp Ser Lys Ala Ala Arg Leu Arg Arg Ile Glu Arg Trp
 1          5          10          15
Gln Ala Thr Val His Ala Ala Glu Ser Val Asp Glu Lys Leu Arg Ile
          20          25          30
Leu Thr Lys Met Gln Phe Met Lys Tyr Met Val Tyr Pro Gln Thr Phe
          35          40          45
Ala Leu Asn Ala Asp Arg Trp Tyr Gln Tyr Phe Thr Lys Thr Val Phe
          50          55          60

```

<210> 312  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<400> 312  
 Met Val Thr Tyr Phe Ile Lys Cys Phe His Tyr Glu Val Ser Phe Leu  
 1 5 10 15  
 Leu Trp Phe Ala Val Val Arg Asn Asp Val Asp Arg Pro Val Ser Leu  
 20 25 30  
 Ser Leu Phe Ser Ser Tyr Ser Leu Phe Ser Thr Tyr Pro Asp Thr Cys  
 35 40 45  
 Pro Leu Phe Lys Leu Pro Thr His Leu Leu Cys Cys Leu Glu Glu Ile  
 50 55 60 64  
 \*

<210> 313  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<400> 313  
 Met Glu Asp Val Arg Glu Lys Val Met Ala Val Pro Ile Met Leu Phe  
 1 5 10 15  
 Tyr Phe Ser Leu Leu Tyr Asn Ser Leu Leu Phe Leu Asn Pro Ile Leu  
 20 25 30  
 Leu Leu Ser Thr Thr His Leu Leu Leu Gly Asp Lys Ala Val \*  
 35 40 45 46

<210> 314  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 314  
 Met Ser Leu Val Leu Asn Gln Ile Glu Leu Ser Glu Lys Gly Met Ala  
 1 5 10 15  
 Val Lys Asn Val Ala Leu Val Ile Thr Trp Ala Tyr Gly Phe Val Lys  
 20 25 30  
 Val Thr Leu Ser Leu Leu Val Phe Cys Val Tyr Cys Met Tyr Val Ile  
 35 40 45  
 Leu His Leu Arg Met Tyr Ile Thr His Lys Gly Ala Cys Arg His Met  
 50 55 60  
 Ser Ala Ser Trp Leu Ala Thr Asn Cys Leu Trp Pro Trp Gly Cys His  
 65 70 75 80  
 Ser Thr Phe His Leu Glu Ile Glu Asn Asn Asn Thr Ile Ile Leu Leu  
 85 90 95  
 Glu Leu Cys Ala \*  
 100

<210> 315

<210> 310  
 <211> 278  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
 Met Ala Gly Pro Glu Leu Leu Leu Asp Ser Asn Ile Arg Leu Trp Val  
 1 5 10 15  
 Val Leu Pro Ile Val Ile Ile Thr Phe Phe Val Gly Met Ile Arg His  
 20 25 30  
 Tyr Val Ser Ile Leu Leu Gln Ser Asp Lys Lys Leu Thr Gln Glu Gln  
 35 40 45  
 Val Ser Asp Ser Gln Val Leu Ile Arg Ser Arg Val Leu Arg Glu Asn  
 50 55 60  
 Gly Lys Tyr Ile Pro Lys Gln Ser Phe Leu Thr Arg Lys Tyr Tyr Phe  
 65 70 75 80  
 Asn Asn Pro Glu Asp Gly Phe Phe Lys Lys Thr Lys Arg Lys Val Val  
 85 90 95  
 Pro Pro Ser Pro Met Thr Asp Pro Thr Met Leu Thr Asp Met Met Lys  
 100 105 110  
 Gly Asn Val Thr Asn Val Leu Pro Met Ile Leu Ile Gly Gly Trp Ile  
 115 120 125  
 Asn Met Thr Phe Ser Gly Phe Val Thr Thr Lys Val Pro Phe Pro Leu  
 130 135 140  
 Thr Leu Arg Phe Lys Pro Met Leu Gln Gln Gly Ile Glu Leu Leu Thr  
 145 150 155 160  
 Leu Asp Ala Ser Trp Val Ser Ser Ala Ser Trp Tyr Phe Leu Asn Val  
 165 170 175  
 Phe Gly Leu Arg Ser Ile Tyr Ser Leu Ile Leu Gly Gln Asp Asn Ala  
 180 185 190  
 Ala Asp Gln Ser Arg Met Met Gln Glu Gln Met Thr Gly Ala Ala Met  
 195 200 205  
 Ala Met Pro Ala Asp Thr Asn Lys Ala Phe Lys Thr Glu Trp Glu Ala  
 210 215 220  
 Leu Glu Leu Thr Asp His Gln Trp Ala Leu Asp Asp Val Glu Glu Glu  
 225 230 235 240  
 Leu Met Gly Gln Arg Pro Pro Leu Arg Arg His Val Gln Lys Gly Ile  
 245 250 255  
 Thr Asp Leu Tyr Phe Leu Lys Thr Glu Gln Gly Leu Ala Val Ser Gly  
 260 265 270  
 Thr Trp Ser Cys Thr \*  
 275 277

<210> 311  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 311  
 Met Leu Phe Val Val Leu Pro Leu Leu Ile Ile Val Phe Asn Ile Pro  
 1 5 10 15  
 Met Arg Glu Ala Val Phe Asp Phe Leu Phe Met Ile Lys Ile Ile Lys  
 20 25 30  
 Val Leu Lys Val Phe Tyr Cys Ile Ala Cys Phe Ile Ile Lys Gln Val  
 35 40 45  
 Leu Val Phe \*  
 50 51



&lt;213&gt; Homo sapiens

&lt;400&gt; 307

```

Met Pro Val Thr Pro Asp Pro Ser Ala Val Ser Leu Phe Val Thr Pro
 1              5              10              15
Trp Pro Leu Leu Leu Cys Leu Pro Trp Pro His Arg Val Pro Gly Gln
              20              25              30
Ser His Pro Gly Leu His Ser Arg Ala Pro Val His Arg Leu Lys Pro
              35              40              45
Gly Pro Pro Ala Arg Leu Gln Leu Pro Ala Ala His Arg Asn Leu Arg
              50              55              60
His Leu Ser Ile Phe *
65              69

```

&lt;210&gt; 308

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 308

```

Met Ser Trp Tyr Thr Cys Gln Cys Leu Phe Phe Leu Ser Asn Thr Leu
 1              5              10              15
Arg Asn Gly Ala Thr Ser Cys His Trp Tyr Cys Ser Pro Asp Asp Met
              20              25              30
Gln Met Val Asp Phe Ser Ser Thr Tyr Glu Arg Ile Phe Arg Pro Phe
              35              40              45
Val Phe Lys Ile Lys Gly Pro Asp Ser Phe Arg Ile Asp Met Ser Pro
              50              55              60
Ile Pro Glu Asp Ile *
65              69

```

&lt;210&gt; 309

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 309

```

Met Val Phe Leu Thr Ala Gln Leu Trp Leu Arg Asn Arg Val Thr Asp
 1              5              10              15
Arg Tyr Phe Arg Ile Gln Glu Val Leu Lys His Ala Arg His Phe Arg
              20              25              30
Gly Arg Lys Asn Arg Cys Tyr Arg Leu Ala Val Arg Thr Val Ile Arg
              35              40              45
Ala Phe Val Lys Cys Thr Lys Ala Arg Tyr Leu Lys Lys Asn Met
              50              55              60
Arg Thr Leu Trp Ile Asn Arg Ile Thr Ala Ala Ser Gln Glu His Gly
              65              70              75              80
Leu Lys Tyr Pro Ala Leu Ile Gly Asn Leu Val Lys Cys Gln Val Glu
              85              90              95
Leu Asn Arg Lys Val Leu Ala Asp Leu Ala Ile Tyr Glu Pro Lys Thr
              100              105              110
Phe Lys Ser Leu Ala Ala Leu Ala Ser Arg Arg Arg His Glu Gly Phe
              115              120              125
Ala Ala Ala Leu Gly Asp Gly Lys Glu Pro Glu Gly Ile Phe Ser Arg
              130              135              140
Val Val Gln Tyr His *
145              149

```

<210> 304  
 <211> 49  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
 Met Gly Phe Leu Phe Leu Leu Asp Ser Ala Leu Met Gln Thr Trp Val  
 1 5 10 15  
 Thr Val Ile Asp Val Ser Leu His His Val Glu Ile Lys Ala Pro Arg  
 20 25 30  
 Ile Arg Leu Met Trp Ser Leu Pro Leu Arg Arg Gln Lys Tyr Thr Met  
 35 40 45 48  
 \*

<210> 305  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 305  
 Met Leu Ala Thr Leu Ala Cys Met Ala Ile Pro Trp Thr His Leu Gly  
 1 5 10 15  
 Cys Ser Cys Leu Leu Ala Cys Leu Pro Phe Ser His His Leu Gly Leu  
 20 25 30  
 Ser Glu Asp Ile Ile Ser Ser Glu Lys Pro Ser Val Thr Met Leu Ser  
 35 40 45  
 Lys Ile Leu Gln His Phe Ser His Pro Leu Ser His Tyr Ser Ala Phe  
 50 55 60  
 Ser Glu Thr Leu Val Leu Pro Glu Thr Tyr Leu Phe Thr Cys Leu Val  
 65 70 75 80  
 Ser Phe Leu Pro His Tyr His Val Ser Phe Leu Arg Val Arg Asp Leu  
 85 90 95  
 Val Arg Asp Asn His Cys Ile Leu Arg Val \*  
 100 105 106

<210> 306  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Met His Thr Pro His Leu Pro Asn Ile Ile Val Tyr Phe Ile Leu Leu  
 1 5 10 15  
 Tyr Ile Cys Ser Gln Tyr Leu Tyr Leu Leu Thr Ile Arg His Asn His  
 20 25 30  
 Leu Thr Gln Ser Leu Phe Tyr Asn Lys Leu Leu Ser Val Leu \*  
 35 40 45 46

<210> 307  
 <211> 70  
 <212> PRT

Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys  
 65 70 75 80  
 Thr Arg Val Glu Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr  
 85 90 95  
 Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe  
 100 105 110  
 Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe  
 115 120 125  
 Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln  
 130 135 140  
 Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val  
 145 150 155 160  
 Asp Pro Ser His Asp Leu Lys Gly Ser Val Val Ile Tyr Asp Val Leu  
 165 170 175  
 Asp Gly Thr Asp Ala Trp Asp Ser Ala Thr Glu Thr Lys Thr Phe Leu  
 180 185 190  
 Val Ser Gln Asp Ile Gln Asp Glu Gly Trp Glu Thr Leu Glu Val Ser  
 195 200 205  
 Ser Ala Val Lys Arg Trp Val Arg Ser Asp Ser Thr Lys Ser Lys Asn  
 210 215 220  
 Lys Leu Glu Val Thr Val Glu Ser His Arg Lys Gly Cys Asp Thr Leu  
 225 230 235 240  
 Asp Ile Ser Val Pro Gly Ser Arg Asn Leu Pro Phe Phe Val Val  
 245 250 255  
 Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu  
 260 265 270  
 Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser  
 275 280 285  
 Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr  
 290 295 300  
 Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser  
 305 310 315 320  
 Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe  
 325 330 335  
 Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu  
 340 345 350  
 Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val  
 355 360 365  
 Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe  
 370 375 380  
 Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro  
 385 390 395 400  
 Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr  
 405 410 415  
 His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg \*  
 420 425 429

&lt;210&gt; 303

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 303

Met Phe Gly Met Ile Lys Arg Arg Val Arg Arg Ala Val Phe Val Gly  
 1 5 10 15  
 Arg Thr Val Leu Cys Gly Ser Cys Asn Ser Gly Ile Ile Met His Arg  
 20 25 30  
 Gly Lys Thr Pro Pro Leu Lys Met Val Cys Arg Phe Glu Glu Ser Phe  
 35 40 45  
 Ser Cys Leu Phe Leu Asn Ser \*  
 50 55

Phe Ile Ile Val Thr Phe Lys Trp Ile Asp Lys Phe Ile Leu Asn Ile  
 65 70 75 80  
 Ser Ile Leu Ile Ser Asn Thr Val Asn Val Asn Ser His Asn Pro His  
 85 90 95  
 Lys Gln Lys Phe Phe Gly Asp Leu Ser Asn Phe  
 100 105 107

<210> 301  
 <211> 228  
 <212> PRT  
 <213> Homo sapiens

<400> 301  
 Met Leu Val Val Lys Gly Val Cys Phe Lys Ala His Lys Asn Val Leu  
 1 5 10 15  
 Ala Ala Phe Ser Gln Tyr Phe Arg Asn Val Gln Gln Met His Ser Arg  
 20 25 30  
 Thr Lys Arg Trp Met Asn Arg Ile Arg Met Leu His His Gln Leu Ile  
 35 40 45  
 Val Ile Thr Pro Gln Val Lys Ser Gln Asn Lys Leu Leu Ile Leu Gln  
 50 55 60  
 Met Ala Ala Ala Gln Asn Cys Leu Ser Asn Ser Gln Ile Thr Ile Thr  
 65 70 75 80  
 Asn Ser Glu Thr Phe Thr Pro Val Asn Asp Ser Ala Pro His Pro Glu  
 85 90 95  
 Ser Asp Ala Thr Cys Gln Gln Pro Val Lys Gln Met Arg Leu Lys Lys  
 100 105 110  
 Ala Ile His Leu Lys Lys Leu Asn Phe Leu Lys Ser Gln Lys Tyr Ala  
 115 120 125  
 Glu Gln Val Ser Glu Pro Lys Ser Asp Asp Gly Leu Thr Lys Arg Leu  
 130 135 140  
 Glu Ser Ala Ser Lys Asn Thr Leu Glu Lys Ala Ser Ser Gln Ser Ala  
 145 150 155 160  
 Glu Glu Lys Glu Ser Glu Glu Val Val Ser Cys Glu Asn Phe Asn Cys  
 165 170 175  
 Ile Ser Glu Thr Glu Arg Pro Glu Asp Pro Ala Ala Leu Glu Asp Gln  
 180 185 190  
 Ser Gln Thr Leu Gln Ser Gln Arg Gln Tyr Ala Cys Glu Leu Cys Gly  
 195 200 205  
 Lys Pro Phe Lys His Pro Ser Asn Leu Glu Leu His Lys Arg Ser His  
 210 215 220  
 Thr Gly Asn \*  
 225 227

<210> 302  
 <211> 430  
 <212> PRT  
 <213> Homo sapiens

<400> 302  
 Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu  
 1 5 10 15  
 Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser  
 20 25 30  
 Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu  
 35 40 45  
 Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val  
 50 55 60

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Met Leu Gly Trp Gln Ile Trp Arg Leu Arg Pro Gln Leu Leu Ser Phe
 1           5           10           15
His Thr Gln Asp Arg Cys His Trp Ser Ile Thr Ser Gln Cys Ser Lys
           20           25           30
Pro Glu Ser Gln Glu Ser Phe Leu Ser Thr Ile His Leu Leu Glu Gly
           35           40           45
Ala Gln Glu Gly Thr Pro Thr Glu *
      50           55 56

```

<210> 298  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

```

<400> 298
Met Ile Tyr Val Phe Ser Leu Ala His Ser Leu Leu Ile Phe Lys Met
 1           5           10           15
Arg Glu Thr Gly Ile Leu Leu Cys Phe Leu Ser Ala Leu Asn Tyr Ile
           20           25           30
Thr Leu Val Thr Ser Gln Lys Leu Ile Leu Ser Lys Lys Met His Val
           35           40           45
Asn His Tyr Leu Pro Lys Lys Thr Ile Ser Lys Phe Leu Tyr Phe Val
           50           55           60
Lys Val Phe His Asp Leu Val Leu
      65           70 72

```

<210> 299  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

```

<400> 299
Met Ser Val Gln Ala Ser Arg Gly Ala Gly Gln His Ser Thr Leu Asp
 1           5           10           15
Glu Lys Gly Ser Glu Arg Ser Leu Ser Cys Ala Asp Gly Phe His Val
           20           25           30
Cys Leu Asn Asp Asn Thr Asn Ser Arg Lys Ile Glu Lys Thr Ser Lys
           35           40           45
Ser Val Ala Ser Ser Pro Ser Tyr Arg Glu Val
      50           55           59

```

<210> 300  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

```

<400> 300
Met Ser Tyr Ser Thr Pro Ala Trp His Glu Gly Cys Arg Tyr Glu Asn
 1           5           10           15
Thr Glu Tyr Gly Cys Phe Leu Leu Ser Thr His Ile Thr Glu Ile Cys
           20           25           30
Lys Asn Val Thr Met Leu Leu Phe Ser Leu Asn Phe Phe Phe Trp Lys
           35           40           45
Ile Val Met Phe His Lys Asn Val Ile Phe Ile Leu Thr Cys Asn Gly
      50           55           60

```

<211> 47  
 <212> PRT  
 <213> Homo sapiens

<400> 294  
 Met Asp Leu Tyr Val Val Ile Phe Trp Leu Val Tyr Ile Phe Ser Thr  
 1 5 10 15  
 Tyr Ile Ile Thr Tyr Ile Lys Gly Asn Val Gly Leu Cys Phe Gln Ile  
 20 25 30  
 Leu Phe Gln Leu Ser Phe Glu Arg Arg Pro Lys Ser Val Arg \*  
 35 40 45 46

<210> 295  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 295  
 Met Ser Phe Pro Ile His Leu Arg Phe Phe Ser Leu Phe Phe Leu His  
 1 5 10 15  
 Trp Leu Leu Leu Ser Gly Phe Ser Ser Leu Leu Pro Trp Ala Ser Ala  
 20 25 30  
 Phe Val Gln Tyr Ser Arg Cys Pro Glu His Thr Pro Ser Leu Cys Pro  
 35 40 45  
 Gly Gly Ala Asn Asn Pro Leu Leu Gln Ala Pro Thr Gln Met Leu Pro  
 50 55 60  
 Pro Leu Gly Cys Leu Leu Cys Ala Leu Pro Ala Ser Pro Ser Pro Tyr  
 65 70 75 80  
 Leu Cys Trp His Leu Leu Tyr His Ala Phe Arg Asn Leu Leu Ile Pro  
 85 90 95  
 Leu Ile Ser Gly Ala Pro Cys Gly Ser Gly Ile Pro Lys Phe Ser Lys  
 100 105 110  
 Cys Leu Ser Val Ser  
 115 117

<210> 296  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<400> 296  
 Met Ala Asp Thr Ala Glu Asn Ser Arg Tyr Asn Val His Ile Pro His  
 1 5 10 15  
 Arg Trp Thr Ile Asn Lys Phe Phe Ile Leu Met Gln Ser Ser Leu Ser  
 20 25 30  
 Tyr Ser Cys Leu Tyr Tyr  
 35 38

<210> 297  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 297

Glu Arg Lys Ala Thr Lys Arg Val Lys Arg Lys Gln Asp Val Thr Gly  
 100 105 110  
 Asn Asp Pro His Ser Pro Ser Leu Ser Ser Gly Gly Pro Ile His Lys  
 115 120 125  
 Ala Asn Thr Ser Gly Arg Leu Lys Val Ser Asp Arg Gly Thr Ala Glu  
 130 135 140  
 Arg Arg Gly Gly Phe Leu Ala Arg Trp Arg Val Phe Thr Val Cys Trp  
 145 150 155 160  
 Val Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu  
 165 170 175  
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser Trp  
 180 185 190  
 Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala Gln Ala  
 195 200 205  
 Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln Pro His Leu  
 210 215 220  
 Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp Val Gly Tyr His  
 225 230 235 240  
 Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu Ala Ala Glu Gly  
 245 250 255  
 Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys Thr Pro Ser Arg  
 260 265 270  
 Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr Gly Leu Gln His  
 275 280 285  
 Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro Leu Asp Asn Ala  
 290 295 300  
 Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser Thr His Met Val  
 305 310 315 320  
 Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Met Pro Thr Arg  
 325 330 335  
 Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr  
 340 345 350  
 Tyr Thr His Tyr Lys Trp Asp Ser Pro Trp Asp Val Trp Leu  
 355 360 365 366

&lt;210&gt; 293

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 293

Met Ala Tyr Ile Ile Gln Pro Ser Ser Thr Ser Val Ile Ser Val Lys  
 1 5 10 15  
 Leu Ser Leu Gly His Cys Ala Ser Ala Thr Leu Thr Ser Leu His Ile  
 20 25 30  
 Ser His Ile His Gln Ala Cys Ser Cys Leu Gly Ala Phe Val Leu Thr  
 35 40 45  
 Met Phe Cys Ser Glu Asn Thr Leu Pro Gln Asp Ile Leu Gln Leu Ser  
 50 55 60  
 Tyr Cys Ile Gln Leu Ser Ala Gln Val Leu Thr Asp Glu Thr Cys His  
 65 70 75 80  
 Pro Tyr Ser Thr Pro Cys Ser Ala Leu Leu Asn Ser Asn Cys Thr Tyr  
 85 90 95  
 Gly Pro Leu Asn Asn Ile His Leu Val Thr Tyr Phe Tyr Leu Ser Ala  
 100 105 110  
 Asn  
 113

&lt;210&gt; 294

<211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 290  
 Met Ala Asn Glu Val Gln Asp Leu Leu Ser Pro Arg Lys Gly Gly His  
 1 5 10 15  
 Pro Pro Ala Val Lys Ala Gly Gly Met Arg Ile Ser Lys Lys Gln Glu  
 20 25 30  
 Ile Gly Thr Leu Glu Arg His Thr Lys Lys Thr Gly Phe Glu Lys Thr  
 35 40 45  
 Ser Ala Ile Ala Asn Val Ala Lys Ile Gln Thr Pro Asp Ala Leu Asn  
 50 55 60  
 Asp Ala Leu Glu Lys Leu Asn Tyr Lys Phe Pro Ala Thr Val His Met  
 65 70 75 80  
 Ala His Gln Lys Pro Thr Pro Ala Leu Glu Lys Val Val Pro Leu Lys  
 85 90 95  
 Arg Ile Tyr Ile Ile Gln Gln Pro Arg Lys Cys  
 100 105 107

<210> 291  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 291  
 Met Leu Leu Trp Val Phe Leu Gln Leu Asn Tyr Lys Ile Gln Ala Ile  
 1 5 10 15  
 Pro Thr Tyr Glu Thr Val Met Thr Phe Phe Lys Ser Phe Pro Glu Asn  
 20 25 30  
 Cys Cys Phe Leu Asp Arg Asp Ile Gly Gln Ser Leu Arg Pro Leu Phe  
 35 40 45  
 Leu Cys Leu Arg Leu His Gly Ile Thr Lys Gly Lys Asp Leu Arg Cys  
 50 55 60  
 Cys Gly Thr Leu Thr Ser Ser Gln Ser His Gly Ser Thr Arg Leu Gln  
 65 70 75 80  
 Ser Thr Ile Thr Thr His Trp Arg Met Gly Ala Thr Trp Ser Thr \*  
 85 90 95

<210> 292  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 292  
 Met Leu Tyr Trp Val Val Ile His Phe Gly Ala Arg Gly Pro Gly Gly  
 1 5 10 15  
 Arg Arg Lys Arg Arg Thr Thr Asn Gly Glu Gly Arg Asn Ala Ala Arg  
 20 25 30  
 His Ala Gly Lys Glu Gly Asn Pro Arg Lys Pro Thr Gly Asn Ala Gln  
 35 40 45  
 Thr Pro Met Asp Pro Arg Lys Arg Lys Lys Gly Ser Leu Thr Pro Gly  
 50 55 60  
 Pro Asn Arg Arg Gln Gln Glu Ser Glu Gly Ala Arg Arg Gln Ser Arg  
 65 70 75 80  
 Arg Gly Glu Asn Gly Ser Glu Ala Ala Gln Ser Pro Ser Arg Gly Thr  
 85 90 95



<400> 287  
 Met Phe Leu Arg Gly Ile Pro Ser Arg Arg Glu Ser Leu Lys Thr Asn  
 1 5 10 15  
 Thr His Arg Ser Trp Arg Trp Ala Pro His Ser Pro Leu Asp Leu Thr  
 20 25 30  
 Ile Arg Asn Leu Leu Cys His Leu Phe Ile Lys Leu Ser Gln Ala Gln  
 35 40 45  
 Lys Ala Cys Pro Asn His Met Leu Arg Ala Lys Gln Met Glu Gln Lys  
 50 55 60  
 Leu Pro Gln Ala Ala Gly Ser His Tyr Gly Trp Asp Glu Ala Arg Thr  
 65 70 75 80  
 Trp Ala His Thr Gly Cys Lys Ala Ala Asp Ala Trp Val Asp Pro Gly  
 85 90 95  
 Val Pro Glu Gln Asp Leu Pro Ala Phe Asn  
 100 105 106

<210> 288  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 288  
 Met Ser Ser Trp Phe Leu Arg Ala Gly His Gly Leu Ile Trp Val Leu  
 1 5 10 15  
 Phe Phe Arg Ile Gly Gln Ala Ala Val Gly Val Ser Ala Gly Pro Gly  
 20 25 30  
 Gly Ser Pro Lys Ala His Leu Gly Arg Val Ala Ser Gln His Pro His  
 35 40 45  
 Gly Ala Glu Ser Arg Ala Cys Leu Leu Ala Arg Gly Leu Pro Lys Ala  
 50 55 60  
 Leu Ser Ser Met Leu Ala Val Asp Cys Arg Pro Arg Ser Gly Pro Leu  
 65 70 75 80  
 His Arg Ala Ala His Ile Met Ala Ala Ser Leu Ile Ser Lys Pro Val  
 85 90 95  
 Arg Gly Cys Leu Ser Glu Asp Asp Ile Pro Ser Pro Leu Ser Asp Ser  
 100 105 110  
 Ala Tyr  
 114

<210> 289  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 289  
 Met Gly Trp Asp Ser Lys Leu Leu Phe Leu Phe Thr Cys Leu Ser Cys  
 1 5 10 15  
 Val Thr Thr Cys Ser Val Ser Thr Cys Phe Gln Ala Pro Leu Gly Ser  
 20 25 30  
 Ser Ser Phe Ala Pro Ser Gly Phe Met Asp Ala Trp Tyr Ser Cys Tyr  
 35 40 45  
 Val Leu Ala \*  
 50 51

<210> 290

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 435 440 445  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 450 455 460  
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 465 470 474

<210> 285  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<400> 285  
 Met Leu Gly Ile Cys Leu Cys Ser Ile Cys Val Leu Arg Leu Cys Leu  
 1 5 10 15  
 Glu Lys Ser Lys Ile Phe Pro Pro Pro Arg Thr Ser Asp His Ser Leu  
 20 25 30  
 Glu Gly Ser Val Thr Pro Val Glu Asn Ala Ala Arg Ser Gly Met \*  
 35 40 45 47

<210> 286  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 286  
 Met Asn Ser Asn Leu Pro Ala Glu Asn Leu Ser Ile Ala Val Asn Met  
 1 5 10 15  
 Thr Lys Thr Leu Pro Thr Ala Val Thr His Gly Phe Asn Ser Thr Asn  
 20 25 30  
 Asp Pro Pro Ser Met Ser Ile Thr Arg Leu Phe Ser Ala Leu Leu Glu  
 35 40 45  
 Cys Phe Gly Ile Val Leu Cys Gly Tyr Ile Ala Gly Arg Ala Asn Val  
 50 55 60  
 Ile Thr Ser Thr Gln Ala Lys Gly Leu Gly Asn Phe Val Ser Arg Phe  
 65 70 75 80  
 Ala Leu Pro Ala Leu Leu Phe Lys Asn Met Val Val Leu Asn Phe Ser  
 85 90 95  
 Asn Val Asp Trp Ala Phe Leu Tyr Ser Ile Leu Ile Ala Lys Ala Ser  
 100 105 110  
 Val Phe Phe Ile Val Cys Val Leu Thr Leu Leu Val Ala Ser Pro Asp  
 115 120 125  
 Ser Arg Phe Ser Lys Ala Gly Leu Phe Pro Ile Phe Ala Thr Gln Ser  
 130 135 140  
 Asn Asp Phe Ala Leu Gly Tyr Pro Ile Gly Lys Leu Ile Phe Ile Phe  
 145 150 155 160  
 Gln Val Phe Lys Lys Phe Asn Phe Asn Leu Phe Arg His Leu Leu Val  
 165 170 175  
 Thr Asp Ser Tyr Ser His Ile  
 180 183

<210> 287  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<210> 284  
 <211> 474  
 <212> PRT  
 <213> Homo sapiens

<400> 284  
 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly  
 1 5 10 15  
 Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30  
 Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe  
 35 40 45  
 Ser Asp Tyr Trp Val Ala Trp Val Arg Gln Ser Pro Asp Lys Gly Leu  
 50 55 60  
 Ala Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser  
 65 70 75 80  
 Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser  
 85 90 95  
 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Asp Ser Asp Thr Ala Met  
 100 105 110  
 Tyr Tyr Cys Ala Arg Gly Ala Arg Gly Thr Ala Pro Ser Tyr His Tyr  
 115 120 125  
 Tyr Gly Leu Asp Val Trp Gly Arg Gly Thr Ser Val Thr Val Ser Ser  
 130 135 140  
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 145 150 155 160  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 165 170 175  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 180 185 190  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 195 200 205  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 210 215 220  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 225 230 235 240  
 Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 245 250 255  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 260 265 270  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 275 280 285  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 290 295 300  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 305 310 315 320  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 325 330 335  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 340 345 350  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 355 360 365  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
 370 375 380  
 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 385 390 395 400  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 405 410 415  
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 420 425 430

<210> 282  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 282  
 Met Cys His Trp Gln Asn Ser Phe Leu Cys Gln Ser Phe Leu Thr Phe  
 1 5 10 15  
 Gly Ser Ile Leu Ala Leu Leu Ala Gly Lys Ala Cys Tyr Pro Glu Ser  
 20 25 30  
 Glu Ser Ile Arg Glu Leu Phe Met Trp Ser Leu Glu Leu Tyr Ser Leu  
 35 40 45  
 Pro Phe Tyr Leu Phe Phe Lys Leu Ser Pro Leu Asn Leu Pro Gly Lys  
 50 55 60  
 Leu Gly Leu Ile Glu Thr Leu Ser Thr Cys Leu Gly Gln Lys Leu Asp  
 65 70 75 80  
 Pro Val Leu Glu Thr Leu Gln Arg Val Arg Ser Met Ala Ser Leu Ile  
 85 90 95  
 Ala Asn Phe Phe Val Pro Phe Ile Gln Lys Lys Gly Gln Leu Ile Thr  
 100 105 110 112  
 \*

<210> 283  
 <211> 231  
 <212> PRT  
 <213> Homo sapiens

<400> 283  
 Met Ala Trp Ile Pro Leu Phe Leu Gly Val Leu Ala Tyr Cys Thr Gly  
 1 5 10 15  
 Ser Val Ala Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser  
 20 25 30  
 Pro Gly Lys Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp  
 35 40 45  
 Lys Tyr Ala Ser Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Val Leu  
 50 55 60  
 Val Ile Tyr Arg His Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
 65 70 75 80  
 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
 85 90 95  
 Gln Val Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser  
 100 105 110  
 Ile Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro  
 115 120 125  
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu  
 130 135 140  
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro  
 145 150 155 160  
 Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala  
 165 170 175  
 Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala  
 180 185 190  
 Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg  
 195 200 205  
 Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr  
 210 215 220  
 Val Ala Pro Thr Glu Cys Ser  
 225 230 231

Gly Ser Ser Ser Leu Ser Leu Thr Arg Lys Asn Ser Pro Lys Ser Gly  
 485 490 495  
 Ser Pro Lys Ser Ser Ser Leu Leu Lys Leu Lys Ala Glu Lys Asn Ala  
 500 505 510  
 Gln Ala Glu Met Gly Lys Asn His Ser Ser Ala Ser Phe Ser Ser Ser  
 515 520 525  
 Ile Thr Ile Asn Thr Thr Cys Cys Ser Ser Ser Ser Ser Ser Ser  
 530 535 540  
 Ser Leu Ser Lys Thr Ser Gly Asp Leu Lys Pro Arg Ser Ala Ser Asp  
 545 550 555 560  
 Ala Gly Ile Arg Gly Thr Pro Lys Val Arg Ala Lys Lys Asp Ala Asp  
 565 570 575  
 Ala Asn Ala Gly Leu Thr Ser Cys Pro Arg Ala Lys Pro Ser Val Arg  
 580 585 590  
 Pro Lys Pro Phe Leu Asn Arg Ala Glu Ser Gln Ser Gln Glu Lys Met  
 595 600 605  
 Asp Ile Ser Thr Leu Arg Arg Gln Leu Arg Pro Thr Gly Gln Leu Arg  
 610 615 620  
 Gly Gly Leu Lys Gly Ser Lys Ser Glu Asp Ser Glu Leu Pro Pro Gln  
 625 630 635 640  
 Thr Ala Ser Glu Ala Pro Ser Glu Gly Ser Arg Arg Ser Ser Ser Asp  
 645 650 655  
 Leu Ile Thr Leu Pro Ala Thr Thr Pro Cys Pro Thr Lys Lys Glu  
 660 665 670  
 Trp Glu Gly Pro Ala Thr Ser Tyr Met Thr Cys Ser Ala Tyr Gln Lys  
 675 680 685  
 Val Gln Asp Ser Glu Ile Ser Phe Pro Ala Gly Val Glu Val Gln Val  
 690 695 700  
 Leu Glu Lys Gln Glu Ser Gly Trp Trp Tyr Val Arg Phe Gly Glu Leu  
 705 710 715 720  
 Glu Gly Trp Ala Pro Ser His Tyr Leu Val Leu Asp Glu Asn Glu Gln  
 725 730 735  
 Pro Asp Pro Ser Gly Lys Glu Leu Asp Thr Val Pro Ala Lys Gly Arg  
 740 745 750  
 Gln Asn Glu Gly Lys Ser Asp Ser Leu Glu Lys Ile Glu Arg Arg Val  
 755 760 765  
 Gln Ala Leu Asn Thr Val Asn Gln Ser Lys Lys Ala Thr Pro Pro Ile  
 770 775 780  
 Pro Ser Lys Pro Pro Gly Gly Phe Gly Lys Thr Ser Gly Thr Pro Ala  
 785 790 795 800  
 Val Lys Met Arg Asn Gly Val Arg Gln Val Ala Val Arg Pro Gln Ser  
 805 810 815  
 Val Phe Val Ser Pro Pro Pro Lys Asp Asn Asn Leu Ser Cys Ala Leu  
 820 825 830  
 Arg Arg Asn Glu Ser Leu Thr Ala Thr Asp Gly Leu Arg Gly Val Arg  
 835 840 845  
 Arg Asn Ser Ser Phe Ser Thr Ala Arg Ser Ala Ala Glu Ala Lys  
 850 855 860  
 Gly Arg Leu Ala Glu Arg Ala Ala Ser Gln Gly Ser Asp Ser Pro Leu  
 865 870 875 880  
 Leu Pro Ala Gln Arg Asn Ser Ile Pro Val Ser Pro Val Arg Pro Lys  
 885 890 895  
 Pro Ile Glu Lys Ser Gln Phe Ile His Asn Asn Leu Lys Asp Val Tyr  
 900 905 910  
 Val Ser Ile Ala Asp Tyr Glu Gly Asp Glu Glu Thr Ala Gly Phe Gln  
 915 920 925  
 Glu Gly Val Ser Met Glu Val Leu Glu Arg Asn Pro Asn Gly Trp Trp  
 930 935 940  
 Tyr Cys Gln Ile Leu Asp Gly Val Lys Pro Phe Lys Gly Trp Val Pro  
 945 950 955 960  
 Ser Asn Tyr Leu Glu Lys Lys Asn \*  
 965 968

&lt;213&gt; Homo sapiens

<400> 281

```

Met Ile Leu Glu Gln Tyr Val Val Val Ser Asn Tyr Lys Lys Gln Glu
 1           5           10           15
Asn Ser Glu Leu Ser Leu Gln Ala Gly Glu Val Val Asp Val Ile Glu
           20           25           30
Lys Asn Glu Ser Gly Trp Trp Phe Val Ser Thr Ser Glu Glu Gln Gly
           35           40           45
Trp Val Pro Ala Thr Tyr Leu Glu Ala Gln Asn Gly Thr Arg Asp Asp
           50           55           60
Ser Asp Ile Asn Thr Ser Lys Thr Gly Glu Val Ser Lys Arg Arg Lys
65           70           75           80
Ala His Leu Arg Arg Leu Asp Arg Arg Trp Thr Leu Gly Gly Met Val
           85           90           95
Asn Arg Gln His Ser Arg Glu Glu Lys Tyr Val Thr Val Gln Pro Tyr
           100          105          110
Thr Ser Gln Ser Lys Asp Glu Ile Gly Phe Glu Lys Gly Val Thr Val
           115          120          125
Glu Val Ile Arg Lys Asn Leu Glu Gly Trp Trp Tyr Ile Arg Tyr Leu
130          135          140
Gly Lys Glu Gly Trp Ala Pro Ala Ser Tyr Leu Lys Lys Ala Lys Asp
145          150          155          160
Asp Leu Pro Thr Arg Lys Lys Asn Leu Ala Gly Pro Val Glu Ile Ile
           165          170          175
Gly Asn Ile Met Glu Ile Ser Asn Leu Leu Asn Lys Lys Ala Ser Gly
           180          185          190
Asp Lys Glu Thr Pro Pro Ala Glu Gly Glu Gly His Glu Ala Pro Ile
           195          200          205
Ala Lys Lys Glu Ile Ser Leu Pro Ile Leu Cys Asn Ala Ser Asn Gly
210          215          220
Ser Ala Val Gly Val Pro Asp Arg Thr Val Ser Arg Leu Ala Gln Gly
225          230          235          240
Ser Pro Ala Val Ala Arg Ile Ala Pro Gln Arg Ala Gln Ile Ser Ser
           245          250          255
Pro Asn Leu Arg Thr Arg Pro Pro Pro Arg Arg Glu Ser Ser Leu Gly
           260          265          270
Phe Gln Leu Pro Lys Pro Pro Glu Pro Pro Ser Val Glu Val Glu Tyr
           275          280          285
Tyr Thr Ile Ala Glu Phe Gln Ser Cys Ile Ser Asp Gly Ile Ser Phe
290          295          300
Arg Gly Gly Gln Lys Ala Glu Val Ile Asp Lys Asn Ser Gly Gly Trp
305          310          315          320
Trp Tyr Val Gln Ile Gly Glu Lys Glu Gly Trp Ala Pro Ala Ser Tyr
           325          330          335
Ile Asp Lys Arg Lys Lys Pro Asn Leu Ser Arg Arg Thr Ser Thr Leu
           340          345          350
Thr Arg Pro Lys Val Pro Pro Pro Ala Pro Pro Ser Lys Pro Lys Glu
           355          360          365
Ala Glu Glu Gly Pro Thr Gly Ala Ser Glu Ser Gln Asp Ser Pro Arg
           370          375          380
Lys Leu Lys Tyr Glu Glu Pro Glu Tyr Asp Ile Pro Ala Phe Gly Phe
385          390          395          400
Asp Ser Glu Pro Glu Leu Ser Glu Glu Pro Val Glu Asp Arg Ala Ser
           405          410          415
Gly Glu Arg Arg Pro Ala Gln Pro His Arg Pro Ser Pro Ala Ser Ser
           420          425          430
Leu Gln Arg Ala Arg Phe Lys Val Gly Glu Ser Ser Glu Asp Val Ala
           435          440          445
Leu Glu Glu Glu Thr Ile Tyr Glu Asn Glu Gly Phe Arg Pro Tyr Ala
450          455          460
Glu Asp Thr Leu Ser Ala Arg Gly Ser Ser Gly Asp Ser Asp Ser Pro
465          470          475          480

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Leu Asp Ser Gly Pro Val His Met Gly Thr Ser Cys Leu Asp Ser Ala  
 165 170 175  
 Ser Glu His Met Gly Thr Ser Ser Leu Asp Ser Ala Ser Glu Leu Val  
 180 185 190  
 Asp Ile Thr Cys Leu Ser Lys Val Ile Thr Pro Leu Gly Phe Trp Lys  
 195 200 205  
 Asn His Gly Asp Phe Cys Pro Gly Lys Arg Tyr Asp Ala Ile Pro Leu  
 210 215 220 224

<210> 280  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<400> 280  
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln  
 20 25 30  
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu  
 35 40 45  
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly  
 50 55 60  
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser  
 65 70 75 80  
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr  
 85 90 95  
 Ile Gly Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile  
 100 105 110  
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val  
 115 120 125  
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe  
 130 135 140  
 Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala  
 145 150 155 160  
 Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile  
 165 170 175  
 Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu  
 180 185 190  
 Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly  
 195 200 205  
 Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe  
 210 215 220  
 Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile  
 225 230 235 240  
 Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu  
 245 250 255  
 Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr  
 260 265 270  
 Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln  
 275 280 285  
 Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro  
 290 295 300 301

<210> 281  
 <211> 969  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 278

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Met Glu Ser Ser Cys Leu Asp Ile Gly Ser Val Pro Met Gly Thr Ser
 1          5          10          15
Cys Leu Asp Ser Trp Pro Val His Ile Ser Cys Leu Asp Ser Gly
 20          25          30
Ser Val Arg Ile Lys Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met
 35          40          45
Gly Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met Gly Thr Ser Cys
 50          55          60
Leu Gly Ser Glu Pro Val Tyr Met Gly Thr Ser Cys Leu Gly Ser Glu
 65          70          75          80
Ser Val His Met Gly Thr Ser Cys Leu Gly Ser Glu Ser Val His Met
 85          90          95
Gly Thr Ser Cys Leu Ala Ser Gly Pro Val His Met Gly Thr Ser Cys
100          105          110
Leu Gly Ser Gly Pro Val His Met Gly Thr Ser Cys Leu Gly Ser Gly
115          120          125
Ser Glu His Met Gly Thr Ser Arg Leu Asp Ser Gly Pro Val His Val
130          135          140
Gly Thr Ser Cys Leu Gly Ser Gly Ser Glu His Val Gly Thr Ser Cys
145          150          155          160
Leu Gly Ser Glu Tyr Val Tyr Thr Gly Thr Ser Arg Leu Asp Ser Gly
165          170          175
Pro Val His Met Gly Thr Ser Cys Leu Asp Ser Ala Ser Glu His Met
180          185          190
Gly Thr Ser Ser Leu Asp Ser Ala Ser Glu Leu Val Asp Ile Thr Cys
195          200          205
Leu Ser Lys Val Ile Thr Pro Leu Gly Phe Trp Lys Asn His Gly Asp
210          215          220
Phe Cys Pro Gly Lys Arg Tyr Asp Ala Ile Pro Leu
225          230          235 236

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&lt;210&gt; 279

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 279

```

Met Glu Ser Ser Cys Leu Asp Ile Gly Ser Val His Met Gly Thr Ser
 1          5          10          15
Cys Leu Asp Ser Trp Pro Val His Ile Ile Ser Cys Leu Asp Ser Gly
 20          25          30
Ser Val Arg Ile Lys Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met
 35          40          45
Gly Thr Ser Cys Leu Asp Ser Gly Pro Val Tyr Met Gly Thr Ser Cys
 50          55          60
Leu Gly Ser Glu Pro Val Tyr Met Gly Thr Ser Cys Leu Gly Ser Glu
 65          70          75          80
Ser Val Tyr Met Gly Thr Ser Cys Leu Gly Ser Glu Ser Val Tyr Met
 85          90          95
Gly Thr Ser Cys Leu Ala Ser Gly Pro Val His Met Gly Thr Ser Cys
100          105          110
Leu Gly Ser Gly Ser Glu His Met Gly Thr Ser Arg Leu Asp Ser Gly
115          120          125
Pro Val His Val Gly Thr Ser Cys Leu Gly Ser Gly Ser Glu His Met
130          135          140
Gly Thr Ser Cys Leu Gly Ser Glu Ser Val Tyr Thr Gly Thr Ser Arg
145          150          155          160

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Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val  
 180 185 190  
 Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu Val Thr Leu Ile  
 195 200 205  
 Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly  
 210 215 220  
 His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr  
 225 230 235 240  
 Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser  
 245 250 255  
 Phe Leu Val  
 259

<210> 277  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 277  
 Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly  
 1 5 10 15  
 Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp  
 20 25 30  
 Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met  
 35 40 45  
 Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly  
 50 55 60  
 Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln  
 65 70 75 80  
 Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr  
 85 90 95  
 Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr  
 100 105 110  
 Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys  
 115 120 125  
 Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg  
 130 135 140  
 Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu  
 145 150 155 160  
 His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro  
 165 170 175  
 Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val  
 180 185 190  
 Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr  
 195 200 205  
 Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu  
 210 215 220  
 Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln  
 225 230 235 240  
 Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu  
 245 250 255  
 Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu  
 260 265 270 272  
 \*

<210> 278  
 <211> 236  
 <212> PRT

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60  
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95  
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295 299

&lt;210&gt; 276

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 276

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr  
 20 25 30  
 Ser Gly Phe Ser Ser Pro Arg Ala Ala Ser Tyr Glu Asp Arg Val Thr  
 35 40 45  
 Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr  
 50 55 60  
 Gly Thr Tyr Thr Cys Met Val Phe Glu Glu Gly Gly Asn Ser Tyr Gly  
 65 70 75 80  
 Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr  
 85 90 95  
 Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val Leu Thr  
 100 105 110  
 Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys  
 115 120 125  
 Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr Arg Ala Phe Ser  
 130 135 140  
 Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp  
 145 150 155 160  
 Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn  
 165 170 175

**PCT/US01/02623**

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<210> 274
<211> 118
<212> PRT
<213> Homo sapiens
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<210> 275
<211> 299
<212> PRT
<213> Homo sapiens
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385

&lt;400&gt; 272

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Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro Phe Leu Leu
 1           5           10           15
Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu Ala Ser Thr Asp
           20           25           30
Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu Ala Ile Ile Phe Thr
           35           40           45
Leu Ile Val Gly Lys Ala Leu Gly Glu Asp Ile Gly Gly Lys Arg Ala
           50           55           60
Val Ala Gly Met Val Leu Thr Val Ile Gly Ile Ser Leu Cys Ile Thr
           65           70           75           80
Ser Ser Val Ser Lys Thr Gln Gly Gln Gln Ser Thr Leu *
           85           90           93

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&lt;210&gt; 273

&lt;211&gt; 486

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

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Met Arg Gly Arg Gly Ser Gln Gln Gln Gln Pro Thr Arg Arg Gln Gly
 1           5           10           15
Gln Lys Leu Pro Ser Pro Ser Pro Ala Gly Lys Tyr Glu Ser Ala Gln
           20           25           30
Pro Gly Gly Thr Gln Pro Glu Pro Gly Leu Gly Ala Arg Met Ala Ile
           35           40           45
His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe Leu Phe Pro
           50           55           60
Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser Gln Gly Leu
           65           70           75           80
Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala Trp Gly Ile
           85           90           95
Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr Phe Val Leu
           100          105          110
Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp Thr Lys Lys
           115          120          125
Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly Thr Leu Gly
           130          135          140
Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp Phe Ser Thr
           145          150          155          160
Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala Ile Cys Phe
           165          170          175
Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu Ala Arg Lys
           180          185          190
Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala Leu Leu Leu
           195          200          205
Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile Ile Thr Leu
           210          215          220
Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser Ser Ala Gly
           225          230          235          240
Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp Phe Val Met
           245          250          255
Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe Leu Gly Ala
           260          265          270
Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys His Gly Val
           275          280          285
Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp Val Val Trp
           290          295          300
Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser Pro Thr Trp
           305          310          315          320

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Ile Gln Glu Ala Arg Ala Asp Leu Ala Arg Arg Gly Leu Arg Phe \*  
 115 120 125 127

<210> 270  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
 Met Lys Phe Arg Ile Val Thr Cys Gln Ser Asp Trp Arg Glu Leu Trp  
 1 5 10 15  
 Val Asp Asp Ala Ile Trp Arg Leu Leu Phe Ser Met Ile Leu Phe Val  
 20 25 30  
 Ile Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe  
 35 40 45  
 Ser Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln Lys Glu Pro Met  
 50 55 60  
 Leu Lys Glu Ser Phe Glu Gly Met Lys Met Arg Ser Thr Lys Gln Glu  
 65 70 75 80  
 Pro Asn Gly Asn Ser Lys Val Asn Lys Ala Gln Glu Asp Asp Leu Lys  
 85 90 95  
 Trp Val Glu Glu Asp Val Pro Ser Ser Val Thr Asp Val Ala Leu Pro  
 100 105 110  
 Ala Leu Leu Asp Ser Asp Glu Glu Arg Met Ile Thr His Phe Glu Arg  
 115 120 125  
 Ser Lys Met Glu  
 130 132

<210> 271  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 271  
 Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro Phe Leu Leu  
 1 5 10 15  
 Asn Gln Gly Gly Ser Leu Leu Tyr Tyr Leu Thr Leu Ala Ser Thr Asp  
 20 25 30  
 Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu Ala Ile Ile Phe Thr  
 35 40 45  
 Leu Ile Val Gly Lys Ala Leu Gly Glu Asp Ile Gly Gly Lys Arg Ala  
 50 55 60  
 Val Ala Gly Met Val Leu Thr Val Ile Gly Ile Ser Leu Cys Ile Thr  
 65 70 75 80  
 Ser Ser Val Pro Trp Thr Ala Glu Leu Gln Leu His Gly Lys Gly Gln  
 85 90 95  
 Leu Gln Thr Leu Ser Gln Lys Cys Lys Arg Glu Ala Ser Gly Thr Gln  
 100 105 110  
 Ser Glu Arg Phe Gly \*  
 115 117

<210> 272  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

Gly Ile Arg Leu His Cys Ala Arg Gly Asn Val Leu Gly Asn Thr His  
                             85                            90                            95  
 Val Val Glu Ser Gln Ser Gly Ser Trp Gly Glu Trp Ser Glu Pro Leu  
                             100                            105                            110  
 Trp Cys Arg Gly Gly Ala Tyr Leu Val Ala Phe Ser Leu Arg Val Glu  
                             115                            120                            125  
 Ala Pro Thr Thr Leu Gly Asp Asn Thr Ala Ala Asn Asn Val Arg Phe  
                             130                            135                            140  
 Arg Cys Ser Asp Gly Glu Glu Leu Gln Gly Pro Gly Leu Ser Trp Gly  
 145                            150                            155                            160  
 Asp Phe Gly Asp Trp Ser Asp His Cys Pro Lys Gly Ala Cys Gly Leu  
                             165                            170                            175  
 Gln Thr Lys Ile Gln Gly Pro Arg Gly Leu Gly Asp Asp Thr Ala Leu  
                             180                            185                            190  
 Asn Asp Ala Arg Leu Phe Cys Cys Arg Ser \*  
                             195                            200                            202

<210> 268  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 268  
 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu  
   1                            5                            10                            15  
 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly  
                             20                            25                            30  
 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp  
                             35                            40                            45  
 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile  
                             50                            55                            60  
 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe  
 65                            70                            75                            80  
 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser  
                             85                            90                            95  
 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Asp Thr Gln \*  
                             100                            105                            110 111

<210> 269  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 269  
 Met Met Lys Ile Pro His Gln Thr Gln Lys Lys Arg Ser Leu Glu Asp  
   1                            5                            10                            15  
 Pro Asn Ser Arg Pro Arg Arg Pro Arg Gly Glu Gly Glu Thr Trp Gly  
                             20                            25                            30  
 Arg Val Thr Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile  
                             35                            40                            45  
 Leu Gly Ser Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu  
                             50                            55                            60  
 Leu Pro Leu Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu  
 65                            70                            75                            80  
 Leu Val Ser Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val  
                             85                            90                            95  
 Ala Thr Phe His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln  
                             100                            105                            110

Val Ser Thr Phe Ile Lys Cys Leu Ala Leu Lys Ser Ile Ile Lys Arg  
                   35                  40                  45  
 Gln Arg Ser Glu Ile Asn Arg Gly Phe Leu Ala Ile Tyr His Ala Leu  
                   50                  55                  60  
 Arg Asn Gln Val Thr Arg Cys Gly Gly Leu \*  
                   65                  70                  74

<210> 265  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

<400> 265  
 Met His Ser Arg Thr Arg Ile Arg Leu Cys Leu Cys Asn Ala Lys Lys  
   1                  5                  10                  15  
 Ser Cys Gln Lys Tyr Leu Ser Ser Leu Lys Leu Ser Thr Leu Leu Ser  
                   20                  25                  30  
 Pro Leu Leu Phe Leu Pro Phe Tyr Thr Pro Ser Leu Lys Gly Trp Gly  
                   35                  40                  45  
 Ile Phe Val Leu Ser Phe Tyr Phe Met Leu Ile Ile Ala Asp Cys Asn  
                   50                  55                  60  
 Leu Phe Lys Ile Ile Ile \*  
                   65                  70

<210> 266  
 <211> 53  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Met Phe Thr His Trp Leu Gly Pro Pro Val Tyr Ile Lys Gln Phe Ile  
   1                  5                  10                  15  
 Val Met Ile Val Ser Ile Leu Thr Leu Phe Pro Val Leu Gln Gly Met  
                   20                  25                  30  
 Leu Arg Asn Phe Leu Tyr Leu Asn Ile Met Phe Val Val Ala Leu Leu  
                   35                  40                  45  
 Lys Ala Ile Leu \*  
                   50                  52

<210> 267  
 <211> 203  
 <212> PRT  
 <213> Homo sapiens

<400> 267  
 Met Glu Arg Gly Ala Gly Ala Lys Leu Leu Pro Leu Leu Leu Leu  
   1                  5                  10                  15  
 Arg Ala Thr Gly Phe Thr Cys Ala Gln Ala Asp Gly Arg Asn Gly Tyr  
                   20                  25                  30  
 Thr Ala Val Ile Glu Val Thr Ser Gly Gly Pro Trp Gly Asp Trp Ala  
                   35                  40                  45  
 Trp Pro Glu Met Cys Pro Asp Gly Phe Phe Ala Ser Gly Phe Ser Leu  
                   50                  55                  60  
 Lys Val Glu Pro Pro Gln Gly Ile Pro Gly Asp Asp Thr Ala Leu Asn  
                   65                  70                  75                  80

Asn Glu Arg Glu Pro Glu Pro Glu Pro Val Glu Ala Asn Ser Glu Glu  
 130 135 140  
 Ser Asp Ser Val Phe Ser Glu Asn Thr Glu Asp Leu Gln Glu Gln Phe  
 145 150 155 160  
 Thr Thr Ser Lys His His Ser His Gly Asn Arg Gln Ala Asn Tyr Ala  
 165 170 175  
 Ser Gly Glu Gln Ala Ser Phe Glu Ser Phe Glu Glu Met Leu Gln Glu  
 180 185 190 192  
 \*

<210> 262  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<400> 262  
 Met Pro Gly Tyr Val Pro Leu Leu Leu Leu Leu Leu Leu Arg Cys  
 1 5 10 15  
 Ser Gln Arg Gly Gly Gly Val Asn Phe Gly Glu Lys Asp Ala Lys Val  
 20 25 30  
 Pro Gly Thr Trp Arg Asp Gly Val Arg Val Pro Gly Glu Gly Ala Ser  
 35 40 45  
 Trp Asp Ser Asp Arg Ala Ser Pro Glu Arg Arg Tyr Gly Ile Gly Glu  
 50 55 60 64  
 \*

<210> 263  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

<400> 263  
 Met Lys Phe Leu Leu Met Ser Leu Pro Tyr Arg His Leu Phe Cys Ile  
 1 5 10 15  
 Thr Gln Ala Ile Leu Ser Glu Ile Ala Glu Gly Ile Arg Asn Asp Pro  
 20 25 30  
 Phe Lys Phe Tyr Leu Tyr Ser Val Leu Ala Leu Phe Leu His Tyr Tyr  
 35 40 45  
 Met Tyr Val Phe Val Ser Arg Phe Ser Ile Tyr Tyr Leu Lys Leu Leu  
 50 55 60  
 Arg Ile Phe Lys Phe Ser \*  
 65 70

<210> 264  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Arg Gln Ile Ala Val Phe Gln Arg Phe Met Phe Pro Phe Leu Leu  
 1 5 10 15  
 Pro Trp Leu Ser Cys Ile Phe Ser Ser Ser Gln Asn Ser Ile Tyr Tyr  
 20 25 30



<210> 259  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<400> 259  
 Met Lys Pro Tyr Cys Met Tyr Pro Phe Leu Ser Gly Leu Leu Ser Ser  
 1 5 10 15  
 Leu Leu Phe Trp Leu Glu Ser Leu Met Leu Leu Cys Val Gln Met Val  
 20 25 30  
 Leu Phe Leu Met Leu Cys Val Leu Asp Tyr Arg Ile Tyr Cys Ile Lys  
 35 40 45  
 Ile Tyr Val Ser Ile Ile Leu Leu Met Ser Ile Trp Ile Ile Ser Ile  
 50 55 60 64  
 \*

<210> 260  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<400> 260  
 Met Cys Tyr Phe Tyr Asn Thr Ile Ile Leu Thr Leu Gln Gly Ser Leu  
 1 5 10 15  
 Met Phe Leu Leu Phe Ser Val Val Thr Leu Tyr Leu Phe Ser His Ser  
 20 25 30  
 His Pro Thr Pro Ile Ser Ile Phe Ser Asp Val Phe Asn Met Tyr Pro  
 35 40 45  
 Trp Ile Tyr Met Tyr Ser Tyr Met Val Phe Ser Val Asn Leu Tyr Lys  
 50 55 60 64  
 \*

<210> 261  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<400> 261  
 Met Leu Met Tyr Arg Gly Glu Ala Leu Glu Asp Phe Thr Gly Pro Asp  
 1 5 10 15  
 Cys Arg Phe Val Asn Phe Lys Lys Gly Asp Pro Val Tyr Val Tyr Tyr  
 20 25 30  
 Lys Leu Ala Arg Gly Trp Pro Glu Val Trp Ala Gly Ser Val Gly Arg  
 35 40 45  
 Thr Phe Gly Tyr Phe Pro Lys Asp Leu Ile Gln Val Val His Glu Tyr  
 50 55 60  
 Thr Lys Glu Glu Leu Gln Val Pro Thr Asp Glu Thr Asp Phe Val Cys  
 65 70 75 80  
 Phe Asp Gly Gly Arg Asp Asp Phe His Asn Tyr Asn Val Glu Glu Leu  
 85 90 95  
 Leu Gly Phe Leu Glu Leu Tyr Asn Ser Ala Ala Thr Asp Ser Glu Lys  
 100 105 110  
 Ala Val Glu Gln Thr Leu Gln Asp Met Glu Lys Asn Pro Glu Leu Ser  
 115 120 125

Leu Lys Ala His Val Gln Ile Val Leu Tyr Trp Val Phe Leu Trp Ser  
           35                          40                          45  
 Arg Gly Asn Asn Phe Leu Thr  
           50                          55

<210> 256  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 256  
 Met Val Ile Leu Asp Val Leu Glu Leu Tyr His Met Trp Phe Leu Gly  
   1                          5                          10                          15  
 Ile Leu Tyr Asp Ala Ile Phe Tyr Cys Phe Val His Ala Ile Asn Ala  
           20                          25                          30  
 Asp Lys Phe Phe Gly Leu Lys Phe Thr Lys Ser Ala Thr Val Ser Gln  
           35                          40                          45  
 Asn Ser Gln \*  
   50  51

<210> 257  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

<400> 257  
 Met Tyr Asp Phe Leu Leu Leu Leu Ser Phe Ile Phe Ile Val Ala Ser  
   1                          5                          10                          15  
 Tyr Trp Ser Phe Leu Ser Thr Ile Phe Leu Asp Val Val Cys Ser Ile  
           20                          25                          30  
 Leu His Cys Pro Val Lys Pro Gln Thr Leu Leu Lys Ser Cys Leu His  
           35                          40                          45  
 Val Asp Cys Lys Ser Thr \*  
   50                          54

<210> 258  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 258  
 Met Trp Pro Gly Cys Gln Val Leu Arg Ala Gly Leu Ser Pro Ala Gly  
   1                          5                          10                          15  
 Arg Ala Arg Phe Pro Pro Asp Thr Tyr Leu Pro Ser Pro Arg Gln Gly  
           20                          25                          30  
 Gly Asn Pro Ala Cys Arg Cys Val Thr Ala Met Asn Ala Val Leu Gln  
           35                          40                          45  
 Val Leu Pro His Pro Ala Pro Asp Thr Asn Arg Ala Asp Glu Gly Cys  
           50                          55                          60  
 Gly Asp Gln Glu Gly Ser Arg Glu Leu Pro Pro Gly Gly Ala Ala Leu  
   65                          70                          75                          80  
 Gly His Arg Gly Gln \*  
           85

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

```

Met Glu Thr Asp Pro Ala Ser Trp Pro Gln Pro Glu Pro Ala Gln Leu
 1           5           10           15
Pro Gly Leu Tyr Ala Asp Phe Arg Ser Arg Thr Pro Arg Asp Ala Pro
           20           25           30
Ala Gly Cys Pro Arg Trp Gly Trp Arg Cys Leu Ser Ala Ala Gln Pro
           35           40           45
Ser Thr Gly Arg Thr Gly Glu Gly Ala Gly Pro Pro Gly Leu Cys Ala
 50           55           60
Asp Gln Pro Cys Gly Ala Ala Gly Gly Gly Gly Ala Glu Lys Gln
 65           70           75           80
Pro Ala Arg Ala Cys Gly Gly Asp Cys Trp Gly Gly Pro Met Pro His
           85           90           95
Gly Arg Glu Pro Glu Ser Gly Ser Ala Ala Lys Val Ser Val Cys Pro
           100           105           110
Gly Glu Glu *
           115

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&lt;210&gt; 253

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 253

```

Met Tyr Phe Ile Trp Ile Gly Thr Val Phe Leu Ile Cys Cys Tyr Leu
 1           5           10           15
Phe Gln Val Ser Ser Val Val Pro Asn Thr *
           20           25 26

```

&lt;210&gt; 254

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 254

```

Met Gly Pro Gly Phe Leu Gln Cys Ser Pro Thr Lys Lys Gly Ser Gln
 1           5           10           15
Thr Ala Pro Leu Asp Gly Ser Pro Glu Asp Gly Pro Ala Gln Trp Val
           20           25           30
Phe Val Glu Gln Ile Arg Asp Asn Lys Thr Asp *
           35           40           43

```

&lt;210&gt; 255

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 255

```

Met Tyr Met Asn Thr Cys Leu Tyr Leu His Val Tyr Val Leu Thr Cys
 1           5           10           15
Ser Gly Cys Asn Val Asp Met Cys Ser Arg Leu Phe Leu Ser Thr Lys
           20           25           30

```

Gly Glu Ser Val Thr Ala Met Glu Leu Glu Phe Lys Leu Leu Ala Ser  
 1635 1640 1645  
 Ser Lys Ala His Thr Ser Arg Phe Ile Ser Ala Asn Leu Pro Cys Asn  
 1650 1655 1660  
 Lys Phe Lys Asn Arg Leu Val Asn Ile Met Pro Tyr Glu Leu Thr Arg  
 1665 1670 1675 1680  
 Val Cys Leu Gln Pro Ile Arg Gly Val Glu Gly Ser Asp Tyr Ile Asn  
 1685 1690 1695  
 Ala Ser Phe Leu Asp Gly Tyr Arg Gln Gln Lys Ala Tyr Ile Ala Thr  
 1700 1705 1710  
 Gln Gly Pro Leu Ala Glu Ser Thr Glu Asp Phe Trp Arg Met Leu Trp  
 1715 1720 1725  
 Glu His Asn Ser Thr Ile Ile Val Met Leu Thr Lys Leu Arg Glu Met  
 1730 1735 1740  
 Gly Arg Glu Lys Cys His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg  
 1745 1750 1755 1760  
 Tyr Gln Tyr Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln  
 1765 1770 1775  
 Tyr Ile Leu Arg Glu Phe Lys Val Thr Asp Ala Arg Asp Gly Gln Ser  
 1780 1785 1790  
 Arg Thr Ile Arg Gln Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Val  
 1795 1800 1805  
 Pro Lys Thr Gly Glu Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys  
 1810 1815 1820  
 Thr Lys Glu Gln Phe Gly Gln Asp Gly Pro Ile Thr Val His Cys Ser  
 1825 1830 1835 1840  
 Ala Gly Val Gly Arg Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu  
 1845 1850 1855  
 Glu Arg Met Arg Tyr Glu Gly Val Val Asp Met Phe Gln Thr Val Lys  
 1860 1865 1870  
 Thr Leu Arg Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Gln Tyr  
 1875 1880 1885  
 Gln Leu Cys Tyr Arg Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His  
 1890 1895 1900  
 Tyr Ala Thr \*  
 1905 1907

<210> 251  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 251  
 Met Ile Trp Ile Tyr Phe Ala Phe Ile Phe Gln Arg Leu His Leu Ile  
 1 5 10 15  
 Pro Gly Lys Ser Ala Arg Gln Val Ser Gly Phe Ser Leu Leu Ser  
 20 25 30  
 Phe Asn Pro Ser Asn Thr Ile Phe Val Lys Leu Asp Trp Trp Cys Phe  
 35 40 45  
 Ile Gln Leu Ile Tyr Ser Ala Tyr Leu Phe Glu Lys Arg Leu Leu Glu  
 50 55 60  
 Ile Asp Asp Val Phe Val Pro Val Ile Leu Lys Val Val Gly Ala Arg  
 65 70 75 80  
 Ile Glu Phe His Ser Gly Ile Gly Phe Gly Ser Gly Leu \*  
 85 90 93

<210> 252  
 <211> 116  
 <212> PRT

Pro His Val Gln Asp Pro Ser Leu Val Arg Trp Phe Tyr Ile Val Val  
 1125 1130 1135  
 Val Pro Ile Asp Arg Val Gly Gly Ser Met Leu Thr Pro Arg Trp Ser  
 1140 1145 1150  
 Thr Pro Glu Glu Leu Glu Leu Asp Glu Leu Leu Glu Ala Ile Glu Gln  
 1155 1160 1165  
 Gly Gly Glu Glu Gln Arg Arg Arg Arg Gln Ala Glu Arg Leu Lys  
 1170 1175 1180  
 Pro Tyr Val Ala Ala Gln Leu Asp Val Leu Pro Glu Thr Phe Thr Leu  
 1185 1190 1195 1200  
 Gly Asp Lys Lys Asn Tyr Arg Gly Phe Tyr Asn Arg Pro Leu Ser Pro  
 1205 1210 1215  
 Asp Leu Ser Tyr Gln Cys Phe Val Leu Ala Ser Leu Lys Glu Pro Met  
 1220 1225 1230  
 Asp Gln Lys Arg Tyr Ala Ser Ser Pro Tyr Ser Asp Glu Ile Val Val  
 1235 1240 1245  
 Gln Val Thr Pro Ala Gln Gln Gln Glu Glu Pro Glu Met Leu Trp Val  
 1250 1255 1260  
 Thr Gly Pro Val Leu Ala Val Ile Leu Ile Ile Leu Ile Val Ile Ala  
 1265 1270 1275 1280  
 Ile Leu Leu Phe Lys Arg Lys Arg Thr His Ser Pro Ser Ser Lys Asp  
 1285 1290 1295  
 Glu Gln Ser Ile Gly Leu Lys Asp Ser Leu Leu Ala His Ser Ser Asp  
 1300 1305 1310  
 Pro Val Glu Met Arg Arg Leu Asn Tyr Gln Thr Pro Gly Met Arg Asp  
 1315 1320 1325  
 His Pro Pro Ile Pro Ile Thr Asp Leu Ala Asp Asn Ile Glu Arg Leu  
 1330 1335 1340  
 Lys Ala Asn Asp Gly Leu Lys Phe Ser Gln Glu Tyr Glu Ser Ile Asp  
 1345 1350 1355 1360  
 Pro Gly Gln Gln Phe Thr Trp Glu Asn Ser Asn Leu Glu Val Asn Lys  
 1365 1370 1375  
 Pro Lys Asn Arg Tyr Ala Asn Val Ile Ala Tyr Asp His Ser Arg Val  
 1380 1385 1390  
 Ile Leu Thr Ser Ile Asp Gly Val Pro Gly Ser Asp Tyr Ile Asn Ala  
 1395 1400 1405  
 Asn Tyr Ile Asp Gly Tyr Arg Lys Gln Asn Ala Tyr Ile Ala Thr Gln  
 1410 1415 1420  
 Gly Pro Leu Pro Glu Thr Met Gly Asp Phe Trp Arg Met Val Trp Glu  
 1425 1430 1435 1440  
 Gln Arg Thr Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys Ser  
 1445 1450 1455  
 Arg Val Lys Cys Asp Gln Tyr Trp Pro Ala Arg Gly Thr Glu Thr Cys  
 1460 1465 1470  
 Gly Leu Ile Gln Val Thr Leu Leu Asp Thr Val Glu Leu Ala Thr Tyr  
 1475 1480 1485  
 Thr Val Arg Thr Phe Ala Leu His Lys Ser Gly Ser Ser Glu Lys Arg  
 1490 1495 1500  
 Glu Leu Arg Gln Phe Gln Phe Met Ala Trp Pro Asp His Gly Val Pro  
 1505 1510 1515 1520  
 Glu Tyr Pro Thr Pro Ile Leu Ala Phe Leu Arg Arg Val Lys Ala Cys  
 1525 1530 1535  
 Asn Pro Leu Asp Ala Gly Pro Met Val Val His Cys Ser Ala Gly Val  
 1540 1545 1550  
 Gly Arg Thr Gly Cys Phe Ile Val Ile Asp Ala Met Leu Glu Arg Met  
 1555 1560 1565  
 Lys His Glu Lys Thr Val Asp Ile Tyr Gly His Val Thr Cys Met Arg  
 1570 1575 1580  
 Ser Gln Arg Asn Tyr Met Val Gln Thr Glu Asp Gln Tyr Val Phe Ile  
 1585 1590 1595 1600  
 His Glu Ala Leu Leu Glu Ala Ala Thr Cys Gly His Thr Glu Val Pro  
 1605 1610 1615  
 Ala Arg Asn Leu Tyr Ala His Ile Gln Lys Leu Gly Gln Val Pro Pro  
 1620 1625 1630

Pro	Pro	Gln	Lys	Val	Met	Cys	Val	Ser	Met	Gly	Ser	Thr	Thr	Val	Arg
610						615					620				
Val	Ser	Trp	Val	Pro	Pro	Ala	Asp	Ser	Arg	Asn	Gly	Val	Ile	Thr	
625					630					635					640
Gln	Tyr	Ser	Val	Ala	Tyr	Glu	Ala	Val	Asp	Gly	Glu	Asp	Arg	Gly	Arg
				645					650					655	
His	Val	Val	Asp	Gly	Ile	Ser	Arg	Glu	His	Ser	Ser	Trp	Asp	Leu	Val
			660					665					670		
Gly	Leu	Glu	Lys	Trp	Thr	Glu	Tyr	Arg	Val	Trp	Val	Arg	Ala	His	Thr
			675				680					685			
Asp	Val	Gly	Pro	Gly	Pro	Glu	Ser	Ser	Pro	Val	Leu	Val	Arg	Thr	Asp
	690					695					700				
Glu	Asp	Val	Pro	Ser	Gly	Pro	Pro	Arg	Lys	Val	Glu	Val	Glu	Pro	Leu
705					710					715					720
Asn	Ser	Thr	Ala	Val	His	Val	Tyr	Trp	Lys	Leu	Pro	Val	Pro	Ser	Lys
			725						730					735	
Gln	His	Gly	Gln	Ile	Arg	Gly	Tyr	Gln	Val	Thr	Tyr	Val	Arg	Leu	Glu
			740					745					750		
Asn	Gly	Glu	Pro	Arg	Gly	Leu	Pro	Ile	Ile	Gln	Asp	Val	Met	Leu	Ala
	755					760					765				
Glu	Ala	Gln	Trp	Arg	Pro	Glu	Glu	Ser	Glu	Asp	Tyr	Glu	Thr	Thr	Ile
	770					775					780				
Ser	Gly	Leu	Thr	Pro	Glu	Thr	Thr	Tyr	Ser	Val	Thr	Val	Ala	Ala	Tyr
785					790					795					800
Thr	Thr	Lys	Gly	Asp	Gly	Ala	Arg	Ser	Lys	Pro	Lys	Ile	Val	Thr	Thr
			805						810					815	
Thr	Gly	Ala	Val	Pro	Gly	Arg	Pro	Thr	Met	Met	Ile	Ser	Thr	Thr	Ala
			820					825					830		
Met	Asn	Thr	Ala	Leu	Leu	Gln	Trp	His	Pro	Pro	Lys	Glu	Leu	Pro	Gly
	835					840						845			
Glu	Leu	Leu	Gly	Tyr	Arg	Leu	Gln	Tyr	Cys	Arg	Ala	Asp	Glu	Ala	Arg
	850					855					860				
Pro	Asn	Thr	Ile	Asp	Phe	Gly	Lys	Asp	Asp	Gln	His	Phe	Thr	Val	Thr
865					870					875					880
Gly	Leu	His	Lys	Gly	Thr	Thr	Tyr	Ile	Phe	Arg	Leu	Ala	Ala	Lys	Asn
			885						890					895	
Arg	Ala	Gly	Leu	Gly	Glu	Glu	Phe	Glu	Lys	Glu	Ile	Arg	Thr	Pro	Glu
			900					905					910		
Asp	Leu	Pro	Ser	Gly	Phe	Pro	Gln	Asn	Leu	His	Val	Thr	Gly	Leu	Thr
	915					920						925			
Thr	Ser	Thr	Thr	Glu	Leu	Ala	Trp	Asp	Pro	Pro	Val	Leu	Ala	Glu	Arg
	930					935					940				
Asn	Gly	Arg	Ile	Ile	Ser	Tyr	Thr	Val	Val	Phe	Arg	Asp	Ile	Asn	Ser
945					950					955					960
Gln	Gln	Glu	Leu	Gln	Asn	Ile	Thr	Thr	Asp	Thr	Arg	Phe	Thr	Leu	Thr
			965					970						975	
Gly	Leu	Lys	Pro	Asp	Thr	Thr	Tyr	Asp	Ile	Lys	Val	Arg	Ala	Trp	Thr
			980					985					990		
Ser	Lys	Gly	Ser	Gly	Pro	Leu	Ser	Pro	Ser	Ile	Gln	Ser	Arg	Thr	Met
	995					1000					1005				
Pro	Val	Glu	Gln	Val	Phe	Ala	Lys	Asn	Phe	Arg	Val	Ala	Ala	Ala	Met
	1010					1015					1020				
Lys	Thr	Ser	Val	Leu	Leu	Ser	Trp	Glu	Val	Pro	Asp	Ser	Tyr	Lys	Ser
1025					1030					1035					1040
Ala	Val	Pro	Phe	Lys	Ile	Leu	Tyr	Asn	Gly	Gln	Ser	Val	Glu	Val	Asp
			1045					1050					1055		
Gly	His	Ser	Met	Arg	Lys	Leu	Ile	Ala	Asp	Leu	Gln	Pro	Asn	Thr	Glu
	1060							1065					1070		
Tyr	Ser	Phe	Val	Leu	Met	Asn	Arg	Gly	Ser	Ser	Ala	Gly	Gly	Leu	Gln
	1075					1080						1085			
His	Leu	Val	Ser	Ile	Arg	Thr	Ala	Pro	Asp	Leu	Leu	Pro	His	Lys	Pro
	1090					1095					1100				
Leu	Pro	Ala	Ser	Ala	Tyr	Ile	Glu	Asp	Gly	Arg	Phe	Asp	Leu	Ser	Met
1105					1110					1115					1120

Arg	Val	Gln	Arg	Asp	Glu	Ala	Ile	Tyr	Glu	Cys	Thr	Ala	Thr	Asn	Ser	100	105	110
Leu	Gly	Glu	Ile	Asn	Thr	Ser	Ala	Lys	Leu	Ser	Val	Leu	Glu	Glu	Glu	115	120	125
Gln	Leu	Pro	Pro	Gly	Phe	Pro	Ser	Ile	Asp	Met	Gly	Pro	Gln	Leu	Lys	130	135	140
Val	Val	Glu	Lys	Ala	Arg	Thr	Ala	Thr	Met	Leu	Cys	Ala	Ala	Gly	Gly	145	150	155
Asn	Pro	Asp	Pro	Glu	Ile	Ser	Trp	Phe	Lys	Asp	Phe	Leu	Pro	Val	Asp	165	170	175
Pro	Ala	Thr	Ser	Asn	Gly	Arg	Ile	Lys	Gln	Leu	Arg	Ser	Gly	Ala	Leu	180	185	190
Gln	Ile	Glu	Ser	Ser	Glu	Glu	Ser	Asp	Gln	Gly	Lys	Tyr	Glu	Cys	Val	195	200	205
Ala	Thr	Asn	Ser	Ala	Gly	Thr	Arg	Tyr	Ser	Ala	Pro	Ala	Asn	Leu	Tyr	210	215	220
Val	Arg	Val	Arg	Arg	Val	Ala	Pro	Arg	Phe	Ser	Ile	Pro	Pro	Ser	Ser	225	230	235
Gln	Glu	Val	Met	Pro	Gly	Gly	Ser	Val	Asn	Leu	Thr	Cys	Val	Ala	Val	245	250	255
Gly	Ala	Pro	Met	Pro	Tyr	Val	Lys	Trp	Met	Met	Gly	Ala	Glu	Glu	Leu	260	265	270
Thr	Lys	Glu	Asp	Glu	Met	Pro	Val	Gly	Arg	Asn	Val	Leu	Glu	Leu	Ser	275	280	285
Asn	Val	Val	Arg	Ser	Ala	Asn	Tyr	Thr	Cys	Val	Ala	Ile	Ser	Ser	Leu	290	295	300
Gly	Met	Ile	Glu	Ala	Thr	Ala	Gln	Val	Thr	Val	Lys	Ala	Leu	Pro	Lys	305	310	315
Pro	Pro	Ile	Asp	Leu	Val	Val	Thr	Glu	Thr	Thr	Ala	Thr	Ser	Val	Thr	325	330	335
Leu	Thr	Trp	Asp	Ser	Gly	Asn	Ser	Glu	Pro	Val	Thr	Tyr	Tyr	Gly	Ile	340	345	350
Gln	Tyr	Arg	Ala	Ala	Gly	Thr	Glu	Gly	Pro	Phe	Gln	Glu	Val	Asp	Gly	355	360	365
Val	Ala	Thr	Thr	Arg	Tyr	Ser	Ile	Gly	Gly	Leu	Ser	Pro	Phe	Ser	Glu	370	375	380
Tyr	Ala	Phe	Arg	Val	Leu	Ala	Val	Asn	Ser	Ile	Gly	Arg	Gly	Pro	Pro	385	390	395
Ser	Glu	Ala	Val	Arg	Ala	Arg	Thr	Gly	Glu	Gln	Ala	Pro	Ser	Ser	Pro	405	410	415
Pro	Arg	Arg	Val	Gln	Ala	Arg	Met	Leu	Ser	Ala	Ser	Thr	Met	Leu	Val	420	425	430
Gln	Trp	Glu	Pro	Pro	Glu	Glu	Pro	Asn	Gly	Leu	Val	Arg	Gly	Tyr	Arg	435	440	445
Val	Tyr	Tyr	Thr	Pro	Asp	Ser	Arg	Arg	Pro	Pro	Asn	Ala	Trp	His	Lys	450	455	460
His	Asn	Thr	Asp	Ala	Gly	Leu	Leu	Thr	Thr	Val	Gly	Ser	Leu	Leu	Pro	465	470	475
Gly	Ile	Thr	Tyr	Ser	Leu	Arg	Val	Leu	Ala	Phe	Thr	Ala	Val	Gly	Asp	485	490	495
Gly	Pro	Pro	Ser	Pro	Thr	Ile	Gln	Val	Lys	Thr	Gln	Gln	Gly	Val	Pro	500	505	510
Ala	Gln	Pro	Ala	Asp	Phe	Gln	Ala	Glu	Val	Glu	Ser	Asp	Thr	Arg	Ile	515	520	525
Gln	Leu	Ser	Trp	Leu	Leu	Pro	Pro	Gln	Glu	Arg	Ile	Ile	Met	Tyr	Glu	530	535	540
Leu	Val	Tyr	Trp	Ala	Ala	Glu	Asp	Glu	Asp	Gln	Gln	His	Lys	Val	Thr	545	550	555
Phe	Asp	Pro	Thr	Ser	Ser	Tyr	Thr	Leu	Glu	Asp	Leu	Lys	Pro	Asp	Thr	565	570	575
Leu	Tyr	Arg	Phe	Gln	Leu	Ala	Ala	Arg	Ser	Asp	Met	Gly	Val	Gly	Val	580	585	590
Phe	Thr	Pro	Thr	Ile	Glu	Ala	Arg	Thr	Ala	Gln	Ser	Thr	Pro	Ser	Ala	595	600	605

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Thr Phe Trp Phe Asn Met Ala Asp Ala Ala Phe Gln Ser Leu Val Cys
865                               870                               880
Phe Ser Ile Pro Tyr Leu Ala Tyr Tyr Asp Ser Asn Val Asp Leu Phe
                               885                               890                               895
Thr Trp Gly Thr Pro Ile Val Thr Ile Ala Leu Leu Thr Phe Leu Leu
900                               905                               910
His Leu Gly Ile Glu Thr Lys Thr Trp Thr Trp Leu Asn Trp Ile Thr
915                               920                               925
Cys Gly Phe Ser Val Leu Leu Phe Phe Thr Val Ala Leu Ile Tyr Asn
930                               935                               940
Ala Ser Cys Ala Thr Cys Tyr Pro Pro Ser Asn Pro Tyr Trp Thr Met
945                               950                               955                               960
Gln Ala Leu Leu Gly Asp Pro Val Phe Tyr Leu Thr Cys Leu Met Thr
965                               970                               975
Pro Val Ala Ala Leu Leu Pro Arg Leu Phe Phe Arg Ser Leu Gln Gly
980                               985                               990
Arg Val Phe Pro Thr Gln Leu Gln Leu Ala Arg Gln Leu Thr Arg Lys
995                               1000                               1005
Ser Pro Arg Arg Cys Ser Ala Pro Lys Glu Thr Phe Ala Gln Gly Arg
1010                               1015                               1020
Leu Pro Lys Asp Ser Gly Thr Glu His Ser Ser Gly Arg Thr Val Lys
1025                               1030                               1035                               1040
Thr Ser Val Pro Leu Ser Gln Pro Ser Trp His Thr Gln Gln Pro Val
1045                               1050                               1055
Cys Ser Leu Glu Ala Ser Gly Glu Pro Ser Thr Val Asp Met Ser Met
1060                               1065                               1070
Pro Val Arg Glu His Thr Leu Leu Glu Gly Leu Ser Ala Pro Ala Pro
1075                               1080                               1085
Met Ser Ser Ala Pro Gly Glu Ala Val Leu Arg Ser Pro Gly Gly Cys
1090                               1095                               1100
Pro Glu Glu Ser Lys Val Arg Ala Ala Ser Thr Gly Arg Val Thr Pro
1105                               1110                               1115                               1120
Leu Ser Ser Leu Phe Ser Leu Pro Thr Phe Ser Leu Leu Asn Trp Ile
1125                               1130                               1135
Ser Ser Trp Ser Leu Val Ser Arg Leu Gly Ser Val Leu Gln Phe Ser
1140                               1145                               1150
Arg Thr Glu Gln Leu Ala Asp Gly Gln Ala Gly Arg Gly Leu Pro Val
1155                               1160                               1165
Gln Pro His Ser Gly Arg Ser Gly Leu Gln Gly Pro Asp His Arg Leu
1170                               1175                               1180
Leu Ile Gly Ala Ser Ser Arg Arg Ser Gln *
1185                               1190                               1194

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&lt;210&gt; 250

&lt;211&gt; 1908

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

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Met Ala Pro Glu Pro Ala Pro Gly Arg Thr Met Val Pro Leu Val Pro
1                               5                               10                               15
Ala Leu Val Met Leu Gly Leu Val Ala Gly Ala His Gly Asp Ser Lys
20                               25                               30
Pro Val Phe Ile Lys Val Pro Glu Asp Gln Thr Gly Leu Ser Gly Gly
35                               40                               45
Val Ala Ser Phe Val Cys Gln Ala Thr Gly Glu Pro Lys Pro Arg Ile
50                               55                               60
Thr Trp Met Lys Lys Gly Lys Lys Val Ser Ser Gln Arg Phe Glu Val
65                               70                               75                               80
Ile Glu Phe Asp Asp Gly Ala Gly Ser Val Leu Arg Ile Gln Pro Leu
85                               90                               95

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Leu Gly Gln Pro Thr Ser Ala Ile Ala Ser Asn Gly Tyr Ser Ser Gln  
 355 360 365  
 Ala Asp Asn Trp Ala Ser Glu Leu Ala Gln Glu Gln Ser Glu Arg  
 370 375 380  
 Glu Leu Arg Tyr Glu Ala Glu Ser Pro Asp Glu Ala Ala Leu Val Tyr  
 385 390 395 400  
 Ala Ala Arg Ala Tyr Asn Cys Val Leu Val Glu Arg Leu His Asp Gln  
 405 410 415  
 Val Ser Val Glu Leu Pro His Leu Gly Arg Leu Thr Phe Glu Leu Leu  
 420 425 430  
 His Thr Leu Gly Phe Asp Ser Val Arg Lys Arg Met Ser Val Val Ile  
 435 440 445  
 Arg His Pro Leu Thr Asp Glu Ile Asn Val Tyr Thr Lys Gly Ala Asp  
 450 455 460  
 Ser Val Val Met Asp Leu Leu Gln Pro Cys Ser Ser Val Asp Ala Arg  
 465 470 475 480  
 Gly Arg His Gln Lys Lys Ile Arg Ser Lys Thr Gln Asn Tyr Leu Asn  
 485 490 495  
 Val Tyr Ala Ala Glu Gly Leu Arg Thr Leu Cys Ile Ala Lys Arg Val  
 500 505 510  
 Leu Ser Lys Glu Glu Tyr Ala Cys Trp Leu Gln Ser His Leu Glu Ala  
 515 520 525  
 Glu Ser Ser Leu Glu Asn Ser Glu Glu Leu Leu Phe Gln Ser Ala Ile  
 530 535 540  
 Arg Leu Glu Thr Asn Leu His Leu Leu Gly Ala Thr Gly Ile Glu Asp  
 545 550 555 560  
 Arg Leu Gln Asp Gly Val Pro Glu Thr Ile Ser Lys Leu Arg Gln Ala  
 565 570 575  
 Gly Leu Gln Ile Trp Val Leu Thr Gly Asp Lys Gln Glu Thr Ala Val  
 580 585 590  
 Asn Ile Ala Tyr Ala Cys Lys Leu Leu Asp His Asp Glu Glu Val Ile  
 595 600 605  
 Thr Leu Asn Ala Thr Ser Gln Glu Ala Cys Ala Ala Leu Leu Asp Gln  
 610 615 620  
 Cys Leu Cys Tyr Val Gln Ser Arg Gly Pro Gln Arg Ala Pro Glu Lys  
 625 630 635 640  
 Thr Lys Gly Lys Val Ser Met Arg Phe Ser Ser Leu Cys Pro Pro Ser  
 645 650 655  
 Thr Ser Thr Ala Ser Gly Arg Arg Pro Ser Leu Val Ile Asp Gly Arg  
 660 665 670  
 Ser Leu Ala Tyr Ala Leu Glu Lys Asn Leu Glu Asp Lys Phe Leu Phe  
 675 680 685  
 Leu Ala Lys Gln Cys Arg Ser Val Leu Cys Cys Arg Ser Thr Pro Leu  
 690 695 700  
 Gln Lys Ser Met Val Val Lys Leu Val Arg Ser Lys Leu Lys Ala Met  
 705 710 715 720  
 Thr Leu Ala Ile Gly Asp Gly Ala Asn Asp Val Ser Met Ile Gln Val  
 725 730 735  
 Ala Asp Val Gly Val Gly Ile Ser Gly Gln Glu Gly Met Gln Ala Val  
 740 745 750  
 Met Ala Ser Asp Phe Ala Val Pro Lys Phe Arg Tyr Leu Glu Arg Leu  
 755 760 765  
 Leu Ile Leu His Gly His Trp Cys Tyr Ser Arg Leu Ala Asn Met Val  
 770 775 780  
 Leu Tyr Phe Phe Tyr Lys Asn Thr Met Phe Val Gly Leu Leu Phe Trp  
 785 790 795 800  
 Phe Gln Phe Phe Cys Gly Phe Ser Ala Ser Thr Met Ile Asp Gln Trp  
 805 810 815  
 Tyr Leu Ile Phe Phe Asn Leu Leu Phe Ser Ser Leu Pro Pro Leu Val  
 820 825 830  
 Thr Gly Val Leu Asp Arg Asp Val Pro Ala Asn Val Leu Leu Thr Asn  
 835 840 845  
 Pro Gln Leu Tyr Lys Ser Gly Gln Asn Met Glu Glu Tyr Arg Pro Arg  
 850 855 860

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro  
 180 185 190  
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu  
 195 200 205  
 Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr  
 210 215 220  
 His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
 225 230 235 240  
 \*

<210> 249  
 <211> 1195  
 <212> PRT  
 <213> Homo sapiens

<400> 249  
 Met Asn Cys Asp Val Leu Trp Cys Val Leu Leu Val Cys Met Ser  
 1 5 10 15  
 Leu Phe Ser Ala Val Gly His Gly Leu Trp Ile Trp Arg Tyr Gln Glu  
 20 25 30  
 Lys Lys Ser Leu Phe Tyr Val Pro Lys Ser Asp Gly Ser Ser Leu Ser  
 35 40 45  
 Pro Val Thr Ala Ala Val Tyr Ser Phe Leu Thr Met Ile Ile Val Leu  
 50 55 60  
 Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu Ile Val Lys  
 65 70 75 80  
 Ala Cys Gln Val Tyr Phe Ile Asn Gln Asp Met Gln Leu Tyr Asp Glu  
 85 90 95  
 Glu Thr Asp Ser Gln Leu Gln Cys Arg Ala Leu Asn Ile Thr Glu Asp  
 100 105 110  
 Leu Gly Gln Ile Gln Tyr Ile Phe Ser Asp Lys Thr Gly Thr Leu Thr  
 115 120 125  
 Glu Asn Lys Met Val Phe Arg Arg Cys Thr Val Ser Gly Val Glu Tyr  
 130 135 140  
 Ser His Asp Ala Asn Ala Gln Arg Leu Ala Arg Tyr Gln Glu Ala Asp  
 145 150 155 160  
 Ser Glu Glu Glu Glu Val Val Pro Arg Gly Gly Ser Val Ser Gln Arg  
 165 170 175  
 Gly Ser Ile Gly Ser His Gln Ser Val Arg Val Val His Arg Thr Gln  
 180 185 190  
 Ser Thr Lys Ser His Arg Arg Thr Gly Ser Arg Ala Glu Ala Lys Arg  
 195 200 205  
 Ala Ser Met Leu Ser Lys His Thr Ala Phe Ser Ser Pro Met Glu Lys  
 210 215 220  
 Asp Ile Thr Pro Asp Pro Lys Leu Leu Glu Lys Val Ser Glu Cys Asp  
 225 230 235 240  
 Lys Ser Leu Ala Val Ala Arg His Gln Glu His Leu Leu Ala His Leu  
 245 250 255  
 Ser Pro Glu Leu Ser Asp Val Phe Asp Phe Phe Ile Ala Leu Thr Ile  
 260 265 270  
 Cys Asn Thr Val Val Val Thr Ser Pro Asp Gln Pro Arg Thr Lys Val  
 275 280 285  
 Arg Val Arg Phe Glu Leu Lys Ser Pro Val Lys Thr Ile Glu Asp Phe  
 290 295 300  
 Leu Arg Arg Phe Thr Pro Ser Cys Leu Thr Ser Gly Cys Ser Ser Ile  
 305 310 315 320  
 Gly Ser Leu Ala Ala Asn Lys Ser Ser His Lys Leu Gly Ser Ser Phe  
 325 330 335  
 Pro Ser Thr Pro Ser Ser Asp Gly Met Leu Leu Arg Leu Glu Glu Arg  
 340 345 350

Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu Arg Leu Arg Thr Val  
 65 70 75 80  
 Leu Leu Asp Val Thr Asp Pro Glu Asn Val Lys Arg Thr Ala Gln Trp  
 85 90 95  
 Val Lys Asn Gln Val Gly Glu Lys Gly Leu Trp Gly Leu Ile Asn Asn  
 100 105 110  
 Ala Gly Val Pro Gly Val Leu Ala Pro Thr Asp Trp Leu Thr Leu Glu  
 115 120 125  
 Asp Tyr Arg Glu Pro Ile Glu Val Asn Leu Phe Gly Leu Ile Ser Val  
 130 135 140  
 Thr Leu Asn Met Leu Pro Leu Val Lys Lys Ala Gln Gly Arg Val Ile  
 145 150 155 160  
 Asn Val Ser Ser Val Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr  
 165 170 175  
 Thr Pro Ser Lys Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg  
 180 185 190  
 Asp Met Lys Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu  
 195 200 205  
 Phe Lys Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu  
 210 215 220  
 Ala Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
 225 230 235 240  
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser Tyr  
 245 250 255  
 Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His Ala Leu  
 260 265 270  
 Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys Asp Ala Lys  
 275 280 285  
 Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala Leu Gln Asp Phe  
 290 295 300  
 Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn Pro Lys Ala Val \*  
 305 310 315 319

&lt;210&gt; 248

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 248

Met Ser Val Pro Thr Met Ala Trp Met Met Leu Leu Leu Gly Leu Leu  
 1 5 10 15  
 Ala Tyr Gly Ser Gly Val Asp Ser Glu Thr Val Val Thr Gln Glu Pro  
 20 25 30  
 Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Leu  
 35 40 45  
 Asn Ser Gly Ser Val Ser Asp Ser Phe Tyr Pro Ser Trp His Gln Gln  
 50 55 60  
 Thr Pro Gly Gln Pro Pro Arg Thr Leu Ile Tyr Asn Thr His Ile Arg  
 65 70 75 80  
 Ala Ser Gly Val Ser Asp Arg Phe Ser Gly Ser Ile Val Gly Asn Lys  
 85 90 95  
 Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Cys Val Tyr  
 100 105 110  
 Tyr Cys Val Leu Tyr Met Gly Asn Asp Ile Ser Leu Phe Gly Gly Gly  
 115 120 125  
 Thr Arg Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr  
 130 135 140  
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu  
 145 150 155 160  
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp  
 165 170 175

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val  
           35                          40                          45  
 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys  
           50                          55                          60  
 Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys  
           65                          70                          75                          80  
 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp  
                           85                          90                          95  
 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His  
                           100                          105                          110  
 Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile  
           115                          120                          125  
 Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His  
           130                          135                          140  
 Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys  
           145                          150                          155                          160  
 Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys  
                           165                          170                          175  
 Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser  
                           180                          185                          190  
 Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala  
           195                          200                          205  
 Pro Arg Gly Arg Ala Ser Glu Pro Lys His Lys Thr Arg Gln Arg \*  
           210                          215                          220                          223

&lt;210&gt; 246

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

Met Arg Arg Ser Phe Trp Thr Val Met Arg Thr Ala Trp Arg Cys Ser  
   1                          5                          10                          15  
 Cys Ser Ser Val Asp Arg Ala Leu Ser His Gln Ala Gly Leu Gln Gly  
           20                          25                          30  
 Gln Cys Leu Ser Ala Cys Leu Leu Gly Asn Leu Gly Tyr Pro Pro Phe  
           35                          40                          45  
 Ile Ser Pro Pro Ala Gln Val Leu Cys Ala Ala Arg Ala Ser Cys His  
           50                          55                          60  
 Leu Gly Ser Leu Met Ala Ile Leu Arg Leu Trp Phe Thr Val Lys Ile  
           65                          70                          75                          80  
 Gly Pro Val \*  
           83

&lt;210&gt; 247

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 247

Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu Trp  
   1                          5                          10                          15  
 Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys Tyr Ile  
           20                          25                          30  
 Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala Ala Arg Thr  
           35                          40                          45  
 Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys Leu Thr Glu Ser  
           50                          55                          60

<210> 244  
 <211> 308  
 <212> PRT  
 <213> Homo sapiens

<400> 244  
 Met Thr Lys Ala Gly Ser Lys Gly Gly Asn Leu Arg Asp Lys Leu Asp  
 1 5 10 15  
 Gly Asn Glu Leu Asp Leu Ser Leu Ser Asp Leu Asn Glu Val Pro Val  
 20 25 30  
 Lys Glu Leu Ala Ala Leu Pro Lys Ala Thr Ile Leu Asp Leu Ser Cys  
 35 40 45  
 Asn Lys Leu Thr Thr Leu Pro Ser Asp Phe Cys Gly Leu Thr His Leu  
 50 55 60  
 Val Lys Leu Asp Leu Ser Lys Asn Lys Leu Gln Gln Leu Pro Ala Asp  
 65 70 75 80  
 Phe Gly Arg Leu Val Asn Leu Gln His Leu Asp Leu Leu Asn Asn Lys  
 85 90 95  
 Leu Val Thr Leu Pro Val Ser Phe Ala Gln Leu Lys Asn Leu Lys Trp  
 100 105 110  
 Leu Asp Leu Lys Asp Asn Pro Leu Asp Pro Val Leu Ala Lys Val Ala  
 115 120 125  
 Gly Asp Cys Leu Asp Glu Lys Gln Cys Lys Gln Cys Ala Asn Lys Val  
 130 135 140  
 Leu Gln His Met Lys Ala Val Gln Ala Asp Gln Glu Arg Glu Arg Gln  
 145 150 155 160  
 Arg Arg Leu Glu Val Glu Arg Glu Ala Glu Lys Lys Arg Glu Ala Lys  
 165 170 175  
 Gln Arg Ala Lys Glu Ala Gln Glu Arg Glu Leu Arg Lys Arg Glu Lys  
 180 185 190  
 Ala Glu Glu Lys Glu Arg Arg Arg Lys Glu Tyr Asp Ala Leu Lys Ala  
 195 200 205  
 Val Lys Arg Glu Gln Glu Lys Lys Pro Lys Lys Glu Ala Asn Gln Ala  
 210 215 220  
 Pro Lys Ser Lys Ser Gly Ser Arg Pro Arg Lys Pro Pro Pro Arg Lys  
 225 230 235 240  
 His Thr Arg Ser Trp Ala Val Leu Lys Leu Leu Leu Leu Leu Leu  
 245 250 255  
 Phe Gly Val Ala Gly Gly Leu Val Ala Cys Arg Val Thr Glu Leu Gln  
 260 265 270  
 Gln Gln Pro Leu Cys Thr Ser Val Asn Thr Ile Tyr Asp Asn Ala Val  
 275 280 285  
 Gln Gly Leu Arg Arg His Glu Ile Leu Gln Trp Val Leu Gln Thr Asp  
 290 295 300  
 Ser Gln Gln \*  
 305 307

<210> 245  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 245  
 Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu  
 1 5 10 15  
 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His  
 20 25 30

Val Gly Leu Pro Gly Gln Arg Gly Glu Arg Gly Phe Pro Gly Leu Pro  
 965 970 975  
 Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly Pro Ser Gly Ala Ser Gly  
 980 985 990  
 Glu Arg Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Leu Ala Gly Pro  
 995 1000 1005  
 Pro Gly Glu Ser Gly Arg Glu Gly Ala Pro Gly Ala Glu Gly Ser Pro  
 1010 1015 1020  
 Gly Arg Asp Gly Ser Pro Gly Ala Lys Gly Asp Arg Gly Glu Thr Gly  
 1025 1030 1035 1040  
 Pro Ala Gly Pro Pro Gly Ala Pro Gly Ala Pro Gly Ala Pro Gly Pro  
 1045 1050 1055  
 Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Thr Gly Pro Ala  
 1060 1065 1070  
 Gly Pro Ala Gly Pro Val Gly Pro Val Gly Ala Arg Gly Pro Ala Gly  
 1075 1080 1085  
 Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly Glu Gln Gly Asp  
 1090 1095 1100  
 Arg Gly Ile Lys Gly His Arg Gly Phe Ser Gly Leu Gln Gly Pro Pro  
 1105 1110 1115 1120  
 Gly Pro Pro Gly Ser Pro Gly Glu Gln Gly Pro Ser Gly Ala Ser Gly  
 1125 1130 1135  
 Pro Ala Gly Pro Arg Gly Pro Pro Gly Ser Ala Gly Ala Pro Gly Lys  
 1140 1145 1150  
 Asp Gly Leu Asn Gly Leu Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg  
 1155 1160 1165  
 Gly Arg Thr Gly Asp Ala Gly Pro Val Gly Pro Pro Gly Pro Pro Gly  
 1170 1175 1180  
 Pro Pro Gly Pro Pro Gly Pro Pro Ser Ala Gly Phe Asp Phe Ser Phe  
 1185 1190 1195 1200  
 Leu Pro Gln Pro Pro Gln Glu Lys Ala His Asp Gly Gly Arg Tyr Tyr  
 1205 1210 1215  
 Arg Ala Asp Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp  
 1220 1225 1230  
 Thr Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu Asn Ile Arg Ser Pro  
 1235 1240 1245  
 Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Lys Met  
 1250 1255 1260  
 Cys His Ser Asp Trp Lys Ser Gly Glu Tyr Trp Ile Asp Pro Asn Gln  
 1265 1270 1275 1280  
 Gly Cys Asn Leu Asp Ala Ile Lys Val Phe Cys Asn Met Glu Thr Gly  
 1285 1290 1295  
 Glu Thr Cys Val Tyr Pro Thr Gln Pro Ser Val Ala Gln Lys Asn Trp  
 1300 1305 1310  
 Tyr Ile Ser Lys Asn Pro Lys Asp Lys Arg His Val Trp Phe Gly Glu  
 1315 1320 1325  
 Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp  
 1330 1335 1340  
 Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr  
 1345 1350 1355 1360  
 Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr  
 1365 1370 1375  
 Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Gln Gly  
 1380 1385 1390  
 Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr  
 1395 1400 1405  
 Ser Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys  
 1410 1415 1420  
 Thr Val Ile Glu Tyr Lys Thr Thr Lys Thr Ser Arg Leu Pro Ile Ile  
 1425 1430 1435 1440  
 Asp Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe  
 1445 1450 1455  
 Asp Val Gly Pro Val Cys Phe Leu  
 1460 1464

Gly Glu Pro Gly Pro Val Gly Val Gln Gly Pro Pro Gly Pro Ala Gly  
 450 455 460  
 Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu  
 465 470 475 480  
 Pro Gly Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro  
 485 490 495  
 Gly Ala Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly  
 500 505 510  
 Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg  
 515 520 525  
 Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro  
 530 535 540  
 Gly Ser Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly  
 545 550 555 560  
 Gln Asp Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln  
 565 570 575  
 Ala Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro  
 580 585 590  
 Gly Lys Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Ala Val Gly  
 595 600 605  
 Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro  
 610 615 620  
 Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Pro Ala Gly Ser Pro  
 625 630 635 640  
 Gly Phe Gln Gly Leu Pro Gly Pro Ala Gly Pro Pro Gly Glu Ala Gly  
 645 650 655  
 Lys Pro Gly Glu Gln Gly Val Pro Gly Asp Leu Gly Ala Pro Gly Pro  
 660 665 670  
 Ser Gly Ala Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Val Gln  
 675 680 685  
 Gly Pro Pro Gly Pro Ala Gly Pro Arg Gly Ala Asn Gly Ala Pro Gly  
 690 695 700  
 Asn Asp Gly Ala Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Ser  
 705 710 715 720  
 Gln Gly Ala Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ala Ala  
 725 730 735  
 Gly Leu Pro Gly Pro Lys Gly Asp Arg Gly Asp Ala Gly Pro Lys Gly  
 740 745 750  
 Ala Asp Gly Ser Pro Gly Lys Asp Gly Val Arg Gly Leu Thr Gly Pro  
 755 760 765  
 Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp Lys Gly Glu Ser  
 770 775 780  
 Gly Pro Ser Gly Pro Ala Gly Pro Thr Gly Ala Arg Gly Ala Pro Gly  
 785 790 795 800  
 Asp Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe Ala Gly Pro  
 805 810 815  
 Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Glu Pro Gly Asp Ala  
 820 825 830  
 Gly Ala Lys Gly Asp Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly  
 835 840 845  
 Pro Pro Gly Pro Ile Gly Asn Val Gly Ala Pro Gly Ala Lys Gly Ala  
 850 855 860  
 Arg Gly Ser Ala Gly Pro Gly Ala Thr Gly Phe Pro Gly Ala Ala  
 865 870 875 880  
 Gly Arg Val Gly Pro Pro Gly Pro Ser Gly Asn Ala Gly Pro Pro Gly  
 885 890 895  
 Pro Pro Gly Pro Ala Gly Lys Glu Gly Gly Lys Gly Pro Arg Gly Glu  
 900 905 910  
 Thr Gly Pro Ala Gly Arg Pro Gly Glu Val Gly Pro Pro Gly Pro Pro  
 915 920 925  
 Gly Pro Ala Gly Glu Lys Gly Ser Pro Gly Ala Asp Gly Pro Ala Gly  
 930 935 940  
 Ala Pro Gly Thr Pro Gly Pro Gln Gly Ile Ala Gly Gln Arg Gly Val  
 945 950 955 960

<210> 243  
 <211> 1464  
 <212> PRT  
 <213> Homo sapiens

<400> 243  
 Met Phe Ser Phe Val Asp Leu Arg Leu Leu Leu Leu Leu Ala Ala Thr  
 1 5 10 15  
 Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp  
 20 25 30  
 Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His  
 35 40 45  
 Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp  
 50 55 60  
 Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn  
 65 70 75 80  
 Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro  
 85 90 95  
 Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly  
 100 105 110  
 Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro  
 115 120 125  
 Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro  
 130 135 140  
 Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala  
 145 150 155 160  
 Pro Gln Leu Ser Tyr Gly Tyr Asp Glu Lys Ser Thr Gly Gly Ile Ser  
 165 170 175  
 Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg Gly Leu Pro Gly Pro  
 180 185 190  
 Pro Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Pro Pro Gly Glu Pro  
 195 200 205  
 Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly  
 210 215 220  
 Pro Pro Gly Lys Asn Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Arg  
 225 230 235 240  
 Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro  
 245 250 255  
 Gly Thr Ala Gly Leu Pro Gly Met Lys Gly His Arg Gly Phe Ser Gly  
 260 265 270  
 Leu Asp Gly Ala Lys Gly Asp Ala Gly Pro Ala Gly Pro Lys Gly Glu  
 275 280 285  
 Pro Gly Ser Pro Gly Glu Asn Gly Ala Pro Gly Gln Met Gly Pro Arg  
 290 295 300  
 Gly Leu Pro Gly Glu Arg Gly Arg Pro Gly Ala Pro Gly Pro Ala Gly  
 305 310 315 320  
 Ala Arg Gly Asn Asp Gly Ala Thr Gly Ala Ala Gly Pro Pro Gly Pro  
 325 330 335  
 Thr Gly Pro Ala Gly Pro Pro Gly Phe Pro Gly Ala Val Gly Ala Lys  
 340 345 350  
 Gly Glu Ala Gly Pro Gln Gly Pro Arg Gly Ser Glu Gly Pro Gln Gly  
 355 360 365  
 Val Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Ala Ala Gly Pro  
 370 375 380  
 Ala Gly Asn Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Ala Asn  
 385 390 395 400  
 Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly  
 405 410 415  
 Pro Ser Gly Pro Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys Gly Asn  
 420 425 430  
 Ser Gly Glu Pro Gly Ala Pro Gly Ser Lys Gly Asp Thr Gly Ala Lys  
 435 440 445



Gln Val Gly Tyr Gly Met Ala Ala Gly Tyr Thr Ile Phe Ile Thr Ser  
 210 215 220  
 Phe Leu Gly Val Leu Val Phe Ser Arg Cys Phe Arg Asp Thr Thr Met  
 225 230 235 240  
 Ile Met Ile Gly Met Val Ser Phe Gly Ser Gly Ala Leu Leu Leu Ala  
 245 250 255  
 Phe Val Lys Glu Thr Tyr Met Phe Tyr Ile Ala Arg Ala Val Met Leu  
 260 265 270  
 Phe Ala Leu Ile Pro Val Thr Thr Ile Arg Ser Ala Met Ser Lys Leu  
 275 280 285  
 Ile Lys Gly Ser Ser Tyr Gly Lys Val Phe Val Ile Leu Gln Leu Ser  
 290 295 300  
 Leu Ala Leu Thr Gly Val Val Thr Ser Thr Leu Tyr Asn Lys Ile Tyr  
 305 310 315 320  
 Gln Leu Thr Met Asp Met Phe Val Gly Ser Cys Phe Ala Leu Ser Ser  
 325 330 335  
 Phe Leu Ser Phe Leu Ala Ile Ile Pro Ile Ser Ile Val Ala Tyr Lys  
 340 345 350  
 Gln Val Pro Leu Ser Pro Tyr Gly Asp Ile Ile Glu Lys \*  
 355 360 365

&lt;210&gt; 242

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 242

Met Phe Leu Phe Leu Phe Phe Leu Val Ala Ile Leu Pro Val Asn Thr  
 1 5 10 15  
 Glu Gly Gly Glu Ile Ile Trp Gly Thr Glu Ser Lys Pro His Ser Arg  
 20 25 30  
 Pro Tyr Met Ala Phe Ile Lys Phe Tyr Asp Ser Asn Ser Glu Pro His  
 35 40 45  
 His Cys Gly Gly Phe Leu Val Ala Lys Asp Ile Val Met Thr Ala Ala  
 50 55 60  
 His Cys Asn Gly Arg Asn Ile Lys Val Thr Leu Gly Ala His Asn Ile  
 65 70 75 80  
 Lys Lys Gln Glu Asn Thr Gln Val Ile Ser Val Val Lys Ala Lys Pro  
 85 90 95  
 His Glu Asn Tyr Asp Arg Asp Ser His Phe Asn Asp Ile Met Leu Leu  
 100 105 110  
 Lys Leu Glu Arg Lys Ala Gln Leu Asn Gly Val Val Lys Thr Ile Ala  
 115 120 125  
 Leu Pro Arg Ser Gln Asp Trp Val Lys Pro Gly Gln Val Cys Thr Val  
 130 135 140  
 Ala Gly Trp Gly Arg Leu Ala Asn Cys Thr Ser Ser Asn Thr Leu Gln  
 145 150 155 160  
 Glu Val Asn Leu Glu Val Gln Lys Gly Gln Lys Cys Gln Asp Met Ser  
 165 170 175  
 Glu Asp Tyr Asn Asp Ser Ile Gln Leu Cys Val Gly Asn Pro Ser Glu  
 180 185 190  
 Gly Lys Ala Thr Gly Lys Gly Asp Ser Gly Gly Pro Phe Val Cys Asp  
 195 200 205  
 Gly Met Ala Pro Gly His Trp Gln Leu Ser Ala Trp Val Leu Gly Thr  
 210 215 220  
 Leu Ser Arg Glu Phe Pro Gln Asn Leu Gln Leu Leu Tyr Arg Gly Phe  
 225 230 235 240  
 Arg Lys Pro Met Lys Gly Pro \*  
 245 247

Arg Tyr Arg Ile Leu Leu Val Thr Val Leu Trp Thr Leu Leu Val Tyr  
 340 345 350  
 Ser Met Leu Ser His Lys Glu Phe Arg Phe Ile Tyr Pro Val Leu Pro  
 355 360 365  
 Phe Cys Met Val Phe Cys Gly Tyr Ser Leu Thr His Leu Lys Thr Trp  
 370 375 380  
 Lys Lys Pro Ala Leu Ser Phe Leu Phe Leu Ser Asn Leu Phe Leu Ala  
 385 390 395 400  
 Leu Tyr Thr Gly Leu Val His Gln Arg Gly Thr Leu Asp Val Met Ser  
 405 410 415  
 His Ile Gln Lys Val Cys Tyr Asn Asn Pro Asn Lys Ser Ser Ala Ser  
 420 425 430  
 Ile Phe Ile Met Met Pro Cys His Ser Thr Pro Tyr Tyr Ser His Val  
 435 440 445  
 His Cys Pro Leu Pro Met Arg Phe Leu Gln Cys Pro Pro Asp Leu Thr  
 450 455 460  
 Gly Lys Ser His Tyr Leu Asp Glu Ala Asp Val Phe Tyr Leu Asn Pro  
 465 470 475 480  
 Leu Asn Trp Leu His Arg Glu Phe His Asp Asp Ala Ser Leu Pro Thr  
 485 490 495  
 His Leu Ile Thr Phe Ser Ile Leu Glu Glu Ile Ser Ala Phe Leu  
 500 505 510  
 Ile Ser Ser Asn Tyr Lys Arg Thr Ala Val Phe Phe His Thr His Leu  
 515 520 525  
 Pro Glu Gly Arg Ile Gly Ser His Ile Tyr Val Tyr Glu Arg Lys Leu  
 530 535 540  
 Lys Gly Lys Phe Asn Met Lys Met Lys Phe  
 545 550 554

&lt;210&gt; 241

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 241

Met Ser Leu Leu Gly Phe Leu Leu Ser Arg Leu Gly Leu Leu Leu Lys  
 1 5 10 15  
 Val Leu Leu Asp Trp Pro Val Glu Val Leu Tyr Gly Ala Ala Ala Leu  
 20 25 30  
 Asn Gly Leu Phe Gly Gly Phe Ser Ala Phe Trp Ser Gly Val Met Ala  
 35 40 45  
 Leu Gly Ser Leu Gly Ser Ser Glu Gly Arg Arg Ser Val Arg Leu Ile  
 50 55 60  
 Leu Ile Asp Leu Met Leu Gly Leu Ala Gly Phe Cys Gly Ser Met Ala  
 65 70 75 80  
 Ser Gly His Leu Phe Lys Gln Met Ala Gly His Ser Gly Gln Gly Leu  
 85 90 95  
 Ile Leu Thr Ala Cys Ser Val Ser Cys Ala Ser Phe Ala Leu Leu Tyr  
 100 105 110  
 Ser Leu Leu Val Leu Lys Val Pro Glu Ser Val Ala Lys Pro Ser Gln  
 115 120 125  
 Glu Leu Pro Ala Val Asp Thr Val Ser Gly Thr Val Gly Thr Tyr Arg  
 130 135 140  
 Thr Leu Asp Pro Asp Gln Leu Asp Gln Gln Tyr Ala Val Gly His Pro  
 145 150 155 160  
 Pro Ser Pro Gly Lys Ala Lys Pro His Lys Thr Thr Ile Ala Leu Leu  
 165 170 175  
 Phe Val Gly Ala Ile Ile Tyr Asp Leu Ala Val Val Gly Thr Val Asp  
 180 185 190  
 Val Ile Pro Leu Phe Val Leu Arg Glu Pro Leu Gly Trp Asn Gln Val  
 195 200 205

Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala Val Tyr Gln Ala  
           195                          200                          205  
 Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala Ile Arg Glu Arg  
           210                          215                          220  
 Leu Gly Pro Leu Val Glu Gln Gly Pro Arg Ala Gly Arg His Cys Gly  
 225                          230                          235                          240  
 Leu Pro Gly Pro Ala Ser Arg Tyr Arg Ser Gly Pro Arg Pro Gly Ala  
                           245                          250                          255  
 Ser Gly Cys Ala Arg Gly Trp Arg Arg Trp Ala Ala Gly Pro Ala Thr  
                           260                          265                          270  
 Ala Trp Thr Arg \*  
           275 276

&lt;210&gt; 240

&lt;211&gt; 554

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 240

Met Arg Arg Pro Leu Ser Lys Cys Gly Met Glu Pro Gly Gly Gly Asp  
   1                          5                          10                          15  
 Ala Ser Leu Thr Leu His Gly Leu Gln Asn Arg Ser His Gly Lys Ile  
           20                          25                          30  
 Lys Leu Arg Lys Arg Lys Ser Thr Leu Tyr Phe Asn Thr Gln Glu Lys  
           35                          40                          45  
 Ser Ala Arg Arg Arg Gly Asp Leu Leu Gly Glu Asn Ile Tyr Leu Leu  
           50                          55                          60  
 Leu Phe Thr Ile Ala Leu Arg Ile Leu Asn Cys Phe Leu Val Gln Thr  
           65                          70                          75                          80  
 Ser Phe Val Pro Asp Glu Tyr Trp Gln Ser Leu Glu Val Ser His His  
                           85                          90                          95  
 Met Val Phe Asn Tyr Gly Tyr Leu Thr Trp Glu Trp Thr Glu Arg Leu  
                           100                          105                          110  
 Arg Ser Tyr Thr Tyr Pro Leu Ile Phe Ala Ser Ile Tyr Lys Ile Leu  
           115                          120                          125  
 His Leu Leu Gly Lys Asp Ser Val Gln Leu Leu Ile Trp Ile Pro Arg  
           130                          135                          140  
 Leu Ala Gln Ala Leu Leu Ser Ala Val Ala Asp Val Arg Leu Tyr Ser  
           145                          150                          155                          160  
 Leu Met Lys Gln Leu Glu Asn Gln Glu Val Ala Arg Trp Val Phe Phe  
                           165                          170                          175  
 Cys Gln Leu Cys Ser Trp Phe Thr Trp Tyr Cys Cys Thr Arg Thr Leu  
                           180                          185                          190  
 Thr Asn Thr Met Glu Thr Val Leu Thr Ile Ile Ala Leu Phe Tyr Tyr  
           195                          200                          205  
 Pro Leu Glu Gly Ser Lys Ser Met Asn Ser Val Lys Tyr Ser Ser Leu  
           210                          215                          220  
 Val Ala Leu Ala Phe Ile Ile Arg Pro Thr Ala Val Ile Leu Trp Thr  
           225                          230                          235                          240  
 Pro Leu Leu Phe Arg His Phe Cys Gln Glu Pro Arg Lys Leu Asp Leu  
                           245                          250                          255  
 Ile Leu His His Phe Leu Pro Val Gly Phe Val Thr Leu Ser Leu Ser  
                           260                          265                          270  
 Leu Met Ile Asp Arg Ile Phe Phe Gly Gln Trp Thr Leu Val Gln Phe  
           275                          280                          285  
 Asn Phe Leu Lys Phe Asn Val Leu Gln Asn Trp Gly Thr Phe Tyr Gly  
           290                          295                          300  
 Ser His Pro Trp His Trp Tyr Phe Ser Gln Gly Phe Pro Val Ile Leu  
           305                          310                          315                          320  
 Gly Thr His Leu Pro Phe Phe Ile His Gly Cys Tyr Leu Ala Pro Lys  
                           325                          330                          335

Ala Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu  
 305 310 315 320  
 Asp Val Ala Val Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala  
 325 330 335  
 Leu Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln  
 340 345 350  
 Leu Ala Leu Asp Ile Tyr Gly Gly Thr Met Leu Ser Ser Gly Ser Gly  
 355 360 365  
 Pro Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile  
 370 375 380  
 Asn Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu  
 385 390 395 400  
 Val Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu  
 405 410 415  
 Val Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile  
 420 425 430  
 Leu Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys  
 435 440 445  
 Phe Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly  
 450 455 460  
 Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly  
 465 470 475 480  
 Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro  
 485 490 495  
 Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr  
 500 505 510  
 Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg  
 515 520 525  
 Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr \*  
 530 535 540 541

&lt;210&gt; 239

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 239

Met Ser Ser Gly Ala Ser Arg Lys Ser Trp Asp Pro Gly Lys Pro Trp  
 1 5 10 15  
 Pro Pro Asp Trp Pro Ile Thr Gly Arg Lys Met Lys Val Leu Trp Ala  
 20 25 30  
 Ala Leu Leu Val Thr Phe Leu Ala Gly Cys Gln Ala Lys Val Glu Gln  
 35 40 45  
 Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln Gln Thr Glu Trp  
 50 55 60  
 Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg Phe Trp Asp Tyr  
 65 70 75 80  
 Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln Glu Glu Leu Leu  
 85 90 95  
 Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met Asp Glu Thr Met  
 100 105 110  
 Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu Gln Leu Thr Pro  
 115 120 125  
 Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu Leu Gln Ala Ala  
 130 135 140  
 Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys Gly Arg Leu Val  
 145 150 155 160  
 Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln Ser Thr Glu Glu  
 165 170 175  
 Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu Arg Lys Arg Leu  
 180 185 190

Lys Tyr Leu Val Lys His Cys Gly Asn Ile Pro Val Phe Val Ile Asn  
 355 360 365  
 Tyr Pro Leu Thr Leu Lys Pro Phe Tyr Met Arg Asp Asn Glu Asp Gly  
 370 375 380  
 Pro Gln His Thr Val Ala Ala Val Asp Leu Leu Val Pro Gly Val Gly  
 385 390 395 400  
 Glu Leu Phe Gly Gly Gly Leu Arg Glu Glu Arg Tyr His Phe Leu Glu  
 405 410 415  
 Glu Arg Leu Ala Arg Tyr Leu Asp Leu Arg Arg Phe Gly Ser Val Pro  
 420 425 430  
 His Gly Gly Phe Gly Met Gly Phe Glu Arg Tyr Leu Gln Cys Ile Leu  
 435 440 445  
 Gly Val Asp Asn Ile Lys Asp Val Ile Pro Phe Pro Arg Phe Pro His  
 450 455 460  
 Ser Cys Leu Leu \*  
 465 468

&lt;210&gt; 238

&lt;211&gt; 542

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser  
 1 5 10 15  
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn  
 20 25 30  
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn  
 35 40 45  
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu  
 50 55 60  
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser  
 65 70 75 80  
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp  
 85 90 95  
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp  
 100 105 110  
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu  
 115 120 125  
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln  
 130 135 140  
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val  
 145 150 155 160  
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His  
 165 170 175  
 Trp Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val  
 180 185 190  
 Leu Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro  
 195 200 205  
 Glu Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu  
 210 215 220  
 Leu Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala  
 225 230 235 240  
 Lys Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu  
 245 250 255  
 Thr Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe  
 260 265 270  
 Gly Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val  
 275 280 285  
 Ala Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe  
 290 295 300

ctattctgac attttactaa catcactctt cctattttaac ttttaaataat gatgaagtca 629  
 ctcccttgct taaaaaatct gatgccatcc catctttcaa aataaaaggc aagcccttac 689  
 ctccaacctc caagactcca catgatctag ccctacact tgtctagctt ttctccaact 749  
 ctccccgcta ggtacttgca ttccattcat attaattcttg cttttctttg aatgcagatc 809  
 tacatgctca cacatgaagt ctttgttcta gctattccat ctgcatagat acagcgcccg 869  
 ctctagagga tccaagctta cgtcg 894

&lt;210&gt; 237

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

Met Leu Gly Val Arg Cys Leu Leu Arg Ser Val Arg Phe Cys Ser Ser  
 1 5 10 15  
 Ala Pro Phe Pro Lys His Lys Pro Ser Ala Lys Leu Ser Val Arg Asp  
 20 25 30  
 Ala Leu Gly Ala Gln Asn Ala Ser Gly Glu Arg Ile Lys Ile Gln Gly  
 35 40 45  
 Trp Ile Arg Ser Val Arg Ser Gln Lys Glu Val Leu Phe Leu His Val  
 50 55 60  
 Asn Asp Gly Ser Ser Leu Glu Ser Leu Gln Val Val Ala Asp Ser Gly  
 65 70 75 80  
 Leu Asp Ser Arg Glu Leu Thr Phe Gly Ser Ser Val Glu Val Gln Gly  
 85 90 95  
 Gln Leu Ile Lys Ser Pro Ser Lys Arg Gln Asn Val Glu Leu Lys Ala  
 100 105 110  
 Glu Lys Ile Lys Val Ile Gly Asn Cys Asp Ala Lys Asp Phe Pro Ile  
 115 120 125  
 Lys Tyr Lys Glu Arg His Pro Leu Glu Tyr Leu Arg Gln Tyr Pro His  
 130 135 140  
 Phe Arg Cys Arg Thr Asn Val Leu Gly Ser Ile Leu Arg Ile Arg Ser  
 145 150 155 160  
 Glu Ala Thr Ala Ala Ile His Ser Phe Phe Lys Asp Ser Gly Phe Val  
 165 170 175  
 His Ile His Thr Pro Ile Ile Thr Ser Asn Asp Ser Glu Gly Ala Gly  
 180 185 190  
 Glu Leu Phe Gln Leu Glu Pro Ser Gly Lys Leu Lys Val Pro Glu Glu  
 195 200 205  
 Asn Phe Phe Asn Val Pro Ala Phe Leu Thr Val Ser Gly Gln Leu His  
 210 215 220  
 Leu Glu Val Met Ser Gly Ala Phe Thr Gln Val Phe Thr Phe Gly Pro  
 225 230 235 240  
 Thr Phe Arg Ala Glu Asn Ser Gln Ser Arg Arg His Leu Ala Glu Phe  
 245 250 255  
 Tyr Met Ile Glu Ala Glu Ile Ser Phe Val Asp Ser Leu Gln Asp Leu  
 260 265 270  
 Met Gln Val Ile Glu Glu Leu Phe Lys Ala Thr Thr Met Met Val Leu  
 275 280 285  
 Ser Lys Cys Pro Glu Asp Val Glu Leu Cys His Lys Phe Ile Ala Pro  
 290 295 300  
 Gly Gln Lys Asp Arg Leu Glu His Met Leu Lys Asn Asn Phe Leu Ile  
 305 310 315 320  
 Ile Ser Tyr Thr Glu Ala Val Glu Ile Leu Lys Gln Ala Ser Gln Asn  
 325 330 335  
 Phe Thr Phe Thr Pro Glu Trp Gly Ala Asp Leu Arg Thr Glu His Glu  
 340 345 350

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<210> 236
<211> 894
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (204)..(548)
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[illegible]

Phe	Ser	Phe	Leu	Asp	Ile	Leu	Arg	Leu	Trp	Glu	Val	Met	Trp	Thr	Glu	
		525					530					535				
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Leu	Pro	Cys	Thr	Asn	Phe	His	Leu	Leu	Leu	Cys	Cys	Ala	Ile	Leu	Glu	
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Ser	Glu	Lys	Gln	Gln	Ile	Met	Glu	Lys	His	Tyr	Gly	Phe	Asn	Glu	Ile	
		555				560				565				570		
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Leu	Lys	His	Ile	Asn	Glu	Leu	Ser	Met	Lys	Ile	Asp	Val	Glu	Asp	Ile	
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Thr	Thr	Pro	Asp	Ser	Asp	Val	Gly	Glu	Asp	Glu	Asn	Val	Val	Met	Thr	
		620				625					630					
cct	tgt	cct	aca	tct	gca	ttt	caa	agt	aat	gcc	ttg	cct	aca	ctc	tct	2031
Pro	Cys	Pro	Thr	Ser	Ala	Phe	Gln	Ser	Asn	Ala	Leu	Pro	Thr	Leu	Ser	
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gcc	agt	gga	gcc	aga	aat	gac	agc	cca	aca	cag	ata	cca	gtg	tcc	tca	2079
Ala	Ser	Gly	Ala	Arg	Asn	Asp	Ser	Pro	Thr	Gln	Ile	Pro	Val	Ser	Ser	
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Asp	Val	Cys	Arg	Leu	Thr	Pro	Ala	*								
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Pro	Val	Ser	Leu	Glu	Glu	Trp	Thr	Lys	Lys	Ile	Asp	Ser	Glu	Gly	Arg		
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Ser	His	Ala	Leu	Arg	Lys	Gln	Ala	Trp	Lys	Phe	Leu	Leu	Gly	Tyr	Phe		
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Pro	Trp	Asp	Ser	Thr	Lys	Glu	Glu	Arg	Thr	Gln	Leu	Gln	Lys	Gln	Lys		
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Glu	Gln	Glu	Lys	Arg	Asn	Ser	Arg	Leu	Arg	Asp	Tyr	Arg	Ser	Leu	Ile		
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Glu	Lys	Asp	Val	Asn	Arg	Thr	Asp	Arg	Thr	Asn	Lys	Phe	Tyr	Glu	Gly		
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Gln	Asp	Asn	Pro	Gly	Leu	Ile	Leu	Leu	His	Asp	Ile	Leu	Met	Thr	Tyr		
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Cys	Met	Tyr	Asp	Phe	Asp	Leu	Gly	Tyr	Val	Gln	Gly	Met	Ser	Asp	Leu		
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Cys	Phe	Ala	Ser	Tyr	Met	Asp	Gln	Met	His	Gln	Asn	Phe	Glu	Glu	Gln		
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Tyr	Leu	Tyr	Phe	Cys	Phe	Arg	Trp	Leu	Leu	Ile	Arg	Phe	Lys	Arg	Glu		
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Thr	Asn	Asp	Gln	Asp	Gly	Leu	Ile	Ser	Gly	Ile	Leu	Arg	Val	Leu	Glu	
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Lys	Asp	Ala	Glu	Val	Ile	Val	Asp	Trp	Arg	Pro	Leu	Asp	Asp	Ala	Leu	
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Lys	Arg	Lys	Pro	His	Thr	Asn	Gly	Asp	Ala	Pro	Ser	His	Arg	Asn	Gly	
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Lys	Ser	Lys	Trp	Ser	Phe	Leu	Phe	Ser	Leu	Thr	Asp	Leu	Lys	Ser	Ile	
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Lys	Gln	Asn	Lys	Glu	Gly	Met	Gly	Trp	Ser	Tyr	Leu	Val	Phe	Cys	Leu	
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Lys	Asp	Asp	Val	Val	Leu	Pro	Ala	Leu	His	Phe	His	Gln	Gly	Asp	Ser	
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aaa	cta	ctgt	att	gaa	tct	ctt	gaa	aaa	tatt	gtgt	gta	ttgt	tgt	gaa	tct	639
Lys	Leu	Leu	Ile	Glu	Ser	Leu	Glu	Lys	Tyr	Val	Val	Leu	Cys	Glu	Ser	
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cca	cag	gat	aaa	aga	aca	ctt	ctt	gtgt	aat	tgt	cag	aat	aag	agt	ctt	687
Pro	Gln	Asp	Lys	Arg	Thr	Leu	Leu	Val	Asn	Cys	Gln	Asn	Lys	Ser	Leu	
			190					195					200			
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Ser	Gln	Ser	Phe	Glu	Asn	Leu	Leu	Asp	Glu	Pro	Ala	Tyr	Gly	Leu	Ile	
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caa	aaa	att	aaa	aag	gac	cct	tatt	acgt	gca	act	atgt	ata	gga	ttt	tcc	783
Gln	Lys	Ile	Lys	Lys	Asp	Pro	Tyr	Thr	Ala	Thr	Met	Ile	Gly	Phe	Ser	
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aaa	gtc	aca	aac	tac	att	ttt	gac	agtt	ttgt	aga	ggc	agc	gat	ccc	tct	831
Lys	Val	Thr	Asn	Tyr	Ile	Phe	Asp	Ser	Leu	Arg	Gly	Ser	Asp	Pro	Ser	
	235				240					245					250	
aca	cat	caa	cga	cca	cct	tca	gaa	atgt	gca	gat	ttt	ctt	agt	gat	gct	879
Thr	His	Gln	Arg	Pro	Pro	Ser	Glu	Met	Ala	Asp	Phe	Leu	Ser	Asp	Ala	
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 aagtagaagc tcggagaaaa agctgctgcc ttctcagctg ctacgagggtg aggagtcagg 180  
 g atg ggg att caa tgg aca tgt gaa tgg ccg tcg tct ctg tca cct 226  
 Met Gly Ile Gln Trp Thr Cys Glu Trp Pro Ser Ser Leu Ser Pro  
 1 5 10 15  
 ggg tgg aag ttc ata gca tgt ctc tgg ttc tcc atg tgg ggg tca cgc 274  
 Gly Trp Lys Phe Ile Ala Cys Leu Trp Phe Ser Met Trp Gly Ser Arg  
 20 25 30  
 cct cca ctt tct caa gct atg agt cac aag caa tgg ccc atg ctg tgt 322  
 Pro Pro Leu Ser Gln Ala Met Ser His Lys Gln Trp Pro Met Leu Cys  
 35 40 45  
 agc tcc att tct aac ccg gaa gct tct gga acg gaa ctg ttc acc tac 370  
 Ser Ser Ile Ser Asn Pro Glu Ala Ser Gly Thr Glu Leu Phe Thr Tyr  
 50 55 60  
 cat ttt cat atg atg gga tac att gaa agg ttt tgg ccg aca gaa gaa 418  
 His Phe His Met Met Gly Tyr Ile Glu Arg Phe Trp Pro Thr Glu Glu  
 65 70 75  
 tta gct caa cgc tgt agt ttg cat aaa gag ctg ccc tgc act gtg ttc 466  
 Leu Ala Gln Arg Cys Ser Leu His Lys Glu Leu Pro Cys Thr Val Phe  
 80 85 90 95  
 aca gag aag cac tgc tct tgc act ttc ctc atg gtg ttt ggg gtt tgc 514  
 Thr Glu Lys His Cys Ser Cys Thr Phe Leu Met Val Phe Gly Val Cys  
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 Met Ala Ser Ala Gly Val Val Ser Gly Lys  
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atggatacag ggctgctgct taggg atg tgc agg tta tac agt tgt gca agg 172  
Met Cys Arg Leu Tyr Ser Cys Ala Arg  
1 5  
atg cca ttg ttc tcc act gtt ctc ttt tct aat gtt tat att aat gat 220  
Met Pro Leu Phe Ser Thr Val Leu Phe Ser Asn Val Tyr Ile Asn Asp  
10 15 20 25  
ttc ctt ctg cag aaa cct gaa aat act aca agc caa cca ctt tct aat 268  
Phe Leu Leu Gln Lys Pro Glu Asn Thr Thr Ser Gln Pro Leu Ser Asn  
30 35 40  
cag cga gtt gta gag gtg gcg atc cct cat gta ggg aaa ttt atg att 316  
Gln Arg Val Val Glu Val Ala Ile Pro His Val Gly Lys Phe Met Ile  
45 50 55  
gaa tca aag gag ggg ggg tat gat gac gag gta cct ttt aca gcc ctc 364  
Glu Ser Lys Glu Gly Gly Tyr Asp Asp Glu Val Pro Phe Thr Ala Leu  
60 65 70  
tgc acc att gct act taa cttttg ctattttaata caaatacttt gggcatgcct 418  
Cys Thr Ile Ala Thr \*  
75  
gcaccctcat acttaatgtc tattgccaca taacatacag ctttgcccc tcatagtcca 478  
aaattacttt accaattatt aacagaactt tgaatttcaa atgaaaattt aagtagaaaa 538  
cttatggaat ttgtcaaaag aattttctgt ttgtggagtt aattctttta tgcagaaata 598  
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Met Phe Arg Ser Asn Pro Gly  
1 5  
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Phe Phe Phe Phe Cys Cys Cys Lys Ser Cys Ile Leu Ala Ile Ser Leu  
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Gly Glu Ile Pro Arg Asn Phe Thr Glu Asn Met Ser Leu Arg Glu  
25 30 35  
agt gag gat tta aag cca gat ctg tct gcc ttc aaa tcc agc gct ctt 317  
Ser Glu Asp Leu Lys Pro Asp Leu Ser Ala Phe Lys Ser Ser Ala Leu  
40 45 50 55  
tat act gat gtg agt tct cct gtc ttt ttt acc tat cag aat tct aga 365  
Tyr Thr Asp Val Ser Ser Pro Val Phe Phe Thr Tyr Gln Asn Ser Arg  
60 65 70  
act ctc cca gag aaa cca ggc aga tac tgc tcc aca ccg gtg agc tgc 413  
Thr Leu Pro Glu Lys Pro Gly Arg Tyr Cys Ser Thr Pro Val Ser Cys  
75 80 85  
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Phe Ser Pro Gly \*  
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Ser Gln Asn Thr Leu His Trp Pro Val Trp Gly Pro Gln Thr Thr Leu  
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cca agt tcc caa gcc agc ttt gtt gcc tgg gcc cat agt cat tcc ccc 470  
Pro Ser Ser Gln Ala Ser Phe Val Gly Trp Ala His Ser His Ser Pro  
80 85 90

ttg gct gtt cct gcg tct tct gac tgt gtc ctc taa atgc cctctggacc 520  
Leu Ala Val Pro Ala Ser Ser Asp Cys Val Leu \*  
95 100 105

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aatatottgc ca atg gct ttg ctt cat atc tgc gtg ggg cac cct ctc 168  
Met Ala Leu Leu His Ile Cys Val Gly His Pro Leu  
1 5 10

ctt tcc ttc ccc aag gct ggg gac ttt tct ttt tca tct caa gat gac 216  
Leu Ser Phe Pro Lys Ala Gly Asp Phe Ser Phe Ser Ser Gln Asp Asp  
15 20 25

ccc tct gag ctg aca gca gga gcc aaa gac aaa gaa ttt tct tgc ctt 264  
Pro Ser Glu Leu Thr Ala Gly Ala Lys Asp Lys Glu Phe Ser Cys Leu  
30 35 40

ctc gtt atc tgc ctc caa ccc gcc ccg agc act cgt tcc ctc ttc tct 312  
Leu Val Ile Cys Leu Gln Pro Ala Pro Ser Thr Arg Ser Leu Phe Ser  
45 50 55 60

tgg cag cta ttt ttg ctc agt ttc tct ctg gtt tct ttt act ttg att 360  
Trp Gln Leu Phe Leu Leu Ser Phe Ser Leu Val Ser Phe Thr Leu Ile  
65 70 75

tat agg ggt gaa ttt aag aaa tct ggt gag gct aag gac tat ttg acc 408  
Tyr Arg Gly Glu Phe Lys Lys Ser Gly Glu Ala Lys Asp Tyr Leu Thr  
80 85 90

caa gtc cag gga ccc ata gac tgt ggg aaa ctc tta gct aca tga aaa 456  
Gln Val Gln Gly Pro Ile Asp Cys Gly Lys Leu Leu Ala Thr \*  
95 100 105

aatgcagccg ctaaacacaa cttgttgccc taagcactca gccactgctt acttgagcga 516

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ttttcagcac tgctgggttc tatcgtgaga acagatgggc tcatggccat gacggttagg 180
aggtctgcct t atg cta gct cat ctc tcc ttt gag cgt agc ctg atc ctt 230
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His Leu Ile Phe Ser Gly Ile Ala Val Ser Ile Lys Ala Leu Thr Lys
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Thr Trp Met Pro Pro Glu Met Gly Ser Ser Pro Val Tyr Lys Ala Phe
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Ser Leu Leu Gln Cys Arg Leu Ser Ala Gln Lys Trp Gly Ser Cys His
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tcc cag aac acc ctt cac tgg cct gtg tgg ggt cct cag acc acc ctt 422

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165 170 175	
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Asn Trp Glu Val Phe Leu Glu Val Leu Asp Gly Val Glu Lys Met Lys	
180 185 190	
tcc atg tca cag ctt gca gtt ttg tca aga cgg tgg aag cct tca gag	922
Ser Met Ser Gln Leu Ala Val Leu Ser Arg Arg Trp Lys Pro Ser Glu	
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Met Lys Leu Asp Pro Phe Gln Glu Val Val Leu Glu Ser Ser Ser Val	
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gac gaa ttg cga gag aag ctt agt gaa atc agt ggg att cct ttg gat	1018
Asp Glu Leu Arg Glu Lys Leu Ser Glu Ile Ser Gly Ile Pro Leu Asp	
225 230 235 240	
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Asp Ile Glu Phe Ala Lys Gly Arg Gly Thr Phe Pro Cys Asp Ile Ser	
245 250 255	
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Val Leu Asp Ile His Gln Asp Leu Asp Trp Asn Pro Lys Val Ser Thr	
260 265 270	
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Leu Asn Val Trp Pro Leu Tyr Ile Cys Asp Asp Gly Gly Val Ile Phe	
275 280 285	
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Tyr Arg Asp Lys Thr Glu Glu Leu Met Glu Leu Thr Asp Glu Gln Arg	
290 295 300	
aat gaa ctg atg aaa aaa gaa agc agt cga ctc cag aag act gga cat	1258
Asn Glu Leu Met Lys Lys Glu Ser Ser Arg Leu Gln Lys Thr Gly His	
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Arg Val Thr Tyr Ser Pro Arg Lys Glu Lys Ala Leu Lys Ile Tyr Leu	
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Asp Gly Ala Pro Asn Lys Asp Leu Thr Gln Asp *	
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 tatcacaagt agtagaagaa cgaaagcaaa tgaagggaaa aaagaaacat gggatacagc 240  
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 Met Gln Tyr Met Tyr Phe Lys Ala Glu Pro Tyr Ala Ala Asp Glu Gly  
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 tct ggg gaa gga cat aaa tgg ttg atg gtg cat gtt gat aaa aga att 394  
 Ser Gly Glu Gly His Lys Trp Leu Met Val His Val Asp Lys Arg Ile  
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 act ctg gca gct ttc aaa caa cat tta gag ccc ttt gtt gga gtt ttg 442  
 Thr Leu Ala Ala Phe Lys Gln His Leu Glu Pro Phe Val Gly Val Leu  
 35 40 45  
 tcc tct cac ttc aag gtc ttt cga gtg tat gcc agc aat caa gag ttt 490  
 Ser Ser His Phe Lys Val Phe Arg Val Tyr Ala Ser Asn Gln Glu Phe  
 50 55 60  
 gag agc gtc cgg ctg aat gag aca ctt tca tca ttt tct gat gac aat 538  
 Glu Ser Val Arg Leu Asn Glu Thr Leu Ser Ser Phe Ser Asp Asp Asn  
 65 70 75 80  
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 Lys Ile Thr Ile Arg Leu Gly Arg Ala Leu Lys Lys Gly Glu Tyr Arg  
 85 90 95  
 gtt aaa gta tac cag ctt ttg gtc aat gaa caa gag cca tgc aag ttt 634  
 Val Lys Val Tyr Gln Leu Leu Val Asn Glu Gln Glu Pro Cys Lys Phe  
 100 105 110  
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 115 120 125  
 gag gaa tta att cct cag ctc agg gag caa tgt ggt tta gag ctc agt 730  
 Glu Glu Leu Ile Pro Gln Leu Arg Glu Gln Cys Gly Leu Glu Leu Ser  
 130 135 140  
 att gac agg ttt cgt cta agg aaa aaa aca tgg aag aat cct ggc act 778  
 Ile Asp Arg Phe Arg Leu Arg Lys Lys Thr Trp Lys Asn Pro Gly Thr  
 145 150 155 160

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cct gat gcc cca caa ccc tgc ggc acc aca gag ccg acc aca agc tcc Pro Asp Ala Pro Gln Pro Cys Gly Thr Thr Glu Pro Thr Thr Ser Ser 145 150 155	781
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Pro Val Val Ala Ile Pro Cys Pro Ile Thr Tyr Leu Pro Val Cys Gly
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tct gac tac atc acc tat ggg aat gaa tgt cac ttg tgt acc gag agc      306
Ser Asp Tyr Ile Thr Tyr Gly Asn Glu Cys His Leu Cys Thr Glu Ser
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agagtaatct tgactgaatg gagaaagttt ctgtgctacc cctacaaacc catgcctcac      534

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aaaggtttgg tatgaaagtc cttccttggg ttctcactcg acttaaaaac catccaagtt      300
ggaattcctc atg agg agc acc tca aag aaa acc agg aag gaa gac cat      349
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gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca gac      397
Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr Asp
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Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn Val
      30              35              40              45

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WO 01/55437

PCT/US01/02623

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	Met Ile Leu
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Met Asp Trp Asn Leu Gln Phe Ser Leu Leu Trp Ala Thr Ala Asp	
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Ile Ser Asp Gln Leu Phe Gln Pro Pro Gln Lys Phe Ser Trp Asp Pro	
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Leu Glu Ser Ala Leu Cys Leu Tyr Ser Ser Gly Ser Ala Lys Asp Leu	
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Lys Gly Glu Met Gln Ser Phe Trp Tyr Pro Ala Arg Lys Ser Pro Pro	
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Leu His Leu Pro Ala Leu Gln Leu Phe Tyr Phe Gly Glu Leu Pro Cys	
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Lys Phe Leu Pro Ala Leu Val Val Pro Gly Ser Thr Leu Pro Pro Ser	
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Arg Pro Leu *	

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	Met Lys Ile Thr Gly Gly
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 Leu Ala Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly  
 325 330 335

ctg ggc ggc ctc tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg 1651  
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 340 345 350

gcg ctg gca gtc ctg agc ccc tgc ccg ccc ctg gtg ggc acc tcg gcg 1699  
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 375 380 385

tcc tac gtg aag gtg gca gcc agc tcc ctg ctg cat ggc ggg ggc cgg 1795  
 Ser Tyr Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg  
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 Pro Ala Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu  
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 Gly Ala Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His  
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 Ser Arg Lys Asp Cys Ala Asp Pro Cys Asp Ser \*  
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 aaaaagaatt ttattaaggt aaaggatttg aggttacatg tggaaaggcc tggatattat 180

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Leu	Trp	Arg	Arg	Leu	Ala	Pro	Gly	Lys	Asp	Glu	Gln	Val	Pro	Ile	Arg	
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Val	Val	Gln	Val	Leu	Gly	Met	Val	Gly	Thr	Ala	Leu	Leu	Ala	Ser	Leu	
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Trp	His	His	Val	Ala	Pro	Val	Ala	Gly	Gln	Leu	His	Ser	Val	Ala	Phe	
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tta	gca	ctg	gcc	ttt	gtg	ctg	gca	ctg	gca	tgc	tgt	gcc	tgc	aat	gtc	979
Leu	Ala	Leu	Ala	Phe	Val	Leu	Ala	Leu	Ala	Cys	Cys	Ala	Ser	Asn	Val	
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Thr	Phe	Leu	Pro	Phe	Leu	Ser	His	Leu	Pro	Pro	Arg	Phe	Leu	Arg	Ser	
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Gly	Thr	Pro	Gly	Pro	Pro	Leu	Asp	Phe	Leu	Glu	Arg	Phe	Pro	Ala	Ser	
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acc	ttc	ttc	tgg	gca	ctg	act	gcc	ctt	ctg	gtc	gct	tca	gct	gct	gcc	1219
Thr	Phe	Phe	Trp	Ala	Leu	Thr	Ala	Leu	Leu	Val	Ala	Ser	Ala	Ala	Ala	
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Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Ser	Val	Pro	Thr	
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Glu	Val	Glu	Glu	Ser	Ser	Pro	Leu	Gln	Glu	Pro	Pro	Ser	Gln	Ala	Ala	
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Gly	Thr	Thr	Pro	Gly	Pro	Asp	Pro	Lys	Ala	Tyr	Gln	Leu	Leu	Ser	Ala	
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aat	ggc	gtg	ctg	cct	ggc	gtg	cag	agc	ttt	tcc	tgc	tta	ccc	tac	ggg	1507
Asn	Gly	Val	Leu	Pro	Ala	Val	Gln	Ser	Phe	Ser	Cys	Leu	Pro	Tyr	Gly	
			295					300					305			
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 catcagggtt aaaaaaaaaa aaaaaa 1081

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 <213> Homo sapiens

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 <222> (590) .. (1927)

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 gcactggagc gggagcgcac tgggcgcggg accgggaggg gcaggggaccg gacggctccc 180  
 gagtcgccc cctgacggta ccgagagggc ggcgcccttc cgagcagagc cgtcccggcc 240  
 actcccttgg gatctgactt ggctcttggc gtcgcgggca ccgtgaagcc ctgggggtgtg 300  
 cgtggctcct cctggtaggc gccctttccc ggctccggc ttgggggtggg ggtggcggtg 360  
 actccagccc cgcctctccc tggagaggag ggctccactc gtccttccg cctcctcccc 420  
 tggggccgca gcgactcggg ccggcttctt gcttccctgc ctgccggcgg tcccgtggc 480  
 tagaagaagt cttcacttcc caggagagcc aaagcgtgtc tggccctagg tgggaaaaga 540  
 actggctgtg acctttgccc tgacctggaa gggcccagcc ttgggctga atg gca 595  
 Met Ala  
 1  
 gca ccc acg ccc gcc cgt ccg gtg ctg acc cac ctg ctg gtg gct ctc 643  
 Ala Pro Thr Pro Ala Arg Pro Val Leu Thr His Leu Leu Val Ala Leu  
 5 10 15  
 ttc ggc atg ggc tcc tgg gct gcg gtc aat ggg atc tgg gtg gag cta 691  
 Phe Gly Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu  
 20 25 30  
 cct gtg gtg gtc aaa gag ctt cca gag ggt tgg agc ctc ccc tct tac 739  
 Pro Val Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr  
 35 40 45 50  
 gtc tct gtg ctt gtg gct ctg ggg aac ctg ggt ctg ctg gtg gtg acc 787



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<210> 224
<211> 1081
<212> DNA
<213> Homo sapiens

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Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro Ala
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tgc gtc gcg gcc cac ggc ttc cgt atc cat gat tat ttg tac ttt caa  153
Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe Gln
          20                      25                      30

gtg ctg agt cct ggg gac att cga tac atc ttc aca gcc aca cct gcc  201
Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro Ala
          35                      40                      45

aag gac ttt ggt ggt atc ttt cac aca agg tat gag cag att cac ctt  249
Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His Leu
          50                      55                      60                      65

gtc ccc gct gaa cct cca gag gcc tgc ggg gaa ctc agc aac ggt ttc  297
Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly Phe
          70                      75                      80

ttc atc cag gac cag att gct ctg gtg gag agg ggg ggc tgc tcc ttc  345
Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser Phe
          85                      90                      95

ctc tcc aag act cgg gtg gtc cag gag cac ggc ggg cgg gcg gtg atc  393
Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val Ile
          100                      105                      110

atc tct gac aac gca gtt gac aat gac agc ttc tac gtg gag atg atc  441
Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met Ile
          115                      120                      125

cag gac agt acc cag cgc aca gct gac atc ccc gcc ctc ttc ctg ctc  489
Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu
          130                      135                      140                      145

ggc cga gac ggc tac atg atc cgc cgc tct ctg gaa cag cat ggg ctg  537
Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu
          150                      155                      160

cca tgg gcc atc att tcc atc cca gtc aat gtc acc agc atc ccc acc  585
Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr
          165                      170                      175

ttt gag ctg ctg caa ccg ccc tgg acc ttc tgg tag aaga gtttgtccca  635
Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp *
          180                      185

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gat cag cct gtg ttg gac atc tgc cca ttt gag gtg aac cgt aac agc	2431
Asp Gln Pro Val Leu Asp Ile Cys Pro Phe Glu Val Asn Arg Asn Ser	
745 750 755	
tac ttg gct acc tta aca gag aag atg gtc cac atc tat aag tgg gag	2479
Tyr Leu Ala Thr Leu Thr Glu Lys Met Val His Ile Tyr Lys Trp Glu	
760 765 770	
tgactgtggt ctcgaaacct tgaaggcatg ctgctgggta gatgtgtttt gctagcgcct	2539
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aaaaaaaa acaaaaaaaaa aaaa	4063

atg aag agc agt cag tac att ccg atg cat ggc aaa cag atc cgt gga Met Lys Ser Ser Gln Tyr Ile Pro Met His Gly Lys Gln Ile Arg Gly 490 495 500	1663
ctg gcg ttt agc agt tac ctc aga ggc ttg cta ctc tct gct tcc cta Leu Ala Phe Ser Ser Tyr Leu Arg Gly Leu Leu Leu Ser Ala Ser Leu 505 510 515	1711
gac aac act att aaa ctg acc agc ctg gag aca aat acc gtg gtc cag Asp Asn Thr Ile Lys Leu Thr Ser Leu Glu Thr Asn Thr Val Val Gln 520 525 530	1759
act tat aat gct gga cgt cct gtc tgg agc tgt tgc tgg tgt ctt gat Thr Tyr Asn Ala Gly Arg Pro Val Trp Ser Cys Cys Trp Cys Leu Asp 535 540 545 550	1807
gag act aac tac atc tat gct gga cta gcc aat ggt tca att ctg gta Glu Thr Asn Tyr Ile Tyr Ala Gly Leu Ala Asn Gly Ser Ile Leu Val 555 560 565	1855
tat gac gtg cga aac acg agc agt cat gtg cag gag tta gta gct cag Tyr Asp Val Arg Asn Thr Ser Ser His Val Gln Glu Leu Val Ala Gln 570 575 580	1903
aaa gcc aga tgc cca ctg gtc tcc ctg tca tac atg ccc aga gct gcc Lys Ala Arg Cys Pro Leu Val Ser Leu Ser Tyr Met Pro Arg Ala Ala 585 590 595	1951
tca gct gca ttt cca tat ggt ggg gtg ctg gct gga acc ttg gag gat Ser Ala Ala Phe Pro Tyr Gly Gly Val Leu Ala Gly Thr Leu Glu Asp 600 605 610	1999
gct tca ttc tgg gaa cag aaa atg gac ttt tct cat tgg cct cat gtg Ala Ser Phe Trp Glu Gln Lys Met Asp Phe Ser His Trp Pro His Val 615 620 625 630	2047
ctg ccc ttg gag cca ggg ggc tgc ata gac ttt cag aca gag aac agc Leu Pro Leu Glu Pro Gly Gly Cys Ile Asp Phe Gln Thr Glu Asn Ser 635 640 645	2095
tcc cgg cac tgt ctt gtg acc tac agg cct gat aaa aat cac acc acc Ser Arg His Cys Leu Val Thr Tyr Arg Pro Asp Lys Asn His Thr Thr 650 655 660	2143
ata cga agt gtg ctg atg gaa atg tcc tac cga ctg gat gac act gga Ile Arg Ser Val Leu Met Glu Met Ser Tyr Arg Leu Asp Asp Thr Gly 665 670 675	2191
aat cca atc tgc tcc tgc cag cct gta cat aca ttt ttt gga gga cct Asn Pro Ile Cys Ser Cys Gln Pro Val His Thr Phe Phe Gly Gly Pro 680 685 690	2239
act tgc aaa cta ttg acc aaa aat gcc att ttc caa agc cca gag aat Thr Cys Lys Leu Leu Thr Lys Asn Ala Ile Phe Gln Ser Pro Glu Asn 695 700 705 710	2287
gat ggc aac atc ctg gtg tgt act ggg gat gaa gca gca aat tct gcc Asp Gly Asn Ile Leu Val Cys Thr Gly Asp Glu Ala Ala Asn Ser Ala 715 720 725	2335
ctg ctg tgg gat gct gcc agt ggc tgc ttg ctc cag gac cta cag acc Leu Leu Trp Asp Ala Ala Ser Gly Ser Leu Leu Gln Asp Leu Gln Thr 730 735 740	2383

gca gag gaa tct gga gct gtc att tta gaa gag caa cta gca ggt gtc Ala Glu Glu Ser Gly Ala Val Ile Leu Glu Glu Gln Leu Ala Gly Val 235 240 245	895
tca gca gag caa gaa gtt aca tgt atc gat gga ggc aag acc ctc ccc Ser Ala Glu Pro Gln Glu Val Thr Cys Ile Asp Gly Gly Lys Thr Leu Pro 250 255 260	943
aaa cag cca tct ccc cag aag tct gag cct ctg cta cct tct gct tct Lys Gln Pro Ser Pro Gln Lys Ser Glu Pro Leu Leu Pro Ser Ala Ser 265 270 275	991
atg gat gag gaa gaa ggg gac act tgt aca ata tgt ctg gaa cag tgg Met Asp Glu Glu Glu Gly Asp Thr Cys Thr Ile Cys Leu Glu Gln Trp 280 285 290	1039
acc aat gct ggg gac cac cgg ctc tca gca tta cgc tgt ggg cat ctc Thr Asn Ala Gly Asp His Arg Leu Ser Ala Leu Arg Cys Gly His Leu 295 300 305 310	1087
ttt ggg tat agg tgc att tcc acg tgg ctt aaa gga caa gta cga aaa Phe Gly Tyr Arg Cys Ile Ser Thr Trp Leu Lys Gly Gln Val Arg Lys 315 320 325	1135
tgt ccc cag tgc aac aag aaa gcc agg cac agt gac att gtc gtc ctt Cys Pro Gln Cys Asn Lys Lys Ala Arg His Ser Asp Ile Val Val Leu 330 335 340	1183
tat gcc cga acc ctg aga gct ttg gac act agt gaa cag gag cgc atg Tyr Ala Arg Thr Leu Arg Ala Leu Asp Thr Ser Glu Gln Glu Arg Met 345 350 355	1231
aaa agt tcc cta ctg aag gaa cag atg cta agg aaa cag gcc gag tta Lys Ser Ser Leu Leu Lys Glu Gln Met Leu Arg Lys Gln Ala Glu Leu 360 365 370	1279
gaa tca gca cag tgc cga ctc caa ctg cag gtc ctc act gat aag tgc Glu Ser Ala Gln Cys Arg Leu Gln Leu Gln Val Leu Thr Asp Lys Cys 375 380 385 390	1327
act agg ctt caa agg cgt gtt cag gac ttg caa aaa ctt acg tca cat Thr Arg Leu Gln Arg Arg Val Gln Asp Leu Gln Lys Leu Thr Ser His 395 400 405	1375
caa agt cag aat tta cag caa ccc agg ggc tcc caa gca tgg gtc ctg Gln Ser Gln Asn Leu Gln Gln Pro Arg Gly Ser Gln Ala Trp Val Leu 410 415 420	1423
agc tgc tca ccc tcc agc cag ggc cag cac aag cac aag tac cac ttc Ser Cys Ser Pro Ser Ser Gln Gly Gln His Lys His Lys Tyr His Phe 425 430 435	1471
caa aag acc ttc aca gta tct cag gca gga aac tgc cgg atc atg gca Gln Lys Thr Phe Thr Val Ser Gln Ala Gly Asn Cys Arg Ile Met Ala 440 445 450	1519
tac tgt gat gct ctg agc tgc ctg gtg ata tca cag cct tct cct cag Tyr Cys Asp Ala Leu Ser Cys Leu Val Ile Ser Gln Pro Ser Pro Gln 455 460 465 470	1567
gcc tct ttt ctt cca ggc ttt ggt gtt aag atg ttg agt act gcc aac Ala Ser Phe Leu Pro Gly Phe Gly Val Lys Met Leu Ser Thr Ala Asn 475 480 485	1615

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Phe	Tyr	Tyr	Thr	Glu	Val	Gln	Leu	Lys	Glu	Glu	Ser	Ala	Ala	Ala	Ala		
				325					330					335			
gct	gct	gct	gcc	gca	ggc	acc	cca	gtc	cct	ggg	act	ccc	acc	tcc	gag	1174	
Ala	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Pro	Val	Pro	Gly	Thr	Pro	Thr	Ser	Glu	
			340					345						350			
cca	gct	ccc	acc	ccc	agc	atg	act	ggc	ctg	cct	ctg	tct	gct	ctt	cca	1222	
Pro	Ala	Pro	Thr	Pro	Ser	Met	Thr	Gly	Leu	Pro	Leu	Ser	Ala	Leu	Pro		
		355					360					365					
cca	cct	ctg	cac	aaa	gcc	cag	tcc	tcc	ggc	cca	gaa	cat	cct	ggc	ccg	1270	
Pro	Pro	Leu	His	Lys	Ala	Gln	Ser	Ser	Gly	Pro	Glu	His	Pro	Gly	Pro		
		370				375					380						
gag	tcc	tcc	ctg	ccc	tca	ggg	gct	ctc	agc	aag	tca	gct	cct	ggg	tcc	1318	
Glu	Ser	Ser	Leu	Pro	Ser	Gly	Ala	Leu	Ser	Lys	Ser	Ala	Pro	Gly	Ser		
385					390				395					400			
ttc	tgg	cac	att	cag	gca	gat	cat	gca	tac	cag	gct	ctg	cca	tcc	ttc	1366	
Phe	Trp	His	Ile	Gln	Ala	Asp	His	Ala	Tyr	Gln	Ala	Leu	Pro	Ser	Phe		
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cag	atc	cca	gtc	tca	cca	cac	atc	tac	acc	agt	gtc	agc	tgg	gct	gct	1414	
Gln	Ile	Pro	Val	Ser	Pro	His	Ile	Tyr	Thr	Ser	Val	Ser	Trp	Ala	Ala		
			420					425					430				
gcc	ccc	tcc	gcc	gcc	tgc	tct	ctc	tct	ccg	gtc	cgg	agc	cgg	tcg	cta	1462	
Ala	Pro	Ser	Ala	Ala	Cys	Ser	Leu	Ser	Pro	Val	Arg	Ser	Arg	Ser	Leu		
		435					440					445					
agc	ttc	agc	gag	ccc	cag	cag	cca	gca	cct	gcg	atg	aaa	tct	cat	ctg	1510	
Ser	Phe	Ser	Glu	Pro	Gln	Gln	Pro	Ala	Pro	Ala	Met	Lys	Ser	His	Leu		
	450					455					460						
atc	gtc	act	tct	cca	ccc	cgg	gcc	cag	agt	ggg	gcc	agg	aaa	gcc	cga	1558	
Ile	Val	Thr	Ser	Pro	Pro	Arg	Ala	Gln	Ser	Gly	Ala	Arg	Lys	Ala	Arg		
465					470					475				480			
ggg	gag	gct	aag	aag	tgc	cgc	aag	gtg	tat	ggc	atc	gag	cac	cgg	gac	1606	
Gly	Glu	Ala	Lys	Lys	Cys	Arg	Lys	Val	Tyr	Gly	Ile	Glu	His	Arg	Asp		
			485					490					495				
cag	tgg	tgc	acg	gcg	tgc	cgg	tgg	aag	aag	gcc	tgc	cag	cgc	ttt	ctg	1654	
Gln	Trp	Cys	Thr	Ala	Cys	Arg	Trp	Lys	Lys	Ala	Cys	Gln	Arg	Phe	Leu		
			500					505					510				
gac	tga	gctgtgctgc	aggttctact	ctgttctctgg	ccctgcgggc	agccactgac	1710										
Asp	*																

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Val Tyr Val Trp Tyr Gly Gly Gln Glu Cys Thr Gly Leu Val Glu Gln	
85 90 95	
cac agc tgg atg gag ggt cag gtg acc gtc tgg ctg ctg gag cag aag	454
His Ser Trp Met Glu Gly Gln Val Thr Val Trp Leu Leu Glu Gln Lys	
100 105 110	
ctg cag gtc tgc tgc agg gtg gag gag gtg tgg ctg gca gag ctg cag	502
Leu Gln Val Cys Cys Arg Val Glu Glu Val Trp Leu Ala Glu Leu Gln	
115 120 125	
ggc ccc tgt ccc cag gca cca ccc ctg gag ccc gga gcc cag gcc ctg	550
Gly Pro Cys Pro Gln Ala Pro Pro Leu Glu Pro Gly Ala Gln Ala Leu	
130 135 140	
gcc tac agg ccc gtc tcc agg aac atc gat gtc cca aag agg aag tcc	598
Ala Tyr Arg Pro Val Ser Arg Asn Ile Asp Val Pro Lys Arg Lys Ser	
145 150 155 160	
gac gca gtg gaa atg gat gag atg atg gcg gcc atg gtg ctg acg tcc	646
Asp Ala Val Glu Met Asp Glu Met Met Ala Ala Met Val Leu Thr Ser	
165 170 175	
ctg tcc tgc agc cct gtt gta cag agt cct ccc ggg acc gag gcc aac	694
Leu Ser Cys Ser Pro Val Val Gln Ser Pro Pro Gly Thr Glu Ala Asn	
180 185 190	
ttc tct gct tcc cgt gcg gcc tgc gac cca tgg aag gag agt ggt gac	742
Phe Ser Ala Ser Arg Ala Ala Cys Asp Pro Trp Lys Glu Ser Gly Asp	
195 200 205	
atc tcc gac agc ggc agc agc act acc agc ggt cac tgg agt ggg agc	790
Ile Ser Asp Ser Gly Ser Ser Thr Thr Ser Gly His Trp Ser Gly Ser	
210 215 220	
agt ggt gtc tcc acc ccc tcc ccc ccc ccc cag gcc agc ccc aag	838
Ser Gly Val Ser Thr Pro Ser Pro Pro His Pro Gln Ala Ser Pro Lys	
225 230 235 240	
tat ttg ggg gat gct ttt ggt tct ccc caa act gat cat ggc ttt gag	886
Tyr Leu Gly Asp Ala Phe Gly Ser Pro Gln Thr Asp His Gly Phe Glu	
245 250 255	
acc gat cct gac cct ttc ctg ctg gac gaa cca gct cca cga aaa aga	934
Thr Asp Pro Asp Pro Phe Leu Leu Asp Glu Pro Ala Pro Arg Lys Arg	
260 265 270	
aag aac tct gtg aag gtg atg tac aag tgc ctg tgg cca aac tgt ggc	982
Lys Asn Ser Val Lys Val Met Tyr Lys Cys Leu Trp Pro Asn Cys Gly	
275 280 285	
aaa gtt ctg cgc tcc att gtg ggc atc aaa cga cac gtc aaa gcc ctc	1030
Lys Val Leu Arg Ser Ile Val Gly Ile Lys Arg His Val Lys Ala Leu	
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cat ctg ggg gac aca gtg gac tct gat cag ttc aag cgg gag gag gat	1078
His Leu Gly Asp Thr Val Asp Ser Asp Gln Phe Lys Arg Glu Glu Asp	
305 310 315 320	
ttc tac tac aca gag gtg cag ctg aag gag gaa tct gct gct gct gct	1126

245	250	255	
agt gag ccc ttt gtg caa aaa ctc tgg gaa caa tac atg gat gag aag			816
Ser Glu Pro Phe Val Gln Lys Leu Trp Glu Gln Tyr Met Asp Glu Lys			
260	265	270	
gac gag tac tta cag cag cta aag cag gag ctt ggc ata gaa ctc cat			864
Asp Glu Tyr Leu Gln Gln Leu Lys Gln Glu Leu Gly Ile Glu Leu His			
275	280	285	
gag gaa gtg act ctg ccc aag ctg cga ggg ggc ctg atg acc atc gac			912
Glu Glu Val Thr Leu Pro Lys Leu Arg Gly Gly Leu Met Thr Ile Asp			
290	295	300	
ccc agc ctg gac aag cag aca gtg aac acc tac atg agc cag gcc ttc			960
Pro Ser Leu Asp Lys Gln Thr Val Asn Thr Tyr Met Ser Gln Ala Phe			
305	310	315	320
cag ctc cct gag tcg gaa atg cca gag gag ggt gac gag aag gaa gaa			1008
Gln Leu Pro Glu Ser Glu Met Pro Glu Glu Gly Asp Glu Lys Glu Glu			
325	330	335	
gcc gtg gtg gaa atc ctc cag act gcc ctg gag cgg ctt cag gtg att			1056
Ala Val Val Glu Ile Leu Gln Thr Ala Leu Glu Arg Leu Gln Val Ile			
340	345	350	
gac atc agg cgt gtg gga cct cga gag cca gag cct gca agc tag			1101
Asp Ile Arg Arg Val Gly Pro Arg Glu Pro Glu Pro Ala Ser *			
355	360	365	

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 <212> DNA  
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<220>  
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 <222> (119)..(1660)

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atg gcg agt gtc ctg tcc cga cgc ctt gga aag cgg tcc ctc ctg gga	166
Met Ala Ser Val Leu Ser Arg Arg Leu Gly Lys Arg Ser Leu Leu Gly	
1 5 10 15	
gcc cgg gtg ttg gga ccc agt gcc tcg gag ggg ccc tcg gct gcc cca	214
Ala Arg Val Leu Gly Pro Ser Ala Ser Glu Gly Pro Ser Ala Ala Pro	
20 25 30	
ccc tcg gag cca ctg cta gaa ggg gcc gct ccc cag cct ttc acc acc	262
Pro Ser Glu Pro Leu Leu Glu Gly Ala Ala Pro Gln Pro Phe Thr Thr	
35 40 45	
tct gat gac acc ccc tgc cag gag cag ccc aag gaa gtc ctt aag gct	310
Ser Asp Asp Thr Pro Cys Gln Glu Gln Pro Lys Glu Val Leu Lys Ala	
50 55 60	
ccc agc acc tcg ggc ctt cag cag gtg gcc ttt cag cct ggg cag aag	358



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1 5 10 15		
gag ctg cag gag atc cag cgc act tcc acg ccg cgg cct gac tgg acc	96	
Glu Leu Gln Glu Ile Gln Arg Thr Ser Thr Pro Arg Pro Asp Trp Thr		
20 25 30		
aag tgc aaa gat gtg gtg gct ggg ggc cca gag cgc tgg cag atg ctg	144	
Lys Cys Lys Asp Val Val Ala Gly Gly Pro Glu Arg Trp Gln Met Leu		
35 40 45		
gct gag ggc aag aac agc gac cag ctg gtg gac gtg ctc ctg gaa gag	192	
Ala Glu Gly Lys Asn Ser Asp Gln Leu Val Asp Val Leu Leu Glu Glu		
50 55 60		
att ggt tcg ggg ctg ctg cgg gag aaa gac ttc ttc cct ggt ctg ggc	240	
Ile Gly Ser Gly Leu Leu Arg Glu Lys Asp Phe Phe Pro Gly Leu Gly		
65 70 75 80		
tat ggg gaa gcc atc cct gct ttt ctt cgg ttt gat ggc ctc gtg gag	288	
Tyr Gly Glu Ala Ile Pro Ala Phe Leu Arg Phe Asp Gly Leu Val Glu		
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 acggccacga gtttgaagct gaggcttga gcctcgccgt ggatgcagcc tacgccaaga 480  
 agcaaaagag ggaggtgggtg aaaagacaag atgtccttta tgagctgatg cagacagagg 540  
 tgaccacgt gcggacgctc aagatcatgc tgaagggtga ctccagggcc ctgcaggagg 600

Arg Glu Cys Arg Leu Gln Ala Gln Asp Leu Arg Gln Glu Gly Gln Gln	
3365 3370 3375	
ctg gtg gac aac agc cac ttc atg tct gcg gag gtg aca gag tgc ctg	10413
Leu Val Asp Asn Ser His Phe Met Ser Ala Glu Val Thr Glu Cys Leu	
3380 3385 3390 3395	
cag gag ctg gaa ggg cgg ctg cag gag ctg gag gag gct tgg gcc ctg	10461
Gln Glu Leu Glu Arg Gly Leu Gln Glu Leu Glu Glu Ala Trp Ala Leu	
3400 3405 3410	
cgc tgg caa cgc tgt gcc gag agc tgg ggc ctg cag aag ctt cgg cag	10509
Arg Trp Gln Arg Cys Ala Glu Ser Trp Gly Leu Gln Lys Leu Arg Gln	
3415 3420 3425	
agg ctg gag cag gct gag gcc tgg ctg gcc tgc tgg gag gga ctc ctg	10557
Arg Leu Glu Gln Ala Glu Ala Trp Leu Ala Cys Trp Glu Gly Leu Leu	
3430 3435 3440	
ctg aag ccc gac tat ggg cac tca gtg tca gat gtg gag ttg ctg ctg	10605
Leu Lys Pro Asp Tyr Gly His Ser Val Ser Asp Val Glu Leu Leu Leu	
3445 3450 3455	
cac aga cac cag gac tta gaa aag ctg ctg gca gcc cag gaa gag aag	10653
His Arg His Gln Asp Leu Glu Lys Leu Leu Ala Ala Gln Glu Glu Lys	
3460 3465 3470 3475	
ttt gcc caa atg caa aag aca gag atg gaa cag gag ctc ctg ctg cag	10701
Phe Ala Gln Met Gln Lys Thr Glu Met Glu Gln Glu Leu Leu Leu Gln	
3480 3485 3490	
cca cag gag ctg aag ccc ggg aga gct ggc agc tcg ctg aca tcc ttt	10749
Pro Gln Glu Leu Lys Pro Gly Arg Ala Gly Ser Ser Leu Thr Ser Phe	
3495 3500 3505	
cag tgg agg ccc tct gga cac cag ggg cta gga gca cag ctg gct gag	10797
Gln Trp Arg Pro Ser Gly His Gln Gly Leu Gly Ala Gln Leu Ala Glu	
3510 3515 3520	
acg agg gac ccc cag gat gca aag ggt acc ccc acc atg gag ggg tct	10845
Thr Arg Asp Pro Gln Asp Ala Lys Gly Thr Pro Thr Met Glu Gly Ser	
3525 3530 3535	
ttg gag ttc aag cag cac ctg ctg cct ggc ggg agg cag cct agc tcg	10893
Leu Glu Phe Lys Gln His Leu Leu Pro Gly Gly Arg Gln Pro Ser Ser	
3540 3545 3550 3555	
agc tcc tgg gac agc tgc cgc ggg acc ttg cag ggc agc tct ctg agc	10941
Ser Ser Trp Asp Ser Cys Arg Gly Thr Leu Gln Gly Ser Ser Leu Ser	
3560 3565 3570	
ctg ttc ctg gat gag agg atg gca gcg gag aaa gta gct tcc ata gcc	10989
Leu Phe Leu Asp Glu Arg Met Ala Ala Glu Lys Val Ala Ser Ile Ala	
3575 3580 3585	
ctc ctt gac ctc acg gga gcc cgg tgt gag agg ctg cgg ggc cgc cac	11037
Leu Leu Asp Leu Thr Gly Ala Arg Cys Glu Arg Leu Arg Gly Arg His	
3590 3595 3600	
ggc agg aaa cac aca ttc tcc tta agg ctg acc agt ggg gca gag atc	11085
Gly Arg Lys His Thr Phe Ser Leu Arg Leu Thr Ser Gly Ala Glu Ile	
3605 3610 3615	
ctg ttt gca gca ccg tcc gaa gag cag gct gag agc tgg tgg cga gcc	11133

His Gln Leu Glu Arg Glu Thr Leu Leu Leu Asp Ala Trp Leu Thr Thr	
3110 3115 3120	
aag gcg gcc acc gcc gag tcc cag gac tac ggg cag gac ctg gag ggt	9645
Lys Ala Ala Thr Ala Glu Ser Gln Asp Tyr Gly Gln Asp Leu Glu Gly	
3125 3130 3135	
gtc aag gtg ctg gaa gag aag ttt gat gct ttc aga aag gaa gtg cag	9693
Val Lys Val Leu Glu Glu Lys Phe Asp Ala Phe Arg Lys Glu Val Gln	
3140 3145 3150 3155	
agc ctg ggc cag gcc aag gtg tat gcc ctg agg aag ttg gca ggc acc	9741
Ser Leu Gly Gln Ala Lys Val Tyr Ala Leu Arg Lys Leu Ala Gly Thr	
3160 3165 3170	
ctg gag cgg ggt gca ccc agg cgc tat ccc cac atc caa gcc cag agg	9789
Leu Glu Arg Gly Ala Pro Arg Arg Tyr Pro His Ile Gln Ala Gln Arg	
3175 3180 3185	
agc cgc att gag gct gct tgg gag agg ttg gac caa gca ata aaa gcc	9837
Ser Arg Ile Glu Ala Ala Trp Glu Arg Leu Asp Gln Ala Ile Lys Ala	
3190 3195 3200	
cgc aca gag aac ttg gct gca gcc cat gag gtc cac agc ttt cag cag	9885
Arg Thr Glu Asn Leu Ala Ala His Glu Val His Ser Phe Gln Gln	
3205 3210 3215	
gca gca gct gag ctg cag gga agg atg cag gag aag acg gcc ctg atg	9933
Ala Ala Ala Glu Leu Gln Gly Arg Met Gln Glu Lys Thr Ala Leu Met	
3220 3225 3230 3235	
aag ggg gag gac gga ggc cac agc ctg tca tct gtg cgg acc ctg cag	9981
Lys Gly Glu Asp Gly Gly His Ser Leu Ser Ser Val Arg Thr Leu Gln	
3240 3245 3250	
caa cag cac agg cgc ctg gag aga gag ctg gaa gct atg gag aag gag	10029
Gln Gln His Arg Arg Leu Glu Arg Glu Leu Glu Ala Met Glu Lys Glu	
3255 3260 3265	
gtg gca cgg cta cag acg gag gcc tgc cga ctg ggc cag cta cat cct	10077
Val Ala Arg Leu Gln Thr Glu Ala Cys Arg Leu Gly Gln Leu His Pro	
3270 3275 3280	
gca gct ccg ggg ggc ctg gcc aag gtg cag gag gcc tgg gcc acc ctg	10125
Ala Ala Pro Gly Gly Leu Ala Lys Val Gln Glu Ala Trp Ala Thr Leu	
3285 3290 3295	
cag gcg aag gcc cag gag cga ggc cag tgg ctg gcg cag gct gca cag	10173
Gln Ala Lys Ala Gln Glu Arg Gly Gln Trp Leu Ala Gln Ala Ala Gln	
3300 3305 3310 3315	
ggc cat gcc ttc ctg ggg cgc tgc cag gaa ctg cta gca tgg gca cag	10221
Gly His Ala Phe Leu Gly Arg Cys Gln Glu Leu Leu Ala Trp Ala Gln	
3320 3325 3330	
gag agg cag gag ctg gcg tcc tcc gag gag ctg gct gag gac gtg gcg	10269
Glu Arg Gln Glu Leu Ala Ser Ser Glu Glu Leu Ala Glu Asp Val Ala	
3335 3340 3345	
ggg gct gag cag ctg ctt ggg cag cat gaa gag ctg ggg caa gaa atc	10317
Gly Ala Glu Gln Leu Leu Gly Gln His Glu Glu Leu Gly Gln Glu Ile	
3350 3355 3360	
agg gag tgc cgc ctt caa gcc cag gac ctg cgg cag gaa gga cag cag	10365

Ala Phe Val Arg Glu Gly His Cys Leu Ala Arg Asp Val Glu Glu Gln	
2855 2860 2865	
gcc cgg cgg ctg ctt cag agg ttc aag agc ctg agg gag ccc ctg cag	8877
Ala Arg Arg Leu Leu Gln Arg Phe Lys Ser Leu Arg Glu Pro Leu Gln	
2870 2875 2880	
gag cgc agg acg gcc ctg gag gcc cgg agc ctc ctc ttg aag ttc ttc	8925
Glu Arg Arg Thr Ala Leu Glu Ala Arg Ser Leu Leu Leu Lys Phe Phe	
2885 2890 2895	
agg gac gcc gac gag gaa atg gcc tgg gtg cag gag aag ctg cct ctg	8973
Arg Asp Ala Asp Glu Glu Met Ala Trp Val Gln Glu Lys Leu Pro Leu	
2900 2905 2910 2915	
gcc gct gcc cag gac tat ggc cag agc ctg agt gcg gtg cgg cac ctg	9021
Ala Ala Ala Gln Asp Tyr Gly Gln Ser Leu Ser Ala Val Arg His Leu	
2920 2925 2930	
cag gag cag cac cag aac ctg gag agt gag atg agc agc cac gag gct	9069
Gln Glu Gln His Gln Asn Leu Glu Ser Glu Met Ser Ser His Glu Ala	
2935 2940 2945	
ctg acc cgg gtg gtg ctg ggc act ggg tac aag ctg gtg cag gct ggg	9117
Leu Thr Arg Val Val Leu Gly Thr Gly Tyr Lys Leu Val Gln Ala Gly	
2950 2955 2960	
cac ttt gcc gcc cac gag gtg gcc gcc cgg gtg cag cag ctg gag aag	9165
His Phe Ala Ala His Glu Val Ala Ala Arg Val Gln Gln Leu Glu Lys	
2965 2970 2975	
gcc atg gcc cac ctg cgg gca gag gcg gcg cgg agg cgg ctt ctg ctg	9213
Ala Met Ala His Leu Arg Ala Glu Ala Ala Arg Arg Arg Leu Leu Leu	
2980 2985 2990 2995	
cag cag gct cag gag gcc cag cag ttt ctg act gag ctc ctg gag gcg	9261
Gln Gln Ala Gln Glu Ala Gln Gln Phe Leu Thr Glu Leu Leu Glu Ala	
3000 3005 3010	
gga tcc tgg ctg gct gag cgg ggc cat gtc ctg gac agc gag gac atg	9309
Gly Ser Trp Leu Ala Glu Arg Gly His Val Leu Asp Ser Glu Asp Met	
3015 3020 3025	
ggc cac agt gct gaa gcc aca cag gcc ctt ctg cgg cgg ctg gag gcc	9357
Gly His Ser Ala Glu Ala Thr Gln Ala Leu Leu Arg Arg Leu Glu Ala	
3030 3035 3040	
acc aag aga gac ctg gaa gcg ttc agc cca cgc atc gag cgg ctg cag	9405
Thr Lys Arg Asp Leu Glu Ala Phe Ser Pro Arg Ile Glu Arg Leu Gln	
3045 3050 3055	
cag aca gca gca ctc ctg gag agc agg aag aac cca gaa agc ccc aag	9453
Gln Thr Ala Ala Leu Leu Glu Ser Arg Lys Asn Pro Glu Ser Pro Lys	
3060 3065 3070 3075	
gtg cta gcc cag ctg cag gca gtt cgg gag gcc cac gca gag ctg ctg	9501
Val Leu Ala Gln Leu Gln Ala Val Arg Glu Ala His Ala Glu Leu Leu	
3080 3085 3090	
cgg agg gcg gag gcc agg ggg cac ggc ctg cag gag cag ctg cag cta	9549
Arg Arg Ala Glu Ala Arg Gly His Gly Leu Gln Glu Gln Leu Gln Leu	
3095 3100 3105	
cac cag ctg gag cga gag acc ctg ctc ctc gac gcc tgg ctg acc acc	9597

Glu Asp Ser	Leu Ala Ser	Glu Gly	Leu Trp	Asp Pro	Leu Ala	Pro Met	
	2600		2605		2610		
gag ccc ctt ctg tgg aag cac aag atg ctg gag tgg gac ctg gag gtg							8109
Glu Pro Leu Leu Trp Lys His Lys Met Leu Glu Trp Asp Leu Glu Val	2615	2620	2625				
cag gcg gga aag atc agt gct ctg gag gcc acg gcc cgc ggc ctg cac							8157
Gln Ala Gly Lys Ile Ser Ala Leu Glu Ala Thr Ala Arg Gly Leu His	2630	2635	2640				
cag ggt ggg cac ccc gag gcc cag agt gcc ctg ggc agg tgc cag gcc							8205
Gln Gly Gly His Pro Glu Ala Gln Ser Ala Leu Gly Arg Cys Gln Ala	2645	2650	2655				
atg ctt ctg agg aag gag gcg ctc ttc agg caa gcc ggg acc cgc cgc							8253
Met Leu Leu Arg Lys Glu Ala Leu Phe Arg Gln Ala Gly Thr Arg Arg	2660	2665	2670	2675			
cat cgc ctg gag gag ctc cgg cag ctg cag gcc ttc ctg cag gac tcc							8301
His Arg Leu Glu Glu Leu Arg Gln Leu Gln Ala Phe Leu Gln Asp Ser	2680	2685	2690				
cag gag gtg gct gcg tgg ctg agg gag aag aac ctg gtg gcc ttg gag							8349
Gln Glu Val Ala Ala Trp Leu Arg Glu Lys Asn Leu Val Ala Leu Glu	2695	2700	2705				
gag ggt ttg ctg gac aca gcc atg ctg cca gca cag tta cag aag cag							8397
Glu Gly Leu Leu Asp Thr Ala Met Leu Pro Ala Gln Leu Gln Lys Gln	2710	2715	2720				
cag aat ttc cag gcg gag ctg gac gcg agc atg cac caa cag cag gag							8445
Gln Asn Phe Gln Ala Glu Leu Asp Ala Ser Met His Gln Gln Gln Glu	2725	2730	2735				
ctg cag cgg gag gga cag agg ctg ctg cag ggg ggc cac cca gcc tgc							8493
Leu Gln Arg Glu Gly Gln Arg Leu Leu Gln Gly Gly His Pro Ala Ser	2740	2745	2750	2755			
gag gcc atc cag gag cga ctg gag gag ctg gga gca ctc tgg ggt gag							8541
Glu Ala Ile Gln Glu Arg Leu Glu Glu Leu Gly Ala Leu Trp Gly Glu	2760	2765	2770				
ctg caa gac aac tcc cag aag aag gtg gcc aag ctc cag aag gcc tgt							8589
Leu Gln Asp Asn Ser Gln Lys Lys Val Ala Lys Leu Gln Lys Ala Cys	2775	2780	2785				
gag gcc ctg cgt ctg cgg cgg agc atg gag gaa ctg gag aac tgg ctg							8637
Glu Ala Leu Arg Leu Arg Arg Ser Met Glu Glu Leu Glu Asn Trp Leu	2790	2795	2800				
gag ccc atc gag gtt gag ctg aga gcc ccc act gtg ggc cag gcc ctg							8685
Glu Pro Ile Glu Val Glu Leu Arg Ala Pro Thr Val Gly Gln Ala Leu	2805	2810	2815				
cct ggg gtg ggc gag ctc ctg ggc aca cag agg gag ctg gag gca gca							8733
Pro Gly Val Gly Glu Leu Leu Gly Thr Gln Arg Glu Leu Glu Ala Ala	2820	2825	2830	2835			
gtg gac aag aag gcc agg cag gct gag gca ctg ctg ggc cag gcc gag							8781
Val Asp Lys Lys Ala Arg Gln Ala Glu Ala Leu Leu Gly Gln Ala Glu	2840	2845	2850				
gcc ttt gtg agg gaa ggc cac tgc ctt gcc cga gat gtg gaa gag cag							8829

Ser	Gln	Leu	Asn	Asn	Arg	Trp	Ala	Ser	Phe	His	Gly	Asn	Leu	Leu	Arg		
2340						2345						2350			2355		
tac	cag	cag	cag	ctc	gaa	ggg	gcc	ttg	gag	ata	cac	gtg	ttg	tcc	cga	7341	
Tyr	Gln	Gln	Gln	Leu	Glu	Gly	Ala	Leu	Glu	Ile	His	Val	Leu	Ser	Arg		
				2360					2365					2370			
gag	ctg	gac	aat	gtc	acc	aag	agg	att	cag	gag	aag	gaa	gcc	ctg	atc	7389	
Glu	Leu	Asp	Asn	Val	Thr	Lys	Arg	Ile	Gln	Glu	Lys	Glu	Ala	Leu	Ile		
			2375					2380					2385				
cag	gcc	ctg	gac	tgt	ggg	aaa	gat	ctg	gag	agc	gtg	cag	agg	ctg	ctg	7437	
Gln	Ala	Leu	Asp	Cys	Gly	Lys	Asp	Leu	Glu	Ser	Val	Gln	Arg	Leu	Leu		
		2390					2395					2400					
cgg	aaa	cac	gag	gag	ctg	gag	cgg	gaa	gtg	cac	ccc	atc	cag	gcc	cag	7485	
Arg	Lys	His	Glu	Glu	Leu	Glu	Arg	Glu	Val	His	Pro	Ile	Gln	Ala	Gln		
		2405				2410					2415						
gtg	gag	tcc	cta	gag	cgt	gaa	gtg	ggc	cgc	ctc	tgc	caa	aga	agc	ccc	7533	
Val	Glu	Ser	Leu	Glu	Arg	Glu	Val	Gly	Arg	Leu	Cys	Gln	Arg	Ser	Pro		
2420				2425					2430					2435			
gag	gca	gcc	cac	ggc	ctc	agg	cac	agg	cag	cag	gag	gtg	gct	gag	agc	7581	
Glu	Ala	Ala	His	Gly	Leu	Arg	His	Arg	Gln	Gln	Glu	Val	Gla	Glu	Ser		
			2440					2445					2450				
tgg	tgg	cag	ctc	cgg	agc	agg	gcc	cag	aag	cgg	agg	gag	gcg	ctg	gat	7629	
Trp	Trp		Gln	Leu	Arg	Ser	Arg	Ala	Gln	Lys	Arg	Arg	Glu	Ala	Leu	Asp	
			2455					2460					2465				
gcc	ttg	cac	caa	gct	cag	aaa	ctc	cag	gca	atg	ctg	cag	gaa	ttg	ctg	7677	
Ala	Leu	His	Gln	Ala	Gln	Lys	Leu	Gln	Ala	Met	Leu	Gln	Glu	Leu	Leu		
		2470				2475					2480						
gtc	agc	gcc	cag	agg	ctg	cgg	gct	cag	atg	gac	acg	agc	ccc	gct	cct	7725	
Val	Ser	Ala	Gln	Arg	Leu	Arg	Ala	Gln	Met	Asp	Thr	Ser	Pro	Ala	Pro		
		2485			2490				2495								
cgc	agc	cct	gtg	gaa	gcc	cgg	cgt	atg	tta	gaa	gag	cat	cag	gag	tgc	7773	
Arg	Ser	Pro	Val	Glu	Ala	Arg	Arg	Met	Leu	Glu	Glu	His	Gln	Glu	Cys		
2500				2505					2510				2515				
aag	gcc	gag	ctg	gac	tcc	tgg	aca	gac	agc	atc	agc	ctg	gcc	cga	agc	7821	
Lys	Ala	Glu	Leu	Asp	Ser	Trp	Thr	Asp	Ser	Ile	Ser	Leu	Ala	Arg	Ser		
			2520					2525					2530				
act	ggg	cag	caa	ctg	ctc	aca	gcg	ggg	cac	ccc	ttc	agc	tcc	gac	att	7869	
Thr	Gly	Gln	Gln	Leu</													

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Ala Arg Gly His Ala Leu Arg Asp Thr Glu Thr Thr Leu Arg Val His	
1830 1835 1840	
aga gat ctc ttg gaa gtc ctc acc cag gtc cag gag aaa gcc acg agc	5805
Arg Asp Leu Leu Glu Val Leu Thr Gln Val Gln Glu Lys Ala Thr Ser	
1845 1850 1855	
ctc ccc aac aat gtg gca cgg gac ctg tgt ggg ctg gag gcg cag ctg	5853
Leu Pro Asn Asn Val Ala Arg Asp Leu Cys Gly Leu Glu Ala Gln Leu	
1860 1865 1870 1875	
aga agc cac cag ggg ctg gag cga gaa ctc gtg ggc acc gag cgg cag	5901
Arg Ser His Gln Gly Leu Glu Arg Glu Leu Val Gly Thr Glu Arg Gln	
1880 1885 1890	
ctg cag gaa ctg ctg gag act gca ggc agg gtg cag aag ctg tgt ccg	5949
Leu Gln Glu Leu Leu Glu Thr Ala Gly Arg Val Gln Lys Leu Cys Pro	
1895 1900 1905	
ggg cct cag gcc cat gcg gtg cag cag agg cag caa gct gtg acg cag	5997
Gly Pro Gln Ala His Ala Val Gln Gln Arg Gln Gln Ala Val Thr Gln	
1910 1915 1920	
gcg tgg gca gtg ctg cag cga cgc atg gag cag cgc agg gcc cag ctg	6045
Ala Trp Ala Val Leu Gln Arg Arg Met Glu Gln Arg Arg Ala Gln Leu	
1925 1930 1935	
gag cgg gca cgc ctc ctg gcc cgc ttc cgc acg gcg gtg cgt gac tat	6093
Glu Arg Ala Arg Leu Leu Ala Arg Phe Arg Thr Ala Val Arg Asp Tyr	
1940 1945 1950 1955	
gcc tcc tgg gca gcc cgc gtg cgc cag gac ctg cag gtg gag gag agt	6141
Ala Ser Trp Ala Ala Arg Val Arg Gln Asp Leu Gln Val Glu Glu Ser	
1960 1965 1970	
tcg caa gag cct agc agt ggc ccg ctg aag ctc agt gcc cac cag tgg	6189
Ser Gln Glu Pro Ser Ser Gly Pro Leu Lys Leu Ser Ala His Gln Trp	
1975 1980 1985	
ctc cgg gcg gag ctg gag gcc cgg gag aag ctg tgg cag cag gcc acc	6237
Leu Arg Ala Glu Leu Glu Ala Arg Glu Lys Leu Trp Gln Gln Ala Thr	
1990 1995 2000	
cag ctg ggg cag cag gca ctt ctt gct gca ggg aca ccc acc aag gag	6285
Gln Leu Gly Gln Gln Ala Leu Leu Ala Ala Gly Thr Pro Thr Lys Glu	
2005 2010 2015	
gtc cag gaa gag ctt cga gcc ctg cag gac cag cgg gac cag gtg tat	6333
Val Gln Glu Glu Leu Arg Ala Leu Gln Asp Gln Arg Asp Gln Val Tyr	
2020 2025 2030 2035	
cag acc tgg gca cgg aag caa gag agg ctg cag gcc gag cag cag gag	6381
Gln Thr Trp Ala Arg Lys Gln Glu Arg Leu Gln Ala Glu Gln Glu	
2040 2045 2050	
cag ctc ttc ctc aga gag tgc ggc cgc ctg gag gag atc ctc gcg gcc	6429
Gln Leu Phe Leu Arg Glu Cys Gly Arg Leu Glu Glu Ile Leu Ala Ala	
2055 2060 2065	
cag gag gtc tcc ctg aaa acc agt gcc ttg ggg agc tcg gtg gaa gag	6477
Gln Glu Val Ser Leu Lys Thr Ser Ala Leu Gly Ser Ser Val Glu Glu	
2070 2075 2080	
gta gag cag ttg att cgc aag cac gag gtc ttc ctg aag gtt ctg act	6525



His Gln Gly Gln Val Gln Arg Val Leu Ser Ser Gly Arg Ser Leu Ala	
1575 1580 1585	
gcc tca ggg cac ccc caa gcc caa cac atc gtg gag cag tgc cag gag	5037
Ala Ser Gly His Pro Gln Ala Gln His Ile Val Glu Gln Cys Gln Glu	
1590 1595 1600	
ctg gaa ggc cac tgg gca gag ctg gag agg gca tgt gaa gcg cgg gcc	5085
Leu Glu Gly His Trp Ala Glu Leu Glu Arg Ala Cys Glu Ala Arg Ala	
1605 1610 1615	
cag tgt ctg cag cag gct gtc act ttc cag cag tac ttt ctg gat gtg	5133
Gln Cys Leu Gln Gln Ala Val Thr Phe Gln Gln Tyr Phe Leu Asp Val	
1620 1625 1630 1635	
tca gag ctg gag ggc tgg gtg gag gag aag cgg ccg ctg gtg agc agt	5181
Ser Glu Leu Glu Gly Trp Val Glu Glu Lys Arg Pro Leu Val Ser Ser	
1640 1645 1650	
cgg gac tat ggc aga gac gag gca gcc acc ctc agg ctc att aac aag	5229
Arg Asp Tyr Gly Arg Asp Glu Ala Ala Thr Leu Arg Leu Ile Asn Lys	
1655 1660 1665	
cac cag gct cta cag gag gaa cta gcc att tac tgg agc tcc atg gag	5277
His Gln Ala Leu Gln Glu Glu Ala Ile Tyr Trp Ser Ser Met Glu	
1670 1675 1680	
gag ctt gac cag acg gcc caa acc ctc act ggc ccc gaa gtc cct gag	5325
Glu Leu Asp Gln Thr Ala Gln Thr Leu Thr Gly Pro Glu Val Pro Glu	
1685 1690 1695	
cag cag cgt gtg gtg cag gag agg ctc cgg gag cag ctg cgg gca ctg	5373
Gln Gln Arg Val Val Gln Glu Arg Leu Arg Glu Gln Leu Arg Ala Leu	
1700 1705 1710 1715	
cag gag ttg gcg gcc aca cgg gac cgg gaa ctg gag ggg acc ctg agg	5421
Gln Glu Leu Ala Ala Thr Arg Asp Arg Glu Leu Glu Gly Thr Leu Arg	
1720 1725 1730	
ctg cat gag ttc ctg agg gag gct gag gac ctg cag ggc tgg ctg gca	5469
Leu His Glu Phe Leu Arg Glu Ala Glu Asp Leu Gln Gly Trp Leu Ala	
1735 1740 1745	
agc cag aag cag gca gcc aaa gga ggg gag agc ctg gga gag gac ccc	5517
Ser Gln Lys Gln Ala Ala Lys Gly Gly Glu Ser Leu Gly Glu Asp Pro	
1750 1755 1760	
gag cac gcc ctg cac ctc tgc acc aag ttt gca aag ttt cag cac caa	5565
Glu His Ala Leu His Leu Cys Thr Lys Phe Ala Lys Phe Gln His Gln	
1765 1770 1775	
gtg gag atg ggc agc cag cgg gtg gcc gcc tgc cgg ctg ctg gcg gag	5613
Val Glu Met Gly Ser Gln Arg Val Ala Ala Cys Arg Leu Leu Ala Glu	
1780 1785 1790 1795	
agc ctg cta gag cgt ggg cac agt gct ggc ccc atg gtc cgt cag agg	5661
Ser Leu Leu Glu Arg Gly His Ser Ala Gly Pro Met Val Arg Gln Arg	
1800 1805 1810	
cag cag gat ctg cag acc gcc tgg tcg gag ctg tgg gag ctg acc cag	5709
Gln Gln Asp Leu Gln Thr Ala Trp Ser Glu Leu Trp Glu Leu Thr Gln	
1815 1820 1825	
gcc cga ggc cac gcg ctc cga gac acc gag acc acc ctc aga gtt cac	5757

Leu Gln Glu Trp Lys Gln Asp Val Ala Glu Leu Met Gln Trp Met Glu	
1320 1325 1330	
gag aag ggg ctg atg gct gcg cat gag ccc tcc gga gcg cgc aga aac	4269
Glu Lys Gly Leu Met Ala Ala His Glu Pro Ser Gly Ala Arg Arg Asn	
1335 1340 1345	
atc ctg cag aca ctc aag cgg cac gaa gca gct gag agc gag cta ctc	4317
Ile Leu Gln Thr Leu Lys Arg His Glu Ala Ala Glu Ser Glu Leu Leu	
1350 1355 1360	
gcc acc cgc aga cac gtg gag gcc ctg cag cag gtt ggg aga gag ctg	4365
Ala Thr Arg Arg His Val Glu Ala Leu Gln Gln Val Gly Arg Glu Leu	
1365 1370 1375	
ttg agt agg agg ccc tgt ggc cag gag gac ata cag acc agg ctt caa	4413
Leu Ser Arg Arg Pro Cys Gly Gln Glu Asp Ile Gln Thr Arg Leu Gln	
1380 1385 1390 1395	
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Arg His Gln Gln Leu Glu Ser Glu Ser Arg Thr Leu Ala Ala Lys Met	
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His Leu Ala Ile Arg Gly Leu Gln Leu Gln Ala Ser Val Glu Leu His	
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Val	Asn	Ser	Ala	Leu	Ser	Pro	Pro	Gly	Glu	Ser	Leu	Arg	Asn	Pro	Gly	
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Arg Arg Leu Thr Lys Ile Leu Leu Gln Leu Gln Glu Thr Glu Leu Leu	
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Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu Gly Ala Val Gly	
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gga gct gga gcc aca gcc ctg gtc ttc ctc tcc ttc tgt gtc atc ttc	929
Gly Ala Gly Ala Thr Ala Leu Val Phe Leu Ser Phe Cys Val Ile Phe	
265 270 275 280	
att gta gtg agg tcc tgc agg aag aaa tcg gca agg cca gca gcg gac	977
Ile Val Val Arg Ser Cys Arg Lys Lys Ser Ala Arg Pro Ala Ala Asp	
285 290 295	
gtg gga gac ata ggc atg aag gat gca aac acc atc agg ggc tca gcc	1025
Val Gly Asp Ile Gly Met Lys Asp Ala Asn Thr Ile Arg Gly Ser Ala	
300 305 310	

agg ggc tca gcc tct cag ggt aac ctg act gag tcc tgg gca gat gat 1366  
 Arg Gly Ser Ala Ser Gln Gly Asn Leu Thr Glu Ser Trp Ala Asp Asp  
                   405                  410                  415

aac ccc cga cac cat ggc ctg gct gcc cac tcc tca ggg gag gaa aga 1414  
 Asn Pro Arg His His Gly Leu Ala Ala His Ser Ser Gly Glu Glu Arg  
                   420                  425                  430

gag atc cag tat gca ccc ctc agc ttt cat aag ggg gag cct cag gac 1462  
 Glu Ile Gln Tyr Ala Pro Leu Ser Phe His Lys Gly Glu Pro Gln Asp  
                   435                  440                  445

cta tca gga caa gaa gcc acc aac aat gag tac tca gag atc aag atc 1510  
 Leu Ser Gly Gln Glu Ala Thr Asn Asn Glu Tyr Ser Glu Ile Lys Ile  
                   450                  455                  460                  465

ccc aag taa gaaaatg cagaggtcgg ggcttgtttg agggttcacg acccctccag 1566  
 Pro Lys \*

caaaggagtc tgaggctgat tccagtagaa ttagcagccc tcaatgctgt gcaacaagac 1626

atcagaactt attcctcttg tctaactgaa aatgcatgcc tgatgaccaa actctccctt 1686

tccccatcca atcggtccac actccccgcc ctggcctctg gtaccaccca ttctcctctg 1746

tacttctcta aggatgacta ctttagattc cgaatatagt gagattgtaa cgtgtttgtc 1806

tctctgtgcc tggcttattt cactcaacat aacatcctct aagttcatct gtgttgtttc 1866

caatgacaga gtaatgtact gaataattca aaatagctaa aa 1908

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<400> 217

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tcgcggccct ggcacctcca accccagat atg ctg ctg ctg ctg ctg ctg ccc 113  
                                   Met Leu Leu Leu Leu Leu Leu Pro  
                                   1                                  5

ctg ctc tgg ggg agg gag agg gtg gaa gga cag aag agt aac cgg aag 161  
 Leu Leu Trp Gly Arg Glu Arg Val Glu Gly Gln Lys Ser Asn Arg Lys  
                   10                  15                  20

gat tac tcg ctg acg atg cag agt tcc gtg acc gtg caa gag ggc atg 209  
 Asp Tyr Ser Leu Thr Met Gln Ser Ser Val Thr Val Gln Glu Gly Met  
                   25                  30                  35                  40

tgt gtc cat gtg cgc tgc tcc ttc tcc tac cca gtg gac agc cag act 257  
 Cys Val His Val Arg Cys Ser Phe Ser Tyr Pro Val Asp Ser Gln Thr  
                   45                  50                  55

ttg acc cac agg ccc aac atc ctt atc ccc ggt acc ctg gag tct ggc Leu Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser Gly 150 155 160	598
tgc ttc cag aat ctg acc tgc tct gtg ccc tgg gcc tgt gag cag ggg Cys Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly 165 170 175	646
acg ccc cct atg atc tcc tgg atg ggg acc tct gtg tcc ccc ctg cac Thr Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu His 180 185 190	694
ccc tcc acc acc cgc tcc tca gtg ctc acc ctc atc cca cag ccc cag Pro Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro Gln 195 200 205	742
cac cac ggc acc agc ctc acc tgt cag gtg acc ttg cct ggg gcc ggc His His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly 210 215 220 225	790
gtg acc acg aac agg acc atc caa ctc aat gtg tcc tac cct cct cag Val Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro Gln 230 235 240	838
aac ttg act gtg act gtc ttc caa gga gaa ggc aca gca tcc aca gct Asn Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr Ala 245 250 255	886
ctg ggg aac agc tca tct ctt tca gtc cta gag ggc cag tct ctg cgc Leu Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu Arg 260 265 270	934
ttg gtc tgt gct gtt gac agc aat ccc cct gcc agg ctg agc tgg acc Leu Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr 275 280 285	982
tgg agg agt ctg acc ctg tac ccc tca cag ccc tca aac cct ctg gta Trp Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu Val 290 295 300 305	1030
ctg gag ctg caa gtg cac ctg ggg gat gaa ggg gaa ttc acc tgt cga Leu Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys Arg 310 315 320	1078
gct cag aac tct ctg ggt tcc cag cac gtt tcc ctg aac ctc tcc ctg Ala Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser Leu 325 330 335	1126
caa cag gag tac aca ggc aaa atg agg cct gta tca gga gtg ttg ctg Gln Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu Leu 340 345 350	1174
ggg gcg gtc ggg gga gct gga gcc aca gcc ctg gtc ttc ctc tcc ttc Gly Ala Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe Leu Ser Phe 355 360 365	1222
tgt gtc atc ttc att gta gtg agg tcc tgc agg aag aaa tcg gca agg Cys Val Ile Phe Ile Val Val Arg Ser Cys Arg Lys Lys Ser Ala Arg 370 375 380 385	1270
cca gca gcg gac gtg gga gac ata ggc atg aag gat gca aac acc atc Pro Ala Ala Asp Val Gly Asp Ile Gly Met Lys Asp Ala Asn Thr Ile 390 395 400	1318

tacccttggt ggtctaaacg gatgctgctg ggtgttgca cccangacga gatgcctttg 2117  
 tttcttttac aataagtcgt tggahgaatg ccattnaagt gaactcccca cctttgcacn 2177  
 ctnttcggg cttaattggt tgggganatn ttggccattg gtcttggtgt tanaaaatgg 2237  
 cngtaccaag aaatcttttt ntocaaaanc ccccttttgc caanggattt tccttngggg 2297  
 gggcnggccca ccccccctnt tc 2319

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 aagaaccctg aggaacagac gttccctcgc ggcctggca cctccaaccc cagat atg 118  
 Met  
 1  
 ctg ctg ctg ctg ctg ctg ccc ctg ctc tgg ggg agg gag agg gtg gaa 166  
 Leu Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Val Glu  
 5 10 15  
 gga cag aag agt aac cgg aag gat tac tgc ctg acg atg cag agt tcc 214  
 Gly Gln Lys Ser Asn Arg Lys Asp Tyr Ser Leu Thr Met Gln Ser Ser  
 20 25 30  
 gtg acc gtg caa gag ggc atg tgt gtc cat gtg cgc tgc tcc ttc tcc 262  
 Val Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe Ser  
 35 40 45  
 tac cca gtg gac agc cag act gac tct gac cca gtt cat ggc tac tgg 310  
 Tyr Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr Trp  
 50 55 60 65  
 ttc cgg gca ggg aat gat ata agc tgg aag gct cca gtg gcc aca aac 358  
 Phe Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr Asn  
 70 75 80  
 aac cca gct tgg gca gtg cag gag gaa act cgg gac cga ttc cac ctc 406  
 Asn Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu  
 85 90 95  
 ctt ggg gac cca cag acc aaa aat tgc acc ctg agc atc aga gat gcc 454  
 Leu Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp Ala  
 100 105 110  
 aga atg agt gat gcg ggg aga tac ttc ttt cgt atg gag aaa gga aat 502  
 Arg Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly Asn  
 115 120 125  
 ata aaa tgg aat tat aaa tat gac cag ctc tct gtg aac gtg aca gcc 550  
 Ile Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala  
 130 135 140 145

220	225	230	
agg gaa aac aga cca aga aat ggt ggc atc tgt gtg gcc aat cat acc			1253
Arg Glu Asn Arg Pro Arg Asn Gly Gly Ile Cys Val Ala Asn His Thr			
235	240	245	
tca ccg atc gat gtg atc atc ttg gcc agc gat ggc tat tat gcc atg			1301
Ser Pro Ile Asp Val Ile Ile Leu Ala Ser Asp Gly Tyr Tyr Ala Met			
250	255	260	265
gtg ggt caa gtg cac ggg gga ctc atg ggt gtg att cag aga gcc atg			1349
Val Gly Gln Val His Gly Gly Leu Met Gly Val Ile Gln Arg Ala Met			
	270	275	280
gtg aag gcc tgc cca cac gtc tgg ttt gag cgc tcg gaa gtg aag gat			1397
Val Lys Ala Cys Pro His Val Trp Phe Glu Arg Ser Glu Val Lys Asp			
	285	290	295
cgc cac ctg gtg gct aag aga ctg act gaa cat gtg caa gat aaa agc			1445
Arg His Leu Val Ala Lys Arg Leu Thr Glu His Val Gln Asp Lys Ser			
	300	305	310
aag ctg cct atc ctc atc ttc cca gaa gga acc tgc atc aat aat aca			1493
Lys Leu Pro Ile Leu Ile Phe Pro Glu Gly Thr Cys Ile Asn Asn Thr			
	315	320	325
tcg gtg atg atg ttc aaa aag gga agt ttt gaa att gga gcc aca gtt			1541
Ser Val Met Met Phe Lys Lys Gly Ser Phe Glu Ile Gly Ala Thr Val			
330	335	340	345
tac cct gtt gct atc aag tat gac cct caa ttt ggc gat gcc ttc tgg			1589
Tyr Pro Val Ala Ile Lys Tyr Asp Pro Gln Phe Gly Asp Ala Phe Trp			
	350	355	360
aac agc agc aaa tac ggg atg gtg acg tac ctg ctg cga atg atg acc			1637
Asn Ser Ser Lys Tyr Gly Met Val Thr Tyr Leu Leu Arg Met Met Thr			
	365	370	375
agc tgg gcc att gtc tgc agc gtg tgg tac ctg cct ccc atg act aga			1685
Ser Trp Ala Ile Val Cys Ser Val Trp Tyr Leu Pro Pro Met Thr Arg			
	380	385	390
gag gca gat gaa gat gct gtc cag ttt gcg aat agg gtg aaa tct gcc			1733
Glu Ala Asp Glu Asp Ala Val Gln Phe Ala Asn Arg Val Lys Ser Ala			
	395	400	405
att gcc agg cag gga gga ctt gtg gac ctg ctg tgg gat ggg ggc ctg			1781
Ile Ala Arg Gln Gly Gly Leu Val Asp Leu Leu Trp Asp Gly Gly Leu			
410	415	420	425
aag agg gag aag gtg aag gac acg ttc aag gag gag cag cag aag ctg			1829
Lys Arg Glu Lys Val Lys Asp Thr Phe Lys Glu Glu Gln Gln Lys Leu			
	430	435	440
tac agc aag atg atc gtg ggg aac cac aag gac agg agc cgc tcc tga			1877
Tyr Ser Lys Met Ile Val Gly Asn His Lys Asp Arg Ser Arg Ser			
	445	450	455
gcctgcctcc agctggctgg ggccaccgtg cgggggtgcca acgggctcag agctggagtt			1937
gcgcgcgcgc ccccccactgc tgtgtccttt ccagaactcca gggctccccg ggctgctctg			1997
gatcccagga ctccggcttt cgccgagccg cagcgggatc cctgtgcacc cggcgcagcc			2057

cagttgacctc	ctgtggccgt	gtttttctgt	cattctgttc	ccaggccttc	tattcaggcg	360
gttgaagggt	gtggactttg	gaatgggggt	tgctgttctt	cggaacttg	cttcctttcc	420
ctggctggcg	ctgtcaggaa	ggaccatctg	aaggctgcaa	tttgttctta	tggaggcagg	480
tgctggcctg	gcctggatct	tccacc	atg ttc	ctg ttg	ctg cct ttt gat agc	533
			Met Phe Leu Leu Leu Pro Phe Asp Ser			
		1		5		
ctg att gtc aac ctt	ctg ggc atc tcc	ctg act gtc ctc	ttc acc ctc			581
Leu Ile Val Asn Leu	Leu Gly Ile Ser Leu	Thr Val Leu Phe	Thr Leu			
10	15	20	25			
ctt ctc gtt ttc	atc ata gtg cca gcc	att ttt gga gtc	tcc ttt ggt			629
Leu Leu Val Phe Ile	Ile Val Pro Ala Ile	Phe Gly Val Ser	Phe Gly			
	30	35	40			
atc cgc aaa ctc	tac atg aaa agt	ctg tta aaa atc	ttt gcg tgg gct			677
Ile Arg Lys Leu Tyr	Met Lys Ser Leu Leu	Lys Ile Phe Ala	Trp Ala			
	45	50	55			
acc ttg aga atg	gag cga gga gcc	aag gag aag aac	cac cag ctt tac			725
Thr Leu Arg Met Glu	Arg Gly Ala Lys Glu	Lys Asn His Gln	Leu Tyr			
	60	65	70			
aag ccc tac acc	aac gga atc att	gca aag gat ccc	act tca cta gaa			773
Lys Pro Tyr Thr Asn	Gly Ile Ile Ala Lys	Asp Pro Thr Ser	Leu Glu			
	75	80	85			
gaa gag atc aaa	gag att cgt cga	agt ggt agt agt	aag gct ctg gac			821
Glu Glu Ile Lys Glu	Ile Arg Arg Ser Gly	Ser Ser Lys Ala	Leu Asp			
	90	95	100	105		
aac act cca gag	ttc gag ctc tct	gac att ttc tac	ttt tgc cgg aaa			869
Asn Thr Pro Glu Phe	Glu Leu Ser Asp Ile	Phe Tyr Phe Cys	Arg Lys			
	110	115	120			
gga atg gag acc	att atg gat gat	gag gtg aca aag	aga ttc tca gca			917
Gly Met Glu Thr Ile	Met Asp Asp Glu	Val Thr Lys Arg	Phe Ser Ala			
	125	130	135			
gaa gaa ctg gag	tcc tgg aac ctg	ctg agc aga acc	aat tat aac ttc			965
Glu Glu Leu Glu Ser	Trp Asn Leu Ser	Arg Thr Asn Tyr	Asn Phe			
	140	145	150			
cag tac atc agc	ctt cgg ctc acg	gtc ctg tgg ggg	tta gga gtg ctg			1013
Gln Tyr Ile Ser Leu	Arg Leu Thr Val	Leu Trp Gly Leu	Gly Val Leu			
	155	160	165			
att cgg tac tgc	ttt ctg ctg ccg	ctc agg ata gca	ctg gct ttc aca			1061
Ile Arg Tyr Cys Phe	Leu Leu Pro Leu	Arg Ile Ala Leu	Ala Phe Thr			
	170	175	180	185		
ggg att agc ctt	ctg gtg gtg ggc	aca act gtg gtg	gga tac ttg cca			1109
Gly Ile Ser Leu Leu	Val Val Gly Thr	Thr Val Val Gly	Tyr Leu Pro			
	190	195	200			
aat ggg agg ttt	aag gag ttc atg	agt aaa cat gtt	cac tta atg tgt			1157
Asn Gly Arg Phe Lys	Glu Phe Met Ser	Lys His Val His	Leu Met Cys			
	205	210	215			
tac cgg atc tgc	gtg cga gcg ctg	aca gcc atc atc	acc tac cat gac			1205
Tyr Arg Ile Cys Val	Arg Ala Leu Thr	Ala Ile Ile Thr	Tyr His Asp			

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gat tcc tgc cag ctg ggc tac tcg gcc ggt ccc tgc atg gga atg acc      834
Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly Met Thr
   230                               235                               240

agc agg tat ttc tat aat ggt aca tcc atg gcc tgt gag act ttc cag      882
Ser Arg Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys Glu Thr Phe Gln
  245                               250                               255                               260

tac ggc ggc tgc atg ggc aac ggt aac aac ttc gtc aca gaa aag gag      930
Tyr Gly Gly Cys Met Gly Asn Gly Asn Phe Val Thr Glu Lys Glu
   265                               270                               275

tgt ctg cag acc tgc cga act gtg gcg gcc tgc aat ctc ccc ata gtc      978
Cys Leu Gln Thr Cys Arg Thr Val Ala Ala Cys Asn Leu Pro Ile Val
   280                               285                               290

cgg ggc ccc tgc cga gcc ttc atc cag ctc tgg gca ttt gat gct gtc     1026
Arg Gly Pro Cys Arg Ala Phe Ile Gln Leu Trp Ala Phe Asp Ala Val
   295                               300                               305

aag ggg aag tgc gtc ctc ttc ccc tac ggg ggc tgc cag ggc aac ggg     1074
Lys Gly Lys Cys Val Leu Phe Pro Tyr Gly Gly Cys Gln Gly Asn Gly
   310                               315                               320

aac aag ttc tac tca gag aag gag tgc aga gag tac tgc ggt gtc cct     1122
Asn Lys Phe Tyr Ser Glu Lys Glu Cys Arg Glu Tyr Cys Gly Val Pro
  325                               330                               335                               340

ggt gat ggt gat gag gag ctg ctg cgc ttc tcc aac tgac aactggccgg     1172
Gly Asp Gly Asp Glu Glu Leu Leu Arg Phe Ser Asn
   345                               350

tctgcaagtc agaggatggc cagtgtctgt cccgggggtcc tgtggcaggc agcgccaagc     1232

aacctgggtc caaataaaaa cttaattgta aactcctgaa aaaaaaaaaa             1280

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<221> CDS
<222> (507)..(1874)

<220>
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<222> (1)...(2319)
<223> n = a,t,c or g

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ctcttgggca ggaaaaccat gtaaaacctc tggaagcagc atcaggacag cagagcagag     180
ccccgtcct cactgtctac ttgcacagaa actocatctg gactcggatg cttttactga     240
agacccatct agcttcaatc atcttttagag tccatccatt ctggagagac ctggcgtttg     300

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 Met Arg Ser Leu  
 1  
 ggg gcc ctg ctc ttg ctg ctg agc gcc tgc ctg gcg gtg agc gct ggc 162  
 Gly Ala Leu Leu Leu Leu Ser Ala Cys Leu Ala Val Ser Ala Gly  
 5 10 15 20  
 cct gtg cca acg ccg ccc gac aac atc caa gtg cag gaa aac ttc aat 210  
 Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln Glu Asn Phe Asn  
 25 30 35  
 atc tct cgg atc tat ggg aag tgg tac aac ctg gcc atc ggt tcc acc 258  
 Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr  
 40 45 50  
 tgc ccc tgg ctg aag aag atc atg gac agg atg aca gtg agc acg ctg 306  
 Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr Val Ser Thr Leu  
 55 60 65  
 gtg ctg gga gag ggc gct aca gag gcg gag atc agc atg acc agc act 354  
 Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser Met Thr Ser Thr  
 70 75 80  
 cgt tgg cgg aaa ggt gtc tgt gag gag acg tct gga gct tat gag aaa 402  
 Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly Ala Tyr Glu Lys  
 85 90 95 100  
 aca gat act gat ggg aag ttt ctc tat cac aaa tcc aaa tgg aac ata 450  
 Thr Asp Thr Asp Arg Lys Phe Leu Tyr His Lys Ser Lys Trp Asn Ile  
 105 110 115  
 acc atg gag tcc tat gtg gtc cac acc aac tat gat gag tat gcc att 498  
 Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp Glu Tyr Ala Ile  
 120 125 130  
 ttc ctg acc aag aaa ttc agc cgc cat cat gga ccc acc att act gcc 546  
 Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro Thr Ile Thr Ala  
 135 140 145  
 aag ctc tac ggg cgg gcg ccg cag ctg agg gaa act ctc ctg cag gac 594  
 Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr Leu Leu Gln Asp  
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 Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu Asp Ser Ile Phe  
 165 170 175 180  
 acc atg gct gac cga ggt gaa tgt gtc cct ggg gag cag gaa cca gag 690  
 Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu Gln Glu Pro Glu  
 185 190 195  
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 Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Val Leu Pro Gln Glu Glu  
 200 205 210  
 gaa gga tca ggg ggt ggg caa ctg gta act gaa gtc acc aag aaa gaa 786  
 Glu Gly Ser Gly Gly Gly Gln Leu Val Thr Glu Val Thr Lys Lys Glu  
 215 220 225



ttg agc aaa gag atc cgt cca gtc tgc cgc aag ttc atg caa gat cca	953
Leu Ser Lys Glu Ile Arg Pro Val Cys Arg Lys Phe Met Gln Asp Pro	
235 240 245	
atg gag atc ttc gtg gat gat gag acg aag ttg acg ctg cat ggg ttg	1001
Met Glu Ile Phe Val Asp Asp Glu Thr Lys Leu Thr Leu His Gly Leu	
250 255 260	
cag cag tac tac gtg aaa ctg aag gac aac gag aag aac cgg aag ctc	1049
Gln Gln Tyr Tyr Val Lys Leu Lys Asp Asn Glu Lys Asn Arg Lys Leu	
265 270 275	
ttt gac ctt ctg gat gtc ctt gag ttc aac cag gtg gtg atc ttt gtg	1097
Phe Asp Leu Leu Asp Val Leu Glu Phe Asn Gln Val Val Ile Phe Val	
280 285 290	
aag tct gtg cag cgg tgc att gcc ttg gcc cag cag ttt aaa gat ttt	1145
Lys Ser Val Gln Arg Cys Ile Ala Leu Ala Gln Gln Phe Lys Asp Phe	
295 300 305 310	
caa cga cga att ctt gtg gct acc aac cta ttt ggc cga ggc atg gac	1193
Gln Arg Arg Ile Leu Val Ala Thr Asn Leu Phe Gly Arg Gly Met Asp	
315 320 325	
atc gag cgg gtg aac att gct ttt aat tat gac atg cct gag gat tct	1241
Ile Glu Arg Val Asn Ile Ala Phe Asn Tyr Asp Met Pro Glu Asp Ser	
330 335 340	
gac acc tac ctg cat cgg gtg gcc aga gca ggc cgg ttt ggc acc aag	1289
Asp Thr Tyr Leu His Arg Val Ala Arg Ala Gly Arg Phe Gly Thr Lys	
345 350 355	
ggc ttg gct atc aca ttt gtg tcc gat gag aat gat gcc aag atc ctc	1337
Gly Leu Ala Ile Thr Phe Val Ser Asp Glu Asn Asp Ala Lys Ile Leu	
360 365 370	
aat gat gtg cag gat cgc ttt gag gtc aat att agt gag ctg cct gat	1385
Asn Asp Val Gln Asp Arg Phe Glu Val Asn Ile Ser Glu Leu Pro Asp	
375 380 385 390	
gag ata gac atc tcc tcc tac att gaa cag aca cgg tag aagactcgcc	1434
Glu Ile Asp Ile Ser Ser Tyr Ile Glu Gln Thr Arg *	
395 400	
cattttggaa tgtgaccgtc tgtccttcag gagaggacac caggggtgggg gtgaaggaga	1494
cactactgcc cccaccctg acagccccc ccccatggct tccatctttt gcacaccac	1554
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gatccccctt cctttcttcc cctgccggcc cagtt atg gca gag aac gat gtg	233
Met Ala Glu Asn Asp Val	
1 5	
gac aat gag ctc ttg gac tat gaa gat gat gag gtg gag aca gca gct	281
Asp Asn Glu Leu Leu Asp Tyr Glu Asp Asp Glu Val Glu Thr Ala Ala	
10 15 20	
ggg gga gat ggg gct gag gcc cct gcc aag aag gat gtc aag ggc tcc	329
Gly Gly Asp Gly Ala Glu Ala Pro Ala Lys Lys Asp Val Lys Gly Ser	
25 30 35	
tat gtc tcc atc cac agc tct ggc ttt cgt gac ttc ctg ctc aag cca	377
Tyr Val Ser Ile His Ser Ser Gly Phe Arg Asp Phe Leu Leu Lys Pro	
40 45 50	
gag ttg ctc cgg gcc att gtc gac tgt ggc ttt gag cat ccg tca gaa	425
Glu Leu Leu Arg Ala Ile Val Asp Cys Gly Phe Glu His Pro Ser Glu	
55 60 65 70	
gtc cag cat gag tgc atc cct cag gcc att ctg gga atg gat gtc ctg	473
Val Gln His Glu Cys Ile Pro Gln Ala Ile Leu Gly Met Asp Val Leu	
75 80 85	
tgc cag gcc aag tgc ggc atg gga aag aca gca gtg ttt gtc ttg gcc	521
Cys Gln Ala Lys Ser Gly Met Gly Lys Thr Ala Val Phe Val Leu Ala	
90 95 100	
aca ctg caa cag ctg gag cca gtt act ggg cag gtg tct gta ctg gtg	569
Thr Leu Gln Gln Leu Glu Pro Val Thr Gly Gln Val Ser Val Leu Val	
105 110 115	
atg tgt cac act cgg gag ttg gct ttt cag atc agc aag gaa tat gag	617
Met Cys His Thr Arg Glu Leu Ala Phe Gln Ile Ser Lys Glu Tyr Glu	
120 125 130	
cgc ttc tct aaa tac atg ccc aat gtc aag gtt gct gtt ttt ttt ggt	665
Arg Phe Ser Lys Tyr Met Pro Asn Val Lys Val Ala Val Phe Phe Gly	
135 140 145 150	
ggt ctg tct atc aag aag gat gaa gag gtg ctg aag aag aac tgc ccg	713
Gly Leu Ser Ile Lys Lys Asp Glu Glu Val Leu Lys Lys Asn Cys Pro	
155 160 165	
cat atc gtc gtg ggg act cca gcc cgt atc cta gcc ctg gct cga aat	761
His Ile Val Val Gly Thr Pro Gly Arg Ile Leu Ala Leu Ala Arg Asn	
170 175 180	
aag agc ctc aac ctc aaa cac att aaa cac ttt att ttg gat gaa tgt	809
Lys Ser Leu Asn Leu Lys His Ile Lys His Phe Ile Leu Asp Glu Cys	
185 190 195	
gat aag atg ctt gaa cag ctc gac atg cgt cgg gat gtc cag gaa att	857
Asp Lys Met Leu Glu Gln Leu Asp Met Arg Arg Asp Val Gln Glu Ile	
200 205 210	
ttt cgc atg acc ccc cac gag aag cag gtc atg atg ttc agt gct acc	905
Phe Arg Met Thr Pro His Glu Lys Gln Val Met Met Phe Ser Ala Thr	
215 220 225 230	

265	270	275	
ttt gac ctt ctg gat gtc ctt gag ttc aac cag gtg gtg atc ttt gtg			1097
Phe Asp Leu Leu Asp Val Leu Glu Phe Asn Gln Val Val Ile Phe Val			
280	285	290	
aag tct gtg cag cgg tgc att gcc ttg gcc cag cta cta gtg gag cag			1145
Lys Ser Val Gln Arg Cys Ile Ala Leu Ala Gln Leu Leu Val Glu Gln			
295	300	305	310
aac ttc cca gcc att gcc atc cac cgt ggg atg ccc cag gag gag agg			1193
Asn Phe Pro Ala Ile Ala Ile His Arg Gly Met Pro Gln Glu Glu Arg			
	315	320	325
ctt tct cgg tat cag cag ttt aaa gat ttt caa cga cga att ctt gtg			1241
Leu Ser Arg Tyr Gln Gln Phe Lys Asp Phe Gln Arg Arg Ile Leu Val			
	330	335	340
gct acc aac cta ttt ggc cga ggc atg gac atc gag cgg gtg aac att			1289
Ala Thr Asn Leu Phe Gly Arg Gly Met Asp Ile Glu Arg Val Asn Ile			
	345	350	355
gct ttt aat tat gac atg cct gag gat tct gac acc tac ctg cat cgg			1337
Ala Phe Asn Tyr Asp Met Pro Glu Asp Ser Asp Thr Tyr Leu His Arg			
	360	365	370
gtg gcc aga gca ggc cgg ttt ggc acc aag ggc ttg gct atc aca ttt			1385
Val Ala Arg Ala Gly Arg Phe Gly Thr Lys Gly Leu Ala Ile Thr Phe			
	375	380	385
gtg tcc gat gag aat gat gcc aag atc ctc aat gat gtg cag gat cgc			1433
Val Ser Asp Glu Asn Asp Ala Lys Ile Leu Asn Asp Val Gln Asp Arg			
	395	400	405
ttt gag gtc aat att agt gag ctg cct gat gag ata gac atc tcc tcc			1481
Phe Glu Val Asn Ile Ser Glu Leu Pro Asp Glu Ile Asp Ile Ser Ser			
	410	415	420
tac att gaa cag aca cgg tag aa gactcgccca ttttggaatg tgaccgtctg			1534
Tyr Ile Glu Gln Thr Arg *			
	425		
tccttcagga gaggacacca ggggtgggggt gaaggagaca ctactgcccc caccctgac			1594
agccccacc ccattggttc catcttttgc atcaccacca ctctgaacc cccatttctg			1654
atttgtcaga attttttttt aacaaaacta aaaatgaaac acatgtgtct gtggtatcta			1714
taaaaaaaaa aa			1726

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (216)..(1424)

<400> 213  
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tat gtc tcc atc cac agc tct ggc ttt cgt gac ttc ctg ctc aag cca Tyr Val Ser Ile His Ser Ser Gly Phe Arg Asp Phe Leu Leu Lys Pro 40 45 50			377
gag ttg ctc cgg gcc att gtc gac tgt ggc ttt gag cat ccg tca gaa Glu Leu Leu Arg Ala Ile Val Asp Cys Gly Phe Glu His Pro Ser Glu 55 60 65 70			425
gtc cag cat gag tgc atc cct cag gcc att ctg gga atg gat gtc ctg Val Gln His Glu Cys Ile Pro Gln Ala Ile Leu Gly Met Asp Val Leu 75 80 85			473
tgc cag gcc aag tcg ggc atg gga aag aca gca gtg ttt gtc ttg gcc Cys Gln Ala Lys Ser Gly Met Gly Lys Thr Ala Val Phe Val Leu Ala 90 95 100			521
aca ctg caa cag ctg gag cca gtt act ggg cag gtg tct gta ctg gtg Thr Leu Gln Gln Leu Glu Pro Val Thr Gly Gln Val Ser Val Leu Val 105 110 115			569
atg tgt cac act cgg gag ttg gct ttt cag atc agc aag gaa tat gag Met Cys His Thr Arg Glu Leu Ala Phe Gln Ile Ser Lys Glu Tyr Glu 120 125 130			617
cgc ttc tct aaa tac atg ccc aat gtc aag gtt gct gtt ttt ttt ggt Arg Phe Ser Lys Tyr Met Pro Asn Val Lys Val Ala Val Phe Phe Gly 135 140 145 150			665
ggt ctg tct atc aag aag gat gaa gag gtg ctg aag aag aac tgc ccg Gly Leu Ser Ile Lys Lys Asp Glu Glu Val Leu Lys Lys Asn Cys Pro 155 160 165			713
cat atc gtc gtg ggg act cca ggc cgt atc cta gcc ctg gct cga aat His Ile Val Val Gly Thr Pro Gly Arg Ile Leu Ala Leu Ala Arg Asn 170 175 180			761
aag agc ctc aac ctc aaa cac att aaa cac ttt att ttg gat gaa tgt Lys Ser Leu Asn Leu Lys His Ile Lys His Phe Ile Leu Asp Glu Cys 185 190 195			809
gat aag atg ctt gaa cag ctc gac atg cgt cgg gat gtc cag gaa att Asp Lys Met Leu Glu Gln Leu Asp Met Arg Arg Asp Val Gln Glu Ile 200 205 210			857
ttt cgc atg acc ccc cac gag aag cag gtc atg atg ttc agt gct acc Phe Arg Met Thr Pro His Glu Lys Gln Val Met Met Phe Ser Ala Thr 215 220 225 230			905
ttg agc aaa gag atc cgt cca gtc tgc cgc aag ttc atg caa gat cca Leu Ser Lys Glu Ile Arg Pro Val Cys Arg Lys Phe Met Gln Asp Pro 235 240 245			953
atg gag atc ttc gtg gat gat gag acg aag ttg acg ctg cat ggg ttg Met Glu Ile Phe Val Asp Asp Glu Thr Lys Leu Thr Leu His Gly Leu 250 255 260			1001
cag cag tac tac gtg aaa ctg aag gac aac gag aag aac cgg aag ctc Gln Gln Tyr Tyr Val Lys Leu Lys Asp Asn Glu Lys Asn Arg Lys Leu			1049

Leu Phe Gly Gly Thr Ser Pro Ser Pro Glu Glu Gly Leu Gly Asp Glu  
 305 310 315 320  
 ttt gac ctt ata gat cat tct gac tta cac att ttg gac ttt agc cct 1186  
 Phe Asp Leu Ile Asp His Ser Asp Leu His Ile Leu Asp Phe Ser Pro  
 325 330 335  
 agt ctg aag act ctg tgc aaa ctg gcc gtg att cag tat aac cta gac 1234  
 Ser Leu Lys Thr Leu Cys Lys Leu Ala Val Ile Gln Tyr Asn Leu Asp  
 340 345 350  
 cag tcc tgt ttg cct cat gat atc agg tgg gag ctg aat gcc atg acc 1282  
 Gln Ser Cys Leu Pro His Asp Ile Arg Trp Glu Leu Asn Ala Met Thr  
 355 360 365  
 acc aac agc aat atc agt cgc ccc atc gtc tcc tcc cat ggg tag gag 1330  
 Thr Asn Ser Asn Ile Ser Arg Pro Ile Val Ser Ser His Gly \*  
 370 375 380  
 gaagtttctg ccacctcccc tctgagcct gctgtcatct tcaactgcccc tgcccatctg 1390  
 tcacccacct gctcctttga cccttggaact tggatatacct ccatgtggag ttgttgggag 1450  
 agaggtgttc tctgtgctgt gaattcagtg gggagctgta gcggggtggg ggctaggttc 1510  
 ctccccctt ggccgaggg cccttcccc ttgggtgtc tgtccccatc cacctcctt 1570  
 cagctgctcc tgggctcag cttctgcccc gggccagccc aggttctgct gggaagggaa 1630  
 gggaatgggg agaaaggag aagcaagcag tgtctgagcc tcaggaagct tcccccccc 1690  
 cttgcctatc ccctccctc tgcttgagcc ttgagccttg actgggagct gaaaggagtt 1750  
 gcagctgttg gcatgagacc tccttctccc cgtcttgggg aggtggggac cagcagataa 1810  
 atccccacct tcctttgant gtcgctgtac tctgaagttc agctagctca gattttataa 1870  
 aaaaaaaaa a 1881

<210> 212  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (216)..(1502)

<400> 212  
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 ccatacgcgc tctccctgtt tagctcttct gttagaaata gtatctttgt tttcctttgc 120  
 tgttctctaa tcccctactc ttacccctt gttttcacct attttgcgag aacccatcca 180  
 gatccccctt cccttcttcc cctgccggcc cagtt atg gca gag aac gat gtg 233  
 Met Ala Glu Asn Asp Val  
 1 5  
 gac aat gag ctg ttg gac tat gaa gat gat gag gtg gag aca gca gct 281  
 Asp Asn Glu Leu Leu Asp Tyr Glu Asp Asp Glu Val Glu Thr Ala Ala

Phe Asn Ala Val Ser Leu Arg Trp Thr Lys Leu Pro Pro Val Lys Ser	
50 55 60	
gcc atc cgt ggg caa gct cct gtg gta ccc tac atg cgc tat gga cac	418
Ala Ile Arg Gly Gln Ala Pro Val Val Pro Tyr Met Arg Tyr Gly His	
65 70 75 80	
tca acc gtc ctc atc gac gac aca gtc ctc ctt tgg ggc ggg cgg aat	466
Ser Thr Val Leu Ile Asp Asp Thr Val Leu Leu Trp Gly Gly Arg Asn	
85 90 95	
gac acc gaa ggg gcc tgc aat gtg ctc tat gcc ttt gac gtc aat acg	514
Asp Thr Glu Gly Ala Cys Asn Val Leu Tyr Ala Phe Asp Val Asn Thr	
100 105 110	
cac aag tgg ttc aca ccc cga gtg tca ggg aca gtt cct ggg gcc cgg	562
His Lys Trp Phe Thr Pro Arg Val Ser Gly Thr Val Pro Gly Ala Arg	
115 120 125	
gat gga cat tca gcc tgt gtc cta ggc aag atc atg tac att ttt ggg	610
Asp Gly His Ser Ala Cys Val Leu Gly Lys Ile Met Tyr Ile Phe Gly	
130 135 140	
ggc tac gag cag cag gcg gac tgt ttt tcc aat gac att cac aag cta	658
Gly Tyr Glu Gln Gln Ala Asp Cys Phe Ser Asn Asp Ile His Lys Leu	
145 150 155 160	
gat acc agc acc atg aca tgg act ctt atc tgt aca aag ggc agc cct	706
Asp Thr Ser Thr Met Thr Trp Thr Leu Ile Cys Thr Lys Gly Ser Pro	
165 170 175	
gca cgc tgg agg gac ttc cac tca gcc aca atg ctg gga agt cac atg	754
Ala Arg Trp Arg Asp Phe His Ser Ala Thr Met Leu Gly Ser His Met	
180 185 190	
tat gtc ttt ggg ggc cgt gcc gac cgc ttt ggg cca ttc cat tcc aac	802
Tyr Val Phe Gly Gly Arg Ala Asp Arg Phe Gly Pro Phe His Ser Asn	
195 200 205	
aat gag att tac tgc aac cgc att cga gtc ttt gac acc aga act gag	850
Asn Glu Ile Tyr Cys Asn Arg Ile Arg Val Phe Asp Thr Arg Thr Glu	
210 215 220	
gct tgg ctg gac tgt ccc ccg act cca gtg ctg cct gag ggg cgc cgg	898
Ala Trp Leu Asp Cys Pro Pro Thr Pro Val Leu Pro Glu Gly Arg Arg	
225 230 235 240	
agc cac tcg gcc ttt ggc tac aat ggg gag ctg tac atc ttt ggt ggt	946
Ser His Ser Ala Phe Gly Tyr Asn Gly Glu Leu Tyr Ile Phe Gly Gly	
245 250 255	
tat aat gca agg ctg aac cgg cac ttc cat gac ctc tgg aag ttt aat	994
Tyr Asn Ala Arg Leu Asn Arg His Phe His Asp Leu Trp Lys Phe Asn	
260 265 270	
cct gtg tcc ttt acc tgg aaa aag att gaa ccg aag ggg aag ggg cca	1042
Pro Val Ser Phe Thr Trp Lys Lys Ile Glu Pro Lys Gly Lys Gly Pro	
275 280 285	
tgt ccc cgc cgg cgc cag tgc tgc tgt att gtt ggt gac aag att gtc	1090
Cys Pro Arg Arg Arg Gln Cys Cys Cys Ile Val Gly Asp Lys Ile Val	
290 295 300	
ctc ttt ggg ggt acc agt cca tct cct gag gaa ggc ctg gga gat gaa	1138

95	100	105	110	
aag ccc cgg gcc cca gga gat gag gaa gcc cag gtg gag aac ctc atc				505
Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu Asn Leu Ile				
	115	120	125	
acc gcc aat gca aca gag ccc cag aaa gca gag aac tga agtgcagcca				554
Thr Ala Asn Ala Thr Glu Pro Gln Lys Ala Glu Asn *				
	130	135		
tcagggtggaa gcctctggaa cctgaggcgg ctgcttgaac ctttggatgc aaatgtcgat				614
gcttaagaaa accggccact tcagcaacag ccctttcccc aggagaagcc aagaacttgt				674
gtgtccccca ccctatcccc tctaacacca ttctccacc tgatgatgca actaacattt				734
gcctccccac tgcagcctgc ggtcctgccc acctcccggtg atgtgtgtgt gtgtgtgtgt				794
gtgtgtgact gtgtgtgttt gctaactgtg gtctttgtgg ctacttgttt gtggatggta				854
ttgtgtttgt tagtgaactg tggactcgct ttcccaggca ggggctgagc cacatggcca				914
tctgtctctc cctgcccctg tgggccctcc atcaccttct gctcctagga ggctgcttgt				974
tgcccgagaa ccagccccct ccntgattt taggggatgg cgtaggggta aggagcaagg				1034
ggcagtggtn ttcaagtngt tttnggtt				1062

<210> 211  
 <211> 1881  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (179)..(1327)

<220>  
 <221> misc\_feature  
 <222> (1)...(1881)  
 <223> n = a,t,c or g

<400> 211	
acgcgtacgg cttggctgtg tttatctcgt tggggactaa ggcgtcggtt ggcgcgcaac	60
gggttctagg ctgcaggcag ctcgaggacc cgcgggccccg ccccggtctg gcctggcaga	120
tagcagaggg agcaggccgt gccggggggg catgttgctg taaccagtgg cccagggg	178
atg tta cgg tgg aca gtg cac ctg gag ggc ggg ccc cgc agg gtg aac	226
Met Leu Arg Trp Thr Val His Leu Glu Gly Gly Pro Arg Arg Val Asn	
1 5 10 15	
cat gct gca gtg gct gtc ggg cat cgg gta tac tcc ttc ggg ggt tac	274
His Ala Ala Val Ala Val Gly His Arg Val Tyr Ser Phe Gly Gly Tyr	
20 25 30	
tgc tct ggt gaa gac tat gag aca ctg cgt cag ata gat gtg cac att	322
Cys Ser Gly Glu Asp Tyr Glu Thr Leu Arg Gln Ile Asp Val His Ile	
35 40 45	
ttc aat gca gtg tcc ttg cgt tgg aca aag ctg ccc ccg gtg aag tct	370

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aga ggt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc tgg gcc      1208
Arg Gly Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Ala
      295                      300                      305

tcc gtc agc aga gcc cca agt cca ccg gaa cat tca ctc cca tgg gct      1256
Ser Val Ser Arg Ala Pro Ser Pro Pro Glu His Ser Leu Pro Trp Ala
      310                      315                      320

tcg gag caa cct tca aga gat ctt tct acc tgc ctt tcc atg tca tga      1304
Ser Glu Gln Pro Ser Arg Asp Leu Ser Thr Cys Leu Ser Met Ser
      325                      330                      335

gaggaagaaa caagaatgac aagtgtatga ctgcctttga gctgtagttc ccgtttattt      1364

acacatgtgg atcctcgttt tccaagaaaa aaaaaa                                1400

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<210> 210
<211> 1062
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (128)..(544)

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<220>
<221> misc_feature
<222> (1)...(1062)
<223> n = a,t,c or g

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<400> 210
gcacgaggcg gatggggaaa caattgagat tgagggaggc aggcagagcg gagcgaaaac      60
aggaggacag aaatagcgaa gcaaggccaa gatcgggacc cccaccaggg aggtgcccag      120
tacagac  atg aaa gta agg cgg gga agc agc tca agc ctc acc cac cgc      169
      Met Lys Val Arg Arg Gly Ser Ser Ser Ser Leu Thr His Arg
      1                      5                      10

cct gcc ccc agc ccc gcc act ccc agg ctc ctc ggg act cgg cgg gtc      217
Pro Ala Pro Ser Pro Ala Thr Pro Arg Leu Leu Gly Thr Arg Arg Val
      15                      20                      25                      30

ctc ctg gga gtc tcg gag ggg acc ggc tgt gca gac gcc atg gag ttg      265
Leu Leu Gly Val Ser Glu Gly Thr Gly Cys Ala Asp Ala Met Glu Leu
      35                      40                      45

gtg ctg gtc ttc ctc tgc agc ctg ctg gcc ccc atg gtc ctg gcc agt      313
Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val Leu Ala Ser
      50                      55                      60

gca gct gaa aag gag aag gaa atg gac cct ttt cat tat gat tac cag      361
Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr Asp Tyr Gln
      65                      70                      75

acc ctg agg att ggg gga ctg gtg ttc gct gtg gtc ctc ttc tcg gtt      409
Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu Phe Ser Val
      80                      85                      90

ggg atc ctc ctt atc cta agt cgc agg tgc aag tgc agt ttc aat cag      457
Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser Phe Asn Gln

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gga gga gca cag ata ttt tcc tgt ata att cca gaa tgt ctt cag aga Gly Gly Ala Gln Ile Phe Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg 40 45 50	440
gcc atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac cac acc Ala Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn His Thr 55 60 65	488
ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act gag tac Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr 70 75 80	536
acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc ttg cat Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His 85 90 95	584
tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt ttt ttc Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe 100 105 110 115	632
acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca aat gaa Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu 120 125 130	680
tta tta ttt ctt cat gtt tat gaa ttt gat gaa gtg atg ttt cca aag Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Val Met Phe Pro Lys 135 140 145	728
aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga tcc aag Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys 150 155 160	776
cac tgc agt gtg tgt aac tgg tgt gtg cac cgt ttc gac cat cac tgt His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe Asp His His Cys 165 170 175	824
gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tac ttc ctc Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu 180 185 190 195	872
atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc gtc gcc att gtg Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val 200 205 210	920
agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta tac cag Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu Tyr Gln 215 220 225	968
gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac acg gtc Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp Thr Val 230 235 240	1016
ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc ttc atg Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met 245 250 255	1064
ctg ggc ttt gtc gtg gtt ctg agc ttc ctc ctg ggt ggc tac ctg ttg Leu Gly Phe Val Val Val Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu 260 265 270 275	1112
ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag tgg tac Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr 280 285 290	1160

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ccc cct tgg gaa tgg ggt agt gag gcc cca gac ttc acc ccc agc cca    1211
Pro Pro Trp Glu Trp Gly Ser Glu Ala Pro Asp Phe Thr Pro Ser Pro
      370                      375                      380

ctg cta aaa tct gtt ttc tga ca gatggggtttt ggggagtcgc ctgctgcact    1264
Leu Leu Lys Ser Val Phe  *
      385

acatgagaaa gggactccca tttgcccttc cctttctcct acagtccctt ttgtcttgtc    1324

tgtctctgggc tgtctgtgtg tgtgccattc tctggacttc agagccccct gagccagtcc    1384

tcccttccca gcctcccttt gggcctccct aactccacct aggctgccag ggaccggagt    1444

cagctggttc aaggccatcg ggagctctgc ctccaagtct acccttcctt tcccggactc    1504

cctctctgtcc cctcctttcc tccctccttc ctccactct ccttcctttt gcttccttgc    1564

cctttccccc tcctcaggtt ctccctcctt tctcactggg ttttccacct tctccttcc    1624

cttcttccct ggctcctagg ctgtgatata tatttttgta ttatctcttt ottcttcttg    1684

tggtgatcat cttgaattac tgtgggatgt aagtttcaaa attttcaaat aaagcctttg    1744

caagataaaa aaaaaaaaaa                                         1763

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<210> 209
<211> 1400
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (288)..(1301)

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<220>
<221> misc_feature
<222> (1)...(1400)
<223> n = a,t,c or g

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gaggtcacga gcccgcaaga agtctcgtat cgcgccccggg aggcgccgga gccagcggc    120

tggcgccaga tccaggctcc tggaagaacc atgtccggca gctactggtc atgccaggca    180

cacactgctg cccaagagga gctgctgttt gaattatctg tgaatgttgg gaagaggaat    240

gccagagctg ccggctgaaa attacccaac caagagaaat ctgcagg  atg gac ttt    296
                                   Met Asp Phe
                                   1

ctg gtc ctc ttc ttg ttc tac ctg gct tcg gtg ctg atg ggt ctt gtt    344
Leu Val Leu Phe Leu Phe Tyr Leu Ala Ser Val Leu Met Gly Leu Val
      5                      10                      15

ctt atc tgc gtc tgc tcg aaa acc cat agc ttg aaa ggc ctg gcc agg    392
Leu Ile Cys Val Cys Ser Lys Thr His Ser Leu Lys Gly Leu Ala Arg
      20                      25                      30                      35

```

acc gtg tct cga gag gat gga ggg gac ccc aac tct gcc aat ccc gga	443
Thr Val Ser Arg Glu Asp Gly Gly Asp Pro Asn Ser Ala Asn Pro Gly	
115 120 125	
ttt ctg gac tat ggt ttt gca gcc cct cat ggg ctc gca acc cca cac	491
Phe Leu Asp Tyr Gly Phe Ala Ala Pro His Gly Leu Ala Thr Pro His	
130 135 140	
ccc aac tca gac tcc atg cga ggt gat gga gat ggg ctt atc ctt gga	539
Pro Asn Ser Asp Ser Met Arg Gly Asp Gly Asp Gly Leu Ile Leu Gly	
145 150 155	
gag gca cct gcc acc ctg cgg cca ttc ctg ttc ggg ggc cgt ggg gaa	587
Glu Ala Pro Ala Thr Leu Arg Pro Phe Leu Phe Gly Gly Arg Gly Glu	
160 165 170	
ggt gtg gac ccc cag ctc tat gtc aca att acc atc tcc atc atc att	635
Gly Val Asp Pro Gln Leu Tyr Val Thr Ile Thr Ile Ser Ile Ile Ile	
175 180 185 190	
gtt ctc gtg gcc act ggc atc atc ttc aag ttc tgc tgg gac cgc agc	683
Val Leu Val Ala Thr Gly Ile Ile Phe Lys Phe Cys Trp Asp Arg Ser	
195 200 205	
cag aag cga cgc aga ccc tca ggg cag caa ggt gcc ctg agg cag gag	731
Gln Lys Arg Arg Arg Pro Ser Gly Gln Gln Gly Ala Leu Arg Gln Glu	
210 215 220	
gag agc cag cag cca ctg aca gac ctg tcc ccg gct gga gtc act gtg	779
Glu Ser Gln Gln Pro Leu Thr Asp Leu Ser Pro Ala Gly Val Thr Val	
225 230 235	
ctg ggg gcc ttc ggg gac tca cct acc ccc acc cct gac cat gag gag	827
Leu Gly Ala Phe Gly Asp Ser Pro Thr Pro Thr Pro Asp His Glu Glu	
240 245 250	
ccc cga ggg gga ccc cgg cct ggg atg ccc cac ccc aag ggg gct cca	875
Pro Arg Gly Gly Pro Arg Pro Gly Met Pro His Pro Lys Gly Ala Pro	
255 260 265 270	
gcc ttc cag ttg aac cgc tca ctc agt ggt cag cgt ttc ctg cac act	923
Ala Phe Gln Leu Asn Arg Ser Leu Ser Gly Gln Arg Phe Leu His Thr	
275 280 285	
tta cct ctc atg tgc gtt tcc cgg cct gat gtt gtg gtg gtg tgc ggc	971
Leu Pro Leu Met Cys Val Ser Arg Pro Asp Val Val Val Val Cys Gly	
290 295 300	
gtg ctc act ctc tcc ctc atg aac acc cac cca cct cgt ttc cgc agc	1019
Val Leu Thr Leu Ser Leu Met Asn Thr His Pro Pro Arg Phe Arg Ser	
305 310 315	
ccc tgc atg ctg ctc cag agg tgg gtg gga ggt gag ctg ggg gct cct	1067
Pro Cys Met Leu Leu Gln Arg Trp Val Gly Gly Glu Leu Gly Ala Pro	
320 325 330	
tgg gcc ctc atc ggt cat ggt ctc gtc cca ttc cac acc att tgt ttc	1115
Trp Ala Leu Ile Gly His Gly Leu Val Pro Phe His Thr Ile Cys Phe	
335 340 345 350	
tct gtc tcc cca tcc tac tcc aag gat gcc ggc atc acc ctg agg gct	1163
Ser Val Ser Pro Ser Tyr Ser Lys Asp Ala Gly Ile Thr Leu Arg Ala	
355 360 365	

acg tgg tgt gaa ctg aga ggt gat gag atg cgt aga tca tct gcc ccc 509  
 Thr Trp Cys Glu Leu Arg Gly Asp Glu Met Arg Arg Ser Ser Ala Pro  
                   30                  35                  40

tgc ctg gtg ggc agc cct ggc ccc acg tgc tga cccaggca cagaaaagcc 560  
 Cys Leu Val Gly Ser Pro Gly Pro Thr Cys \*  
                   45                  50

acatacgtgt actgggcacg ctctatggaa gaacggtgaa ttgttgctct ggcaaataat 620

atccagcaga gatcagtggg cccaggggtgc actggtaaga aatgggttcc agtcgattcc 680

tgtgtggttt tgaggatcat ggtgagctag gatctaccaa agcagctgtt taaaaagtg 740

tgaccatgct gacagcagac tcaagagagg gtgtggggcc gggtgcggtg gctcacgcct 800

gtaatccttg gccttgggag gccaaaggcg gctgatcgcc gggtagcgag atcgaattgg 860

gaa 863

<210> 208  
 <211> 1763  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (66)..(1232)

<400> 208

acggaattcc cgggtcgacg atttcgtgct gaaaatctgg gtcacagctg aggaagacct 60

cagac atg gag tcc agg atg tgg cct gcg ctg ctg tcc cac ctc 107  
 Met Glu Ser Arg Met Trp Pro Ala Leu Leu Ser His Leu  
           1                  5                  10

ctc cct ctc tgg cca ctg ctg ttg ctg ccc ctc cca ccg cct gct cag 155  
 Leu Pro Leu Trp Pro Leu Leu Leu Leu Pro Leu Pro Pro Pro Ala Gln  
   15                  20                  25                  30

gac tct tca tcc tcc cct cga acc cca cca gcc cca gcc cgc ccc ccg 203  
 Asp Ser Ser Ser Ser Pro Arg Thr Pro Pro Ala Pro Ala Arg Pro Pro  
                   35                  40                  45

tgt gcc agg gga ggc ccc tcg gcc cca cgt cat gtg tgc gtg tgg gag 251  
 Cys Ala Arg Gly Gly Pro Ser Ala Pro Arg His Val Cys Val Trp Glu  
           50                  55                  60

cga gca cct cca cca agc cga tct cct cgg gtc cca aga tca cgt cgg 299  
 Arg Ala Pro Pro Pro Ser Arg Ser Pro Arg Val Pro Arg Ser Arg Arg  
           65                  70                  75

caa gtc ctg cct ggc act gca ccc cca gcc acc cca tca ggc ttt gag 347  
 Gln Val Leu Pro Gly Thr Ala Pro Pro Ala Thr Pro Ser Gly Phe Glu  
   80                  85                  90

gag ggg ccg ccc tca tcc caa tac ccc tgg gct atc gtg tgg ggt ccc 395  
 Glu Gly Pro Pro Ser Ser Gln Tyr Pro Trp Ala Ile Val Trp Gly Pro  
   95                  100                  105                  110

tac tat ttt tta tcc ctt tct aac atc ttt ata ttg acg att ggc ctg 100  
 Tyr Tyr Phe Leu Ser Leu Ser Asn Ile Phe Ile Leu Thr Ile Gly Leu  
 10 15 20  
 acg tgt gcc tct ggc ccc ctt gac ttt acc cct gtg ttt ctg ctt gga 148  
 Thr Cys Ala Ser Gly Pro Leu Asp Phe Thr Pro Val Phe Leu Leu Gly  
 25 30 35 40  
 aag ggc tcc ctg aag tgc aaa tat ggt cct gtt gca cat ttg ccc cct 196  
 Lys Gly Ser Leu Lys Cys Lys Tyr Gly Pro Val Ala His Leu Pro Pro  
 45 50 55  
 gaa gct ctg gaa agc ggt ccc caa atc cca tcc gga tgt aac tgg aag 244  
 Glu Ala Leu Glu Ser Gly Pro Gln Ile Pro Ser Gly Cys Asn Trp Lys  
 60 65 70  
 gaa att cca aca tcc tcc tag tc cagccgaggg gggtcccacc acggatttcc 297  
 Glu Ile Pro Thr Ser Ser \*  
 75  
 ttttcagggc tcccattgca ttactggaca acttctaact attgaaaatt ttccattggg 357  
 agaattctcc gtgtgtcatt tttctgtagt tccatttaat gcagtgatag ttatttttta 417  
 tcttctgtgt tttctctact tcttgattaa attatgacct cctcaaattg aagggaata 477  
 taaactcatt tctttttatt atcccacagt aattgtcagg ctcagacttc tctgtgagca 537  
 tcaccgactg accagggtag cgctggctgg gatgttacat ggagcagtta cactagcatt 597  
 ttagtttcaa atggatgcag attcagc 624

<210> 207  
 <211> 863  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (387)..(542)

<400> 207  
 ccagggtgagg cacaggtggg tctgcaaggc cccttgagct ccaagcacct gcatgtgtct 60  
 aggcaaaacc tccagcacat cggatttccc ttgtgaagta cgtaaagcca cagattaagt 120  
 ggggatggat ctctcgctc tgcgttcaag ggggcaaata tccaggataa atgccccctt 180  
 ttctacacc attttccacc agccttgagg agtcagcttc ccatggcttc cttccaacgg 240  
 aagcaggaga aagggtggg ctagttaaac cgcagcactt tcagtttttag ggtgtgtcgt 300  
 gtaggttagt gatttgtgct ctgcagagac tctccaggga gagcaaaaag agcaggtgga 360  
 atcatcagct tggccagaag acgcag atg acg ccc cgt gag cca gct cag gaa 413  
 Met Thr Pro Arg Glu Pro Ala Gln Glu  
 1 5  
 aga cgg ccc cac ctt gaa ggg ccc acg ctg aaa gcc agt gat ggg gag 461  
 Arg Arg Pro His Leu Glu Gly Pro Thr Leu Lys Ala Ser Asp Gly Glu  
 10 15 20 25

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```
<220>  
<221> CDS  
<222> (284) .. (421)
```

```
<210> 206
<211> 624
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (29) .. (265)
```

<400> 206  
cgaatatggtt caggaaaaat ctttaatt atg aaa act ctg aaa atc ttc aca 52  
Met Lys Thr Leu Lys Ile Phe Thr  
1 5

ctggaagagc ccgccccctg aatctatgga gaaaagcggg ctaggccccc tcgggttctt 779  
ccccccccca ggggggggttt tggcgacatc c 810

```
<210> 204
<211> 743
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (224) .. (514)
```

<400>	204
atttggccct cgaggccaag aattcg'gcac gaggaatat ctttttttaa aacatacttt 60	
aaaaaatctt ttcttacctg tgaaagctta tggcacatag taggcattta gcaaagtgtg 120	
gtttccttcc ttttagaccg acatttggtt gggactgggt ttaactacct tgaggacttt 180	
tcttatctca cccatctcaa atgtctcctc ccctgtaggg tgt   atg gcc atc agc Met Gly Ile Ser 1 235	
tgc aag ttg ctt ctt ctg act aga gtc tgc tac ctg atc acc ccg tta Cys Lys Leu Leu Leu Thr Arg Val Cys Tyr Leu Ile Thr Pro Leu 5                10               15            20 283	
gat ctt gag agg ttt ccc ttc cca aac act gag cag gtg aca ttt ccg Asp Leu Glu Arg Phe Pro Phe Pro Asn Thr Glu Gln Val Thr Phe Pro 25                  30              35 331	
gaa cgc aga gtt agc gtc ttc ctg ctg cct ctg agc tgg tgt ttg gac Glu Arg Arg Val Ser Val Phe Leu Leu Pro Leu Ser Trp Cys Leu Asp 40                  45              50 379	
aca agg ctg ccc aga gag cct ggc tgc agg tgt cga cac agc tct cca Thr Arg Leu Pro Arg Glu Pro Gly Cys Arg Cys Arg His Ser Ser Pro 55                  60              65 427	
cag gac gtg gtt ggc ggc agt cac ctg gtc acc aca act ctt cta agc Gln Asp Val Val Gly Gly Ser His Leu Val Thr Thr Thr Leu Leu Ser 70                  75              80 475	
ctc cca gct cgg gaa ttc tgg acc tct tgc atc ctc taa attggatgct Leu Pro Ala Arg Glu Phe Trp Thr Ser Cys Ile Leu * 85                90                  95 524	
gtctgatatt tcmetaaggga taccatgctt gatgagatca aaggaggaga ggatgactca 584	
gaaaagaccc agaagagctc acagtgtctt tagcaggatg cttagtgaca tggagtcttc 644	
tgacagcaat agtgcttgga gacattttta cacctatggc cacagggccc atgcatacac 704	
cccccccccc cccccacaca aaacctgggtg acctaaaggy 743	

<210> 205

**PCT/US01/02623**

<400> 203

285



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cta ctt att act ctt caa ttc cat ttc aga gtc tgt tac gtg aac ata      301
Leu Leu Ile Thr Leu Gln Phe His Phe Arg Val Cys Tyr Val Asn Ile
    65                      70                      75

att acc ctt atc cct ctt gca caa atc ttt ctt taa tctg ttggatgact      351
Ile Thr Leu Ile Pro Leu Ala Gln Ile Phe Leu *
    80                      85                      90

ctgaaaggat tagtttcagt ttggggcctg agctgtgtcc agacacacaa ctgctattag      411

ttcctaccat agttctacct gggtcagaag aatgagaaaa ataatcctta ctttttcctc      471

ctctatgagc aggaggtgct tactttttac tgatttgacc agctgaacat ttaagataa      531

tattcagcac tgtagatgaa gattagaaat tactgcgcaa actttaagtg agaataaaag      591

aattttgtggc gttctacgag actctaaaca cactatcttc cctattgtct ccttaattca      651

aacaagcatt tgggcttttt tcttcattcc actcgacccc tccccgaagc tcaccgccct      711

tcgcccctcc ccgctcccc ccttcacccc tctcc                                746

<210> 202
<211> 824
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (527) .. (775)

<400> 202
gggctcgcgc gggggccggt gtagaggggg aagggcgaga aggggggggg gggagtgaag      60
caatggggga gatggcgagg cggtgcagtg ggtggggagg ccggtcgttg ggcgcggtgg      120
ggcgaggaaa gggaaggggg gtcaggaggg gtgggggtgag ggggcaaggg caggggggtg      180
gcgcccaggg tgaggggtg gtagggaggg gggcgggggc gacgcgggga taaaaggacg      240
gagggatggc ggcaggtggt ggggttgggc agttgcgatg ggggtgtggt catgtggcag      300
tgaaaagtag agggagaaag atctcggcgc ttggcaaagg cgctggtaac tagttttcta      360
gtagtctgtg cactgtgctt tcatagagcc atctgtaatc tatcttttct tggcatctgt      420
gacgctgggg ttattttctc cccacacttt gtctgctctg acccttataa tgaaaccaa      480
ggttaaatgt agactcactc aacaccacac acattaaaac aattgg      atg gaa aat      535
                                Met Glu Asn
                                1

aat ctc atc ttg aca tgc tgg ggg aga tgt gct gca cac cca gta gag      583
Asn Leu Ile Leu Thr Cys Trp Gly Arg Cys Ala Ala His Pro Val Glu
    5                      10                      15

tta atg gga gtt aca gcc aaa acc aag gtg aag cct ctg ctc cca agg      631
Leu Met Gly Val Thr Ala Lys Thr Lys Val Lys Pro Leu Leu Pro Arg
    20                      25                      30                      35

```

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<210> 201
<211> 746
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (65)..(337)
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<400> 201															
atttggccct cgaggccaag aattcggcac gaggatttga ccttcttaaa tgtgaacatt															60
tcat atg ttc ctt gtg ttt tgt aat ata att act gtc atc acc atg aca															109
Met Phe Leu Val Phe Cys Asn Ile Ile Thr Val Ile Thr Met Thr															
1 5 10 15															
tct tta ttt ctt att ctt ctc tca tgt ata ttt att ttg ata acc tgt															157
Ser Leu Phe Leu Ile Leu Ser Cys Ile Phe Ile Leu Ile Thr Cys															
20 25 30															
tgc tat aaa tgt aga tac att tct ttc tcc ttt aca ttt tcc gtc aca															205
Cys Tyr Lys Cys Arg Tyr Ile Ser Phe Ser Phe Thr Phe Ser Val Thr															
35 40 45															
ccc tcc ggt ttc ttt gtt agc atc ctc cag tat ctt gcc cac att ctc															253
Pro Ser Gly Phe Phe Val Ser Ile Leu Gln Tyr Leu Ala His Ile Leu															
50 55 60															

<400> 199  
gacggagggtg cgccaaggat ccccggtggcc at atg gcg cgt ccg act agc agt 53  
Met Ala Arg Pro Thr Ser Ser  
1 5

cta tgc ctg ctt ctc tac ttc ttc tct act ggt aaa agc gtg cct gta 101  
Leu Cys Leu Leu Leu Tyr Phe Phe Ser Thr Gly Lys Ser Val Pro Val  
10 15 20

tcc atc tta ccc ggc gtt gtg cgc atg ctg ctg cca ccg cct cct cat 149  
Ser Ile Leu Pro Gly Val Val Arg Met Leu Leu Pro Pro Pro His  
25 30 35

ctt ctg ccc ggc caa ccg gcc tgc ccc gct gca gtg atg tgc gac aag 197  
Leu Leu Pro Gly Gln Pro Ala Cys Pro Ala Ala Val Met Cys Asp Lys  
40 45 50 55

gag ttc atg tgg gcc ctg aaa aac gga gac ttg gat gag gtg aaa gac 245  
Glu Phe Met Trp Ala Leu Lys Asn Gly Asp Leu Asp Glu Val Lys Asp  
60 65 70

tat gtg gcc aag gga gaa gat gtc aac cgg aca cta gaa ggt gga agg 293  
Tyr Val Ala Lys Gly Glu Asp Val Asn Arg Thr Leu Glu Gly Gly Arg  
75 80 85

aaa cct ctt cat tat gca gca gat tgt ggg cag ctt gaa atc ctg gaa 341  
Lys Pro Leu His Tyr Ala Ala Asp Cys Gly Gln Leu Glu Ile Leu Glu  
90 95 100

ttt ctg ctg ctg aaa gga gca gat att aat gct cca gat aaa cat cat 389  
Phe Leu Leu Leu Lys Gly Ala Asp Ile Asn Ala Pro Asp Lys His His  
105 110 115

att act cct ctt ctg tct gct gtc tat gag ggt cat gtt tcc tgt gtg 437  
Ile Thr Pro Leu Leu Ser Ala Val Tyr Glu Gly His Val Ser Cys Val  
120 125 130 135

aaa ttg ctt ctg tca aag tga gc tccagtgtg tgaatctctg cttaaagcac 490  
Lys Leu Leu Leu Ser Lys \*  
140

catatgacat tcacctgtaa tcccagcact tcgaaaggcc aaggcgggag gatcaattga 550

gcagcctggg caacataggg agacctcatc tctacaaaaa ataaaaataa attagccagg 610

tatggtggtg catgcctggn gtcccagcca ctactcaggt ggttgagttg agaggattgc 670

ttgagcccac ggaattgagg ctgcagcgag tggatgatcac accactgcac tccagcctgg 730

gtgacagagt gagacctct ctctaannaa aaaaa 765

<210> 200  
<211> 703  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (227) .. (376)

<400> 200

<400> 198

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<210> 199
<211> 765
<212> DNA
<213> Homo sapiens
```

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<220>
<221> CDS
<222> (33) .. (458)

<220>
<221> misc_feature
<222> (1) ... (765)
<223> n = a,t,c or g
```

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<213> Homo sapiens

<220>
<221> CDS
<222> (127) .. (294)

<400> 197
tatcgtcgta aacatcacta cgcctagctt ggcacgagcc taatacagac cctatctcaa      60
aaacaaacaa aaagagattg ctcatgggca cttgggccct gaatgtgcta atgagatgtg      120
gcattc    atg ggc cat ctg ctg tgt gtg tgg ggt ttt aca tac atc ctt      168
          Met Gly His Leu Leu Cys Val Trp Gly Phe Thr Tyr Ile Leu
              1              5              10

cct tgt ata tcc tta agg cat tca cct ctt cag cct cca gga tgg gaa      216
Pro Cys Ile Ser Leu Arg His Ser Pro Leu Gln Pro Pro Gly Trp Glu
   15              20              25              30

ggt ttt tgc agg aat gta tct ttt cct ctc ttg agg gcc tca ctt gct      264
Gly Phe Cys Arg Asn Val Ser Phe Pro Leu Leu Arg Ala Ser Leu Ala
          35              40              45

cct cac cat agg agg aag gac gga ttt atc t gattggagag actgtaaata      315
Pro His His Arg Arg Lys Asp Gly Phe Ile
          50              55

aagactgact ggaacatatg gaccaggggc gggctctgctg catggacgtt gggctgtgtg      375
ggttgctcac tctcctgccc tcttcttgcc tatgcagaac tgatttctca cctctgcctt      435
cctgtctgtt cctggtgggt taggaacgta caggagagaa gggatgaaga ttagtttctc      495
ttaccccctg aagcattatt ttccacaggg cctctccacc tgttcagtgt tgagtaagtg      555
ctgaatgagt ggacagggaa acagccttg gaaaagcttac tatcccgcac atccctacta      615
agtgatggca atgaatcagg ggagccgggt gtccacaccc caagcgccca cccttggtgg      675
gttgtaagaa tcccctgggt agggagggca tgacggtaaa catctccctc cgggttatct      735
cctgccatct ggctgggttg atcccccttc taatccccct gggggggggt ccccccttcc      795
aatcaggctt gggggaccac agggggcctt tggtttacta acctggggcc tggccacaac      855
cgttatttta tggggacccc cgaagccatg gggcccaacc cttttgggcc ctctttttct      915
caacattcat atgcgtgcc                                          934

```

```

<210> 198
<211> 814
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (232) .. (483)

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<220>
<221> misc_feature
<222> (1) ... (814)

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aag aca gac cag ttc ctg agg gat gca gtg gaa acc aga ctg aga atg 635  
Lys Thr Asp Gln Phe Leu Arg Asp Ala Val Glu Thr Arg Leu Arg Met  
180 185 190

ctg atc cca tac att gag cac tgg ccc cgg gcc ctc agc atc ctc atg 683  
Leu Ile Pro Tyr Ile Glu His Trp Pro Arg Ala Leu Ser Ile Leu Met  
195 200 205

ctc cct cac aac atc ccg tcc agc ctg agc ctg ctc acc agc atg gtg 731  
Leu Pro His Asn Ile Pro Ser Ser Leu Ser Leu Leu Thr Ser Met Val  
210 215 220

gat gac atg tgg cat tac gct ggg gac cag tcc act gat ttt aac tgg 779  
Asp Asp Met Trp His Tyr Ala Gly Asp Gln Ser Thr Asp Phe Asn Trp  
225 230 235 240

tac acc cgc cga gcc atg ctg gct gcc atc tac aac aca aca gag ctg 827  
Tyr Thr Arg Arg Ala Met Leu Ala Ala Ile Tyr Asn Thr Thr Glu Leu  
245 250 255

gtg atg atg cag gac tcc tct cca gac ttt gag gac act tgg cgc ttc 875  
Val Met Met Gln Asp Ser Ser Pro Asp Phe Glu Asp Thr Trp Arg Phe  
260 265 270

ctg gaa aac cgg gtt aat gat gca atg aac atg ggc cac act gcc aag 923  
Leu Glu Asn Arg Val Asn Asp Ala Met Asn Met Gly His Thr Ala Lys  
275 280 285

cag gta aag tcc aca gga gag gca ctg gtg caa gga ctc atg ggt gca 971  
Gln Val Lys Ser Thr Gly Glu Ala Leu Val Gln Gly Leu Met Gly Ala  
290 295 300

gca gtg acg ctc aag aac ttg aca ggt cta aac cag cgt cgg tga gag 1019  
Ala Val Thr Leu Lys Asn Leu Thr Gly Leu Asn Gln Arg Arg \*  
305 310 315

gaaggggtat aagctacaat gcctagaaga gaatgagcgg acagattgaa agagctttga 1079

aaagtataag gtgccatcca cataacctgg tgttcacgag aacacactaa aggactcctg 1139

agtcactacc acagccacct ggaaaccaca aggcatttga tgctaccgtt ctggtcaggg 1199

attgggctgc ttcttcagtt cctaatacca gaccaagcct cctgatgcct ttctgcaactg 1259

caactgtgtg attgaaaaat gagatgttca tccaagcagt caagccacag aaaccagca 1319

tgtccctgtc acaatctcat gggcaccttg atcatgtctt aaccttcct taaccttggg 1379

gctcccaagc cagagtcaag gtctgacgcc acctcaaggt gacagctcat ctccagcaca 1439

gcacaggcgt gtgcacacag aggtgttctt tgcagcccc tccctctcag gtgtcctgag 1499

atgctgctcc tgggagcccc ctcaaaaaac tgctcacct gagacaagtg cctgctggac 1559

agaggtgtga ttccaggcct ggtgtcacat gacaccagca tgcattgcag gattattagt 1619

gtatttttgag tctgtaaaaa taataaatat gtttgaagta gtaaaaaaaa aaa 1672

<210> 197  
<211> 934  
<212> DNA

cactgagggga ggcaaagtgc agcaggaatt ataacttgaa ttccaaaccc agactatgcc 729  
tagagcaagg gttctccacc ctggatgtgt cacaagccag caggatgctt tcaccccccc 789  
ccagcaacac caagggaacc cccccaacca ccagtggcac ccatcaagcc ccccc 844

<210> 196  
<211> 1672  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (60)..(1016)

<400> 196  
cctgcgggtac cgggtccggaa ttcccgggtc gacccacgcg tccggtgcc gcttccaaa 59  
atg gcg gcg gcg gta tct ggt gcg ctt ggc cgg gcg ggc tgg agg 107  
Met Ala Ala Ala Val Ser Gly Ala Leu Gly Arg Ala Gly Trp Arg  
1 5 10 15  
ctc ctg cag ctg cga tgc ctg ccc gtg gcc cgt tgc cga caa gcc ctg 155  
Leu Leu Gln Leu Arg Cys Leu Pro Val Ala Arg Cys Arg Gln Ala Leu  
20 25 30  
gtg ccg cgt gcc ttc cat gct tca gct gtg ggg cta agg tct tca gat 203  
Val Pro Arg Ala Phe His Ala Ser Ala Val Gly Leu Arg Ser Ser Asp  
35 40 45  
gag cag aag cag cag cct ccc aac tca ttt tct cag cag cat tct gag 251  
Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe Ser Gln Gln His Ser Glu  
50 55 60  
aca cag ggg gca gaa aaa cct gat cca gag tct tct cat tca ccc ccc 299  
Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu Ser Ser His Ser Pro Pro  
65 70 75 80  
agg tat aca gac cag ggc ggc gag gag gag gac tat gaa agt gag 347  
Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu Asp Tyr Glu Ser Glu  
85 90 95  
gag cag ttg cag cac cgc atc ctg acg gca gcc ctt gag ttt gtg ccc 395  
Glu Gln Leu Gln His Arg Ile Leu Thr Ala Ala Leu Glu Phe Val Pro  
100 105 110  
gcc cac ggg tgg aca gca gag gcg att gca gaa gga gcc cag tct ctg 443  
Ala His Gly Trp Thr Ala Glu Ala Ile Ala Glu Gly Ala Gln Ser Leu  
115 120 125  
ggg ctc tcc agt gca gca gcc agc atg ttc ggg aag gat ggc agt gag 491  
Gly Leu Ser Ser Ala Ala Ala Ser Met Phe Gly Lys Asp Gly Ser Glu  
130 135 140  
cta ata ctg cat ttt gtg acc cag tgc aat acc cgg ctc aca cgt gtg 539  
Leu Ile Leu His Phe Val Thr Gln Cys Asn Thr Arg Leu Thr Arg Val  
145 150 155 160  
cta gaa gag gag cag aag ctg gta cag ttg ggc cag gcg gag aag agg 587  
Leu Glu Glu Glu Lys Leu Val Gln Leu Gly Gln Ala Glu Lys Arg  
165 170 175

gcacctgtgc ataccgcatg agccaccaga ccgtcatgct ctgtgacttg tctgtctgcc 485  
 caattctatt ttgagcttct tgagggcagg gatctcattt tttatctctg tatcttcagt 545  
 ggccggcaca ttgagcctgc tcaatgaatg cgtgagagaa tggaagtacg gaagaagagc 605  
 gacagcctga cagcgcccca aatgttgctc cttactctaa ggcttctga tcacaccac 665  
 caaaaactca tgaggcccggt cgaaatgggt ctagccctga caaggggact ttttaattca 725  
 ccggcgcaacc ccctctcgcc ctccaggacg gacggatgat cgcacctccc cctctctggg 785  
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 taatgaacac aggccctgga accatcatct gagtatagta atttgagata taattttaag 180  
 attactggaa gacagtgtaa taggcttg atg tct gtc ctc atc tgg tgt ttg 232  
 Met Ser Val Leu Ile Trp Cys Leu  
 1 5  
 ata ttc ttt cct ctt gag tat tcc agg ccc aag aga ggc ttg aaa gtt 280  
 Ile Phe Phe Pro Leu Glu Tyr Ser Arg Pro Lys Arg Gly Leu Lys Val  
 10 15 20  
 gat aat gtg tgt ttt tcc act gtt gcc ctt tca aca ggg tct aga att 328  
 Asp Asn Val Cys Phe Ser Thr Val Ala Leu Ser Thr Gly Ser Arg Ile  
 25 30 35 40  
 tcc aac tgg tct aac tgt gaa act tgt ctt ctt gct gaa atg ttt ttc 376  
 Ser Asn Trp Ser Asn Cys Glu Thr Cys Leu Leu Ala Glu Met Phe Phe  
 45 50 55  
 ctt gat ttg ggg ttt tct tga aa ttattgccaa agtcatatga cataaattgt 429  
 Leu Asp Leu Gly Phe Ser \*  
 60  
 aaatgccaca aaatttatcc tgctattctt gagataaaac atggaaatct gaaagttgaa 489  
 ggctaggact tggaagaga acttaagaag ctaccatttc aaaatcotta atgaagggat 549  
 tatattacct gcttgctttg accttgaaag tctcttgaat gatcttggtc atctgtcaga 609  
 caatccctgc gtcaatgatt aataaaaaca ctctagcctg aggggtgggct tgtgtctgaa 669



gct gag cca aga gca gat ggc agc cgc cgg act aca cgc tat gac att 489  
Ala Glu Pro Arg Ala Asp Gly Ser Arg Arg Thr Thr Arg Tyr Asp Ile  
135 140 145

gac atg acc aag tgt atc tac tgt ggt ttc tgc cag gaa gcc tgc cct 537  
Asp Met Thr Lys Cys Ile Tyr Cys Gly Phe Cys Gln Glu Ala Cys Pro  
150 155 160

gtt gac gct atc gtg gag ggc ccc aac ttt gag ttc tcc acc gag acg 585  
Val Asp Ala Ile Val Glu Gly Pro Asn Phe Glu Phe Ser Thr Glu Thr  
165 170 175

cat gag gag ttg ctg tac aac aag gag aag cta ctc aac aat ggt gac 633  
His Glu Glu Leu Leu Tyr Asn Lys Glu Lys Leu Leu Asn Asn Gly Asp  
180 185 190 195

aag tgg gag gcc gag atc gcg gcc aac atc cag gct gac tac ctg tat 681  
Lys Trp Glu Ala Glu Ile Ala Ala Asn Ile Gln Ala Asp Tyr Leu Tyr  
200 205 210

cgg tga cccggccacc ggtgaccttg ccacctggcc agccttggtg cccctatagc 737  
Arg \*

ccataaagaa actctgatcc caaaaaaaaa aaaaaaaaa 775

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atg ata gag ttg gct ttt gcc tca ttc tta aaa tgt gct tca ttt tct 107  
Met Ile Glu Leu Ala Phe Ala Ser Phe Leu Lys Cys Ala Ser Phe Ser  
1 5 10 15

ttg gtg ata ctg gtc tct ttt agt ttc cca ctt tgg ttt ttc ctc agc 155  
Leu Val Ile Leu Val Ser Phe Ser Phe Pro Leu Trp Phe Phe Leu Ser  
20 25 30

tgc ttt gca tgc tct tac tca ttt tcc tgc ctc tta agt aga att tca 203  
Cys Phe Ala Cys Ser Tyr Ser Phe Ser Cys Leu Leu Ser Arg Ile Ser  
35 40 45

atc ctt agc ccc ttt tgt cac ctt ctt cct agg caa tcc cat gac ctt 251  
Ile Leu Ser Pro Phe Cys His Leu Leu Pro Arg Gln Ser His Asp Leu  
50 55 60

tgt act aat gat ttg taa atctct agtcccagcc taggcctttg tgtaaaactcc 305  
Cys Thr Asn Asp Leu \*  
65 70

tccattaagt gcctactagg agatctgcat gcctagatgt tctaattgtga tctcaaactg 365

aacatagtca aaactcaact cccgtgcacc cctgtcatgc catccacacc atgccgtgct 425

<400> 193																	
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Met Tyr Arg																	
1																	
ctg agc tca tca atg ctg tta cgg gct ttg gcc cag gcc atg cgc aca																	105
Leu Ser Ser Ser Met Leu Leu Arg Ala Leu Ala Gln Ala Met Arg Thr																	
5 10 15																	
gga cat ctt att gga caa agc ctt cat agc agc gca gtg gcg gca acg																	153
Gly His Leu Ile Gly Gln Ser Leu His Ser Ser Ala Val Ala Ala Thr																	
20 25 30 35																	
tac aag tat gtg aat aag aag gaa cag gag tct gag gtg gac atg aag																	201
Tyr Lys Tyr Val Asn Lys Lys Glu Gln Glu Ser Glu Val Asp Met Lys																	
40 45 50																	
tcc gaa act gac aat gca gct cgg att ctg atg tgg aca gaa ctc atc																	249
Ser Glu Thr Asp Asn Ala Ala Arg Ile Leu Met Trp Thr Glu Leu Ile																	
55 60 65																	
cga gga ctg ggc atg acc cta aga tac ctc ttt cga gag cct gcc acc																	297
Arg Gly Leu Gly Met Thr Leu Arg Tyr Leu Phe Arg Glu Pro Ala Thr																	
70 75 80																	
atc aac tac ccc ttt gag aag ggc cca ctg agt ccg cgc ttc cgt ggg																	345
Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg Gly																	
85 90 95																	
gag cat gca ctg cgc cgc tac ccg tct ggg gag gag cgt tgc atc gcc																	393
Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile Ala																	
100 105 110 115																	
tgc aag ctc tgt gag gcc atc tgt cct gca cag gcc atc acc att gag																	441
Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile Glu																	
120 125 130																	

gag gat ctg ctt tgc tgt tac tct tcc atg gtc tct cgg aag aac aaa	472
Glu Asp Leu Leu Cys Cys Tyr Ser Ser Met Val Ser Arg Lys Asn Lys	
75 80 85	
atc agg cgc aat cgg cag cta gag agg ctg gct tcc cac atc aag gaa	520
Ile Arg Arg Asn Arg Gln Leu Glu Arg Leu Ala Ser His Ile Lys Glu	
90 95 100 105	
ctg gag ccc aag ctg aag aag att ctg cag atg aac cca agg atg cgg	568
Leu Glu Pro Lys Leu Lys Lys Ile Leu Gln Met Asn Pro Arg Met Arg	
110 115 120	
aag ttc caa gtg gat atg acc ttg gat gcc aac aca gcc aac aac ttc	616
Lys Phe Gln Val Asp Met Thr Leu Asp Ala Asn Thr Ala Asn Asn Phe	
125 130 135	
ctc ctc att tct gac gac ctc agg agc gtc cga agt ggg cgc atc aga	664
Leu Leu Ile Ser Asp Asp Leu Arg Ser Val Arg Ser Gly Arg Ile Arg	
140 145 150	
cag aat cgg caa gac ctt gcc gag aga ttt gac gtg tcc gtt tgc atc	712
Gln Asn Arg Gln Asp Leu Ala Glu Arg Phe Asp Val Ser Val Cys Ile	
155 160 165	
ctg ggc tcc cct cgc ttt acc tgt ggc cgc cac tgc tgg gag gtg gac	760
Leu Gly Ser Pro Arg Phe Thr Cys Gly Arg His Cys Trp Glu Val Asp	
170 175 180 185	
gtg gga aca agc aca gaa tgg gac ctg gga gtc tgc aga gaa tct gtt	808
Val Gly Thr Ser Glu Trp Asp Leu Gly Val Cys Arg Glu Ser Val	
190 195 200	
cac cgc aaa ggg agg atc cag ctg acc aca gag ctt gga ttc tgg act	856
His Arg Lys Gly Arg Ile Gln Leu Thr Thr Glu Leu Gly Phe Trp Thr	
205 210 215	
gtg agt ttg agg gat gga ggc cgc ctc tct gcc agc acc gtg ccg ctg	904
Val Ser Leu Arg Asp Gly Gly Arg Leu Ser Ala Ser Thr Val Pro Leu	
220 225 230	
act ttc ctc ttc gta gac cgc aag tta cag cga gtg ggg att ttt ctg	952
Thr Phe Leu Phe Val Asp Arg Lys Leu Gln Arg Val Gly Ile Phe Leu	
235 240 245	
gat atg ggc atg cag aac gtt tcc ttt ttt gat gct gaa ggt ggt tcc	1000
Asp Met Gly Met Gln Asn Val Ser Phe Phe Asp Ala Glu Gly Gly Ser	
250 255 260 265	
cat gtc tat aca ttc agg agc gta tct gct gag gag cca ctg tgc cca	1048
His Val Tyr Thr Phe Arg Ser Val Ser Ala Glu Glu Pro Leu Cys Pro	
270 275 280	
ttt ttg gct cct tca att cca cct aat ggt gat caa ggt gtc ttg agc	1096
Phe Leu Ala Pro Ser Ile Pro Pro Asn Gly Asp Gln Gly Val Leu Ser	
285 290 295	
atc tgt cct ttg atg aac tca ggc act act gat gct cca gtc cgt cct	1144
Ile Cys Pro Leu Met Asn Ser Gly Thr Thr Asp Ala Pro Val Arg Pro	
300 305 310	
ggg gag gcc aaa taa gccctcactc caaaaaaac aaaaaacagg gtaagaaaat	1199
Gly Glu Ala Lys *	
315	

cta cgt gga cgt tcg gcc aag gga cca agg tgg aaa tca aac gaa ctg 916  
 Leu Arg Gly Arg Ser Ala Lys Gly Pro Arg Trp Lys Ser Asn Glu Leu  
 285 290 295

tgg ctg cac cat ctg tct tca tct tcc cgc cat ctg atg agc agt tga 964  
 Trp Leu His His Leu Ser Ser Ser Ser Arg His Leu Met Ser Ser  
 300 305 310

aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga gaggccaaag 1024

tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt gtcacagagc 1084

aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact 1144

acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc tcgcccgtca 1204

caaagagctt caacagggga gagtgttaga gggagaagtg ccccccactg ctcctcagtt 1264

ccagccttga cccctccca tcctttgggc cttttgaccc tttttccac agggggacct 1324

tacccctatt tgcggttctt ccaggttcat cttttcaact tnaacccct tcttcttct 1384

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canctgttaa aaaa 1458

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 <213> Homo sapiens

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acgggggggtg gggggatgtg cttgagtgtt tgtactcatg gtcttattct cggagtgaca 180

aagctggaac acaatacctc tatgc atg aaa agg ttg tca ctt gtc aca act 232  
 Met Lys Arg Leu Ser Leu Val Thr Thr  
 1 5

aac agg ctt tca cct cat gga aat ttt ttt acc ttg tgt act ttt ccc 280  
 Asn Arg Leu Ser Pro His Gly Asn Phe Phe Thr Leu Cys Thr Phe Pro  
 10 15 20 25

ctg gca gtg gac atg gct gca ctc ttc caa gaa gca agc agc tgt ccc 328  
 Leu Ala Val Asp Met Ala Ala Leu Phe Gln Glu Ala Ser Ser Cys Pro  
 30 35 40

gtc tgc tca gac tat ctg gaa aaa cca atg tcc ctg gag tgt gga tgc 376  
 Val Cys Ser Asp Tyr Leu Glu Lys Pro Met Ser Leu Glu Cys Gly Cys  
 45 50 55

gcc gtc tgc ctc aag tgc att aat tca ctg cag aag gag ccc cat ggg 424  
 Ala Val Cys Leu Lys Cys Ile Asn Ser Leu Gln Lys Glu Pro His Gly  
 60 65 70

agg tgt ttt cat ttg gtg atc agg act gaa cag aga gaa ctc acc atg	148
Arg Cys Phe His Leu Val Ile Arg Thr Glu Gln Arg Glu Leu Thr Met	
30 35 40	
gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt gtc	196
Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val	
45 50 55	
cag tgt gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct	244
Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro	
60 65 70	
ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc	292
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser	
75 80 85 90	
agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag	340
Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
95 100 105	
tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac	388
Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp	
110 115 120	
tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg	436
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr	
125 130 135	
ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat	484
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr	
140 145 150	
tac tgt gcg aaa tcc cat ccg ggg tat tac tat gat agt agt ggt tac	532
Tyr Cys Ala Lys Ser His Pro Gly Tyr Tyr Tyr Asp Ser Ser Gly Tyr	
155 160 165 170	
tcc tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc	580
Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser	
175 180 185	
tca agt gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct	628
Ser Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser	
190 195 200	
gta gga gac aga gtc acc atc act tgc cgg gcc agt cag agt att agt	676
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser	
205 210 215	
agc tgg ttg gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc	724
Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu	
220 225 230	
ctg atc tat aag gcg tct agt tta gaa agt ggg gtc cca tca agg ttc	772
Leu Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe	
235 240 245 250	
agc ggc agt gga tct ggg aca gaa ttc act ctc acc atc agc agc ctg	820
Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu	
255 260 265	
cag cct gat gat ttt gca act tat tac tgc caa cag tat aat agt tat	868
Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr	
270 275 280	

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tct tac tgg ttt gta aga ctt ctt tct att aat aga ggt tgg aaa tag      682
Ser Tyr Trp Phe Val Arg Leu Leu Ser Ile Asn Arg Gly Trp Lys  *
      35                      40                      45

cagttatcta ggtttttaaat gttggtttga taaacactga attttactta gtttgcatta    742
gagagcttac tgtaactct taaacattta aattccctgt tctcagttct aattttcagt    802
gtgaaatcag gtaagataca tttgcagggtg aaaaagtttg aaatgtaaaa agataaccaa    862
attaatttaa tatttccttg ggaatttgat tactttttct gggagaggag ttctgggcaa    922
caacataaat actgttattt gtggatattt gcaggttacg tttggtcttc aaataagtca    982
acattatttt ctttcacaaa acttggtttt ctggctttct ataatttccc aattaacatt   1042
taaataaaag accaaattaa acaattaaac tttatttaat ttggtctttt gtttaaattgc   1102
tttgtggcta cctagcttac cttttcagct ttttaaggaaa aaaaaaatca gaacttttta   1162
ttttggttcg gtcggagaca gcctcactct ggcaaccagc ctgcaatgca agcgcgtgat   1222
cttagcttac tggcacctct ccttccaggg tcaaaaaaat ccccttgctt aagttccccc   1282
cctaccccat cattgggatt atagccacgc gcgccagccc agctaatttt ggggtaccagg   1342
tttctcattt ccttctggtg gcgcgaaccc cgccctaag acctccctct ccggcgctaa   1402
cggggggatc cgcgacctct cctccttgg cgccctccc cccgtctacg tctccataag   1462
tgctgcctgc ttgcgcggcc cgcccgcccc acagctctgc tcccctctgg cgcgctgggc   1522
cccgctccac tagaccgtat accttcttcc ctgcgcgcct ggccctcaca ccgatacca   1582
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 <213> Homo sapiens

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<220>  
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      1                      5                      10

aag aga tct ctc gag gat ccg aat tcg cgg ccg cgt cga cgg att ttc      100
Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro Arg Arg Arg Ile Phe
      15                      20                      25

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gac cag ggc cac agc cat ctg ggg gac ccc t gaggatctac ctgcccaggc 1257  
 Asp Gln Gly His Ser His Leu Gly Asp Pro  
 395 400

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 tcaccaggct ttgcaaacc agcctcccag tgctcatttg ggaatgctca tgagttactc 1497  
 cattcaaggg tgagggagta gggagggaga ggcaccatgc atgtgggtga ttatctgcaa 1557  
 gctgtttgc cgtgatgctg gaagcctgtg ccactacatc ctggagtctg aactgagcc 1617  
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 tacactagcg cgcgacagct agagcgatga cggcgaggac gtctcgagc ctaccagcaa 1797  
 cggaagacg tgctcccgg cgtcgtatgg attaacaagc tccaagtagg gtgtacaacg 1857  
 ccgcagcatg aactcccagg 1877

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<220>  
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 <222> (539) .. (682)

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 ttctagacct ttggatagcc attaatatgg ttccacgtta ataacagtgg aaccatactg 180  
 tatgttctgt ttgtgttttc agtggaaaaa cattacagaa atactctgaa caaccttctg 240  
 tcaagtaaatt ttttcgagaa cttatatgat tatagatctg aactaattta tttaatcaat 300  
 ctggtatttg ccttcctttt tattttctag gttctggctt ttataaacat tgaaaatata 360  
 ctcataggtc agtctttgag tgttcttatt ttcttgggat aaagtgaatt gctgagtcaa 420  
 aagaatttgc tcattttcaa tgcatttgat acatactacc acattgcttt cagaaaagtt 480  
 atgctagttt tcccaaccag cgtttgatgg gcaaaaaaaa cctggtgaga ttgaattt 538  
 atg ttt att ggg ctt ggt att tct ttt tta aat tgc ccc tcg ctt ttt 586  
 Met Phe Ile Gly Leu Gly Ile Ser Phe Leu Asn Cys Pro Ser Leu Phe  
 1 5 10 15  
 gct cat ttt att ctc ttt tgc cca ttg ccc ctc ttt ggg ata ttt atc 634  
 Ala His Phe Ile Leu Phe Cys Pro Leu Pro Leu Phe Gly Ile Phe Ile  
 20 25 30

gag gag gtg aag gct cgc ctc cag ccc tac atg gca gag gcg cac gag Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala Glu Ala His Glu 135 140 145 150	486
ctg gtg ggc tgg aat ttg gag ggc ttg cgg cag caa ctg aag ccc tac Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln Leu Lys Pro Tyr 155 160 165	534
acg atg gat ctg atg gag cag gtg gcc ctg cgc gtg cag gag ctg cag Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val Gln Glu Leu Gln 170 175 180	582
gag cag ttg cgc gtg gtg ggg gaa gac acc aag gcc cag ttg ctg ggg Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala Gln Leu Leu Gly 185 190 195	630
ggc gtg gac gag gct tgg gct ttg ctg cag gga ctg cag agc cgc gtg Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu Gln Ser Arg Val 200 205 210	678
gtg cac cac acc ggc cgc ttc aaa gag ctc ttc cac cca tac gcc gag Val His His Thr Gly Arg Phe Lys Glu Leu Phe His Pro Tyr Ala Glu 215 220 225 230	726
agc ctg gtg agc ggc atc ggg cgc cac gtg cag gag ctg cac cgc agt Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu Leu His Arg Ser 235 240 245	774
gtg gct ccg cac gcc ccc gcc agc ccc gcg cgc ctc agt cgc tgc gtg Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu Ser Arg Cys Val 250 255 260	822
cag gtg ctc tcc cgg aag ctc acg ctc aag gcc aag gcc ctg cac gca Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys Ala Leu His Ala 265 270 275	870
cgc atc cag cag aac ctg gac cag ctg cgc gaa gag ctc agc aga gcc Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu Leu Ser Arg Ala 280 285 290	918
ttt gca ggc act ggg act gag gaa ggg gcc ggc ccg gac ccc cag atg Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro Asp Pro Gln Met 295 300 305 310	966
ctc tcc gag gag gtg cgc cag cga ctt cag gct ttc cgc cag gac acc Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr 315 320 325	1014
tac ctg cag ata gct gcc ttc act cgc gcc atc gac cag gag act gag Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp Gln Glu Thr Glu 330 335 340	1062
gag gtc cag cag cag ctg gcg cca cct cca cca ggc cac agt gcc ttc Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly His Ser Ala Phe 345 350 355	1110
gcc cca gag ttt caa caa aca gac agt ggc aag gtt ctg agc aag ctg Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu 360 365 370	1158
cag gcc cgt ctg gat gac ctg tgg gaa gac atc act cac agc ctt cat Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His 375 380 385 390	1206



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agttggccag ttctttgata ctgagctgta acaatcacca tccttgcttg aagaagtcct 553
tgctttctttg aatctctcat ttggcttgac atcaaagctg aaaaagggtta ctgatgacgg 613
tatggacctt ttcaatatgc aaattatgta atggtacaaa cgactttata tcagtataat 673
aaagtgcctta acgattcatt tttattgctg cctgtccata ccggaagctg taaaatagaa 733
taatttaatt tatgggaacg actcacatct tggaaaatga agggggaaaa acctgaattc 793
cctagtggcc acctctgcca ttagcctggg cacttctctgg gggacagagg tggaaccccg 853
gcgggaaagg cttccccggc ttctacaccg gcccgctgc aggttaacc 902

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<210> 189
<211> 1877
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (37)..(1236)

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<400> 189
gtaggcactg tgcaaaacat actagtggat atagag  atg aat aag aaa aag ccc 54
                                         Met Asn Lys Lys Lys Pro
                                         1 5

ctg cac tca aag agc tct cgg att cat caa caa att att gtg cag tta 102
Leu His Ser Lys Ser Ser Arg Ile His Gln Gln Ile Ile Val Gln Leu
          10          15          20

gat agc ctc cct cca cct gtc ttc tca gag cag gta atg gca agc atg 150
Asp Ser Leu Pro Pro Pro Val Phe Ser Glu Gln Val Met Ala Ser Met
          25          30          35

gct gcc gtg ctc acc tgg gct ctg gct ctt ctt tca gcg ttt tcg gcc 198
Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser Ala Phe Ser Ala
          40          45          50

acc cag gca cgg aaa ggc ttc tgg gac tac ttc agc cag acc agc ggg 246
Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser Gln Thr Ser Gly
          55          60          65          70

gac aaa ggc agg gtg gag cag atc cat cag cag aag atg gct cgc gag 294
Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys Met Ala Arg Glu
          75          80          85

ccc gcg acc ctg aaa gac agc ctt gag caa gac ctc aac aat atg aac 342
Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu Asn Asn Met Asn
          90          95          100

aag ttc ctg gaa aag ctg agg cct ctg agt ggg agc gag gct cct cgg 390
Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser Glu Ala Pro Arg
          105          110          115

ctc cca cag gac ccg gtg ggc atg cgg cgg cag ctg cag gag gag ttg 438
Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu Gln Glu Glu Leu
          120          125          130

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<210> 188
<211> 902
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (257)..(430)
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267

590	595	600	
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gtc tca gca gat gga gat gag gtt gtc cct agt cag agt acc agt aga Val Ser Ala Asp Gly Asp Glu Val Val Pro Ser Gln Ser Thr Ser Arg 625 630 635			2043
gaa cct gag aga aat cat act cac aga agt ttg ttt tcc gtg gag tct Glu Pro Glu Arg Asn His Thr His Arg Ser Leu Phe Ser Val Glu Ser 640 645 650			2091
gat gat aca gac aca gaa aat gag aga aga gat atg gca gga gca tct Asp Asp Thr Asp Thr Glu Asn Glu Arg Arg Asp Met Ala Gly Ala Ser 655 660 665			2139
ggg ggt ggt gca gct cct ttg cct caa aaa gtc cct ccc aca acg gca Gly Gly Val Ala Ala Pro Leu Pro Gln Lys Val Pro Pro Thr Thr Ala 670 675 680			2187
gta gaa gcg aca gta gga gca tgt gca agt tcc tca act cag agt acc Val Glu Ala Thr Val Gly Ala Cys Ala Ser Ser Ser Thr Gln Ser Thr 685 690 695 700			2235
cga ggt ggt cat gca gat aat gga agg gat gtg aca agt gtg gaa ccc Arg Gly Gly His Ala Asp Asn Gly Arg Asp Val Thr Ser Val Glu Pro 705 710 715			2283
cca agt gtg agt cca gca cgt cac cag ctt aca agt gca ctc agt cgt Pro Ser Val Ser Pro Ala Arg His Gln Leu Thr Ser Ala Leu Ser Arg 720 725 730			2331
atg act cag ggg cta cgc tgg gta cgt ttt aca tta gga cga tca agt Met Thr Gln Gly Leu Arg Trp Val Arg Phe Thr Leu Gly Arg Ser Ser 735 740 745			2379
tcc cta agt cag aac cag agt cct ttg aga caa ctt gat aat ggg gta Ser Leu Ser Gln Asn Gln Ser Pro Leu Arg Gln Leu Asp Asn Gly Val 750 755 760			2427
agt gga aga gaa gat gat gat gat gtt gaa atg cta att cca att tct Ser Gly Arg Glu Asp Asp Asp Asp Val Glu Met Leu Ile Pro Ile Ser 765 770 775 780			2475
gat gga tct tca gac ttt gat gtg aat gac tgc tcc aga cct ctt ctt Asp Gly Ser Ser Asp Phe Asp Val Asn Asp Cys Ser Arg Pro Leu Leu 785 790 795			2523
gat ctt gcc tca gat caa gga caa ggg ctt aga caa cca tat aat gca Asp Leu Ala Ser Asp Gln Gly Gln Gly Leu Arg Gln Pro Tyr Asn Ala 800 805 810			2571
aca aat cct gga gta agg cca agt aat cga gat ggc ccc tgt gag cgc Thr Asn Pro Gly Val Arg Pro Ser Asn Arg Asp Gly Pro Cys Glu Arg 815 820 825			2619
tgt ggt att gtc cac act gcc cag ata cca gac act tgc tta gaa gta Cys Gly Ile Val His Thr Ala Gln Ile Pro Asp Thr Cys Leu Glu Val 830 835 840			2667
aca ctg aaa aac gaa acg agt gat gat gag gct ttg tta ctt tgt tag Thr Leu Lys Asn Glu Thr Ser Asp Asp Glu Ala Leu Leu Leu Cys *			2715

335	340	345	
cag ata agg gta cat ttt tgt gct gat aaa gtg aat gct gca agg gga Gln Ile Arg Val His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly 350 355 360			1227
ttt aat gct act tac caa gta gat ggg ttc tgt ttg cca tgg gaa ata Phe Asn Ala Thr Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile 365 370 375 380			1275
ccc tgt gga ggt aac tgg ggg tgt tat act gag cag cag cgt tgt gat Pro Cys Gly Gly Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Cys Asp 385 390 395			1323
ggg tat tgg cat tgc cca aat gga agg gat gaa acc aat tgt acc atg Gly Tyr Trp His Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met 400 405 410			1371
tgc cag aag gaa gaa ttt cca tgt tcc cga aat ggt gtc tgt tat cct Cys Gln Lys Glu Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro 415 420 425			1419
cgt tct gat cgc tgc aac tac cag aat cat tgc cca aat ggc tca gat Arg Ser Asp Arg Cys Asn Tyr Gln Asn His Cys Pro Asn Gly Ser Asp 430 435 440			1467
gaa aaa aac tgc ttt ttt tgc caa cca gga aat ttc cat tgt aaa aac Glu Lys Asn Cys Phe Phe Cys Gln Pro Gly Asn Phe His Cys Lys Asn 445 450 455 460			1515
aat cgt tgt gtg ttt gaa agt tgg gtg tgt gat tct caa gat gac tgt Asn Arg Cys Val Phe Glu Ser Trp Val Cys Asp Ser Gln Asp Asp Cys 465 470 475			1563
ggt gat ggc agc gat gaa gaa aat tgc cca gta atc gtg cct aca aga Gly Asp Gly Ser Asp Glu Glu Asn Cys Pro Val Ile Val Pro Thr Arg 480 485 490			1611
gtc atc act gct gcc gtc ata ggg agc ctc atc tgt ggc ctg tta ctc Val Ile Thr Ala Ala Val Ile Gly Ser Leu Ile Cys Gly Leu Leu Leu 495 500 505			1659
gtc ata gca ttg gga tgt act tgt aag ctt tat tct ctg aga atg ttt Val Ile Ala Leu Gly Cys Thr Cys Lys Leu Tyr Ser Leu Arg Met Phe 510 515 520			1707
gaa aga aga tca ttt gaa aca cag ttg tca aga gtg gaa gca gaa ttg Glu Arg Arg Ser Phe Glu Thr Gln Leu Ser Arg Val Glu Ala Glu Leu 525 530 535 540			1755
tta aga aga gaa gct cct ccc tcg tat gga caa ttg att gct cag ggt Leu Arg Arg Glu Ala Pro Pro Ser Tyr Gly Gln Leu Ile Ala Gln Gly 545 550 555			1803
tta att cca cca gtt gaa gat ttt cct gtt tgt tca cct aat cag gct Leu Ile Pro Pro Val Glu Asp Phe Pro Val Cys Ser Pro Asn Gln Ala 560 565 570			1851
tct gtt ttg gaa aat ctg agg cta gcg gta cga tct cag ctt gga ttt Ser Val Leu Glu Asn Leu Arg Leu Ala Val Arg Ser Gln Leu Gly Phe 575 580 585			1899
act tca gtc agg ctt cct atg gca ggc aga tca agc aac att tgg aac Thr Ser Val Arg Leu Pro Met Ala Gly Arg Ser Ser Asn Ile Trp Asn			1947

80	85	90	
cag gat ttt gat att caa gga tcc aga agg tgc aat ttg gac tgg ttg Gln Asp Phe Asp Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu 95 100 105			459
aca ata gaa aca tac aag aat att gaa agt tac aga gct tgt ggt tcc Thr Ile Glu Thr Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser 110 115 120			507
aca att cca cct ccg tat atc tct tca caa gac cac atc tgg att agg Thr Ile Pro Pro Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg 125 130 135 140			555
ttt cat tcg gat gac aac atc tct aga aag ggt ttc aga ctg gca tat Phe His Ser Asp Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr 145 150 155			603
ttt tca ggg aaa tct gag gaa cca aat tgt gct tgt gat cag ttt cgt Phe Ser Gly Lys Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg 160 165 170			651
tgt ggt aat gga aag tgt ata cca gaa gcc tgg aaa tgc aat aac atg Cys Gly Asn Gly Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met 175 180 185			699
gat gaa tgt gga gat agt tcc gat gaa gag atc tgt gcc aaa gaa gca Asp Glu Cys Gly Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala 190 195 200			747
aat cct cca act gct gct gct ttt caa ccc tgt gct tac aac cag ttc Asn Pro Pro Thr Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe 205 210 215 220			795
cag tgt tta tcc cgt ttt acc aaa gtt tac act tgc ctc ccc gaa tct Gln Cys Leu Ser Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser 225 230 235			843
tta aaa tgt gat ggg aac att gac tgc ctt gac cta gga gat gag ata Leu Lys Cys Asp Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile 240 245 250			891
gac tgt gat gtg cca aca tgt ggg caa tgg cta aaa tat ttt tat ggt Asp Cys Asp Val Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly 255 260 265			939
act ttt aat tct ccc aat tat cca gac ttt tat cct cct gga agc aat Thr Phe Asn Ser Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn 270 275 280			987
tgc acc tgg tta ata gac act ggt gat cac cgt aaa gtc att tta cgc Cys Thr Trp Leu Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg 285 290 295 300			1035
ttc act gac ttt aaa ctt gat ggt act ggt tat ggt gat tat gtc aaa Phe Thr Asp Phe Lys Leu Asp Gly Thr Gly Tyr Gly Asp Tyr Val Lys 305 310 315			1083
ata tat gat gga tta gag gag aat cca cac aag ctt ttg cgt gtg ttg Ile Tyr Asp Gly Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu 320 325 330			1131
aca gct ttt gat tct cat gca cct ctt aca gtt gtt tct tct tct gga Thr Ala Phe Asp Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly 1179			

	100	105	110	
gca ttg aaa gaa tgt cta act gct taa tacct gaaggaaaat atctctgaga				629
Ala Leu Lys Glu Cys Leu Thr Ala *				
	115	120		
cttcctccag ccttgtgatt tggttgatta atataattta actcctagaa agttgagata				689
aatcgatatgg atgataaaaa gctataatga tccagccttt tatgaagaat gcaaaatgga				749
atacctgaag gaaaggggaag aattcagaaa aactggaatt cctacaaaga aaaggctaca				809
gaagcttcca acaagcatgt aggcagatac tcaaatagaca ttcaggaact ctaatatcca				869
tggaagtcatt tttatagtcc ttaaataatg gactcaagca tatatgtttg ctttacctta				929
attatggaaa tattaacttt atctgaaata aatattttat ttgtaaacgc ggccgcgaat				989
tcggatcctc gagagatctc tttttttggg ttgtgtgggg tatcttcacg gtcg				1043

<210> 187  
 <211> 3405  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (136)..(2715)

<220>  
 <221> misc\_feature  
 <222> (1)...(3405)  
 <223> n = a,t,c or g

caggccccgg tccggaattc ccgggtcgac gatttcgtgc ggccggcggcg gcggcgtcgg				60
cgtcggcgtc gtctacctcc agcttctcct cctcctcctc ccgtctcctc ctctctctct				120
ccatctgctg tgggtt atg gcc tgt cgc tgg agc aca aaa gag tct ccg cgg				171
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg				
1 5 10				
tgg agg tct gcg ttg ctc ttg ctt ttc ctc gct ggg gtg tac gga aat				219
Trp Arg Ser Ala Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn				
15 20 25				
ggt gct ctt gca gaa cat tct gaa aat gtg cat att tca gga gtg tca				267
Gly Ala Leu Ala Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser				
30 35 40				
act gct tgt gga gag act cca gag caa ata cga gca cca agt ggc ata				315
Thr Ala Cys Gly Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile				
45 50 55 60				
atc aca agc cca ggc tgg cct tct gaa tat cct gca aaa atc aac tgt				363
Ile Thr Ser Pro Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys				
65 70 75				
agc tgg ttc ata agg gca aac cca ggc gaa atc att act ata agt ttt				411
Ser Trp Phe Ile Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe				

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aggtgtcaga ctgcaggaaa ggagctcact ctgctggggt ggatatctga ggcagagatc 481
tgctgggtata ggggaccaac tggctaagta agtttcccca agactcacgg aatttccaca 541
acaggtgatt taggatctga aaacctgaca attatgggta cacatgaggg gggcagcctg 601
cacaatgttc tccaggtgag gagactgggt gttgagttgc cttttgaaag ggggtggtag 661
ccccctgggt tttctttcca cacaccgga ctgggagctc cctggggggg agcaggggaa 721
tcccccttct gggcccccgg c 742

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<210> 186
<211> 1043
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (245)..(604)

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<220>
<221> misc_feature
<222> (1)...(1043)
<223> n = a,t,c or g

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<400> 186
cgctgccna ggatagcctg cggtagcgggt ccggaattcc cgggtcgacc cacgcgtccg 60
gtagccttca ggaatgttct ctcttttctg tggggttacc tttgggttat cttctctatt 120
aagtgtggat ccctgaaaaa tggcataccc tgggtggtttt tctagcccct gctgaaatcc 180
tttgaaggaa tgtacttatt tgtcaagatt cgtctaaaaa tgtggtctcc agaaatgaac 240
atag atg tgc tgt gag ctg ctt gca gtt gtg att gcg aca ctg ata att 289
Met Cys Cys Glu Leu Leu Ala Val Val Ile Ala Thr Leu Ile Ile
1 5 10 15
aag att ggt tta gtt gtt ctg ttg tac ttc atc aaa ttg ttg att cac 337
Lys Ile Gly Leu Val Val Leu Leu Tyr Phe Ile Lys Leu Leu Ile His
20 25 30
att gaa ttt atc aaa cgt cat tct att cta aaa tgt gaa agt att ttt 385
Ile Glu Phe Ile Lys Arg His Ser Ile Leu Lys Cys Glu Ser Ile Phe
35 40 45
aac tta aat gta gga att cgc atg tat cca gga caa gta aat ttt tgt 433
Asn Leu Asn Val Gly Ile Arg Met Tyr Pro Gly Gln Val Asn Phe Cys
50 55 60
gaa aca ttg cag atg tta gat gga ttt ggg aga att ttc caa act aag 481
Glu Thr Leu Gln Met Leu Asp Gly Phe Gly Arg Ile Phe Gln Thr Lys
65 70 75
tgg acg aac tta tat agc tac ata aat agt aat ttt acc aaa tgt tgc 529
Trp Thr Asn Leu Tyr Ser Tyr Ile Asn Ser Asn Phe Thr Lys Cys Cys
80 85 90 95
aag aac tct gga gtt ctt atg gta gta aaa tgc cgg aaa gaa aat tct 577
Lys Asn Ser Gly Val Leu Met Val Val Lys Cys Arg Lys Glu Asn Ser

```

Phe Asn Cys Val Ser Pro Gly Ile Leu Pro Ile Ser Leu Cys Leu Ala  
 30 35 40 45

ttc aat cat gat aga agc acc ttt ttc ttt tca ata ata tta ttg tta 253  
 Phe Asn His Asp Arg Ser Thr Phe Phe Phe Ser Ile Ile Leu Leu Leu  
 50 55 60

aaa gcc tta att att ttg tct tct ctg ctt caa act aag taa ttctgac 302  
 Lys Ala Leu Ile Ile Leu Ser Ser Leu Leu Gln Thr Lys \*  
 65 70 75

ttccttaatc ttttatcaca ggctctgttc tccaaacttt cagtcttttc tgttggtcca 362

tattccattg gtttctcctc ctactcattc agaggcaaata taagggtggt ttttaagttt 422

tggtttgtag actatgtcgt tatgtgagaa atttacttta gggttgatt gtcaacccca 482

tagcacaagc caggctactta atttaggcatt tagtcagtga tatagattga atatttgtcc 542

ctgcgcaaata ctcatgttga attgcaatcc ccagtgttgg ggggtggcgt tgggtggaagg 602

cgaaggatc aaggcgaccg gcggccccca cccctcgggg gcttttctta acgggtgttg 662

aaattttgtg cccccccccc caaaaaaaag ggtgggggaa acgtttcccc ccttt 717

<210> 185  
 <211> 742  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (128)..(361)

<400> 185

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tcaaagggaac acccagccta cctctctggt ctacgtttt cccagtcattg aggagctcac 120

ttctccc atg aag ccc atc ctg ctg gtc ctc agc tct atc acc cgt gcc 169  
 Met Lys Pro Ile Leu Leu Val Leu Ser Ser Ile Thr Arg Ala  
 1 5 10

ctc ctt ctg cag ata tca agt gtg tct tgg cag tcc tgc atg tgg agg 217  
 Leu Leu Leu Gln Ile Ser Ser Val Ser Trp Gln Ser Cys Met Trp Arg  
 15 20 25 30

gca atg cct gat tgt ctc cag act gat tac ccc ata agc ctt ggc ttt 265  
 Ala Met Pro Asp Cys Leu Gln Thr Asp Tyr Pro Ile Ser Leu Gly Phe  
 35 40 45

cat caa aga aca agg ctt cta gat gct ctc tgc cca gtc act caa tgc 313  
 His Gln Arg Thr Arg Leu Leu Asp Ala Leu Cys Pro Val Thr Gln Cys  
 50 55 60

cat cac tct gcc tgg ccc tgt gtt tgc cag gga gca cag aca ccc atc 361  
 His His Ser Ala Trp Pro Cys Val Cys Gln Gly Ala Gln Thr Pro Ile  
 65 70 75

tgaggaatcc atgccatgag gagtttatgg tctgtgaaga atacaggcag gaatttgaga 421